

ID XX AAY28444 standard; protein; 1203 AA.
XX AC AAY28444;
XX DT 03-DEC-1999 (first entry)
XX DE Human ptc-2 protein.
XX KW Patched-2; ptc-2; human; hedgehog receptor; nototropic; neuroprotective;
KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
KW graft; transplant; treatment; nervous system injury; chemical injury;
KW vascular injury; infection; inflammatory; tumor-induced injury; ageing;
KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
KW lesion-induced death; neuron regeneration; damage repair; skeletal;
KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
XX OS Homo sapiens.
XX FN WO9929854-A1.
XX PD 17-JUN-1999.
XX PF 08-DEC-1998; 98WO-US026009.
XX PR 08-DEC-1997; 97US-0067940P.
XX PA (ONTO-) ONTOGENY INC.
XX PI Bumcrot DA;
XX DR WPI; 1999-561298/47...
XX DR N-PSDB; AAX89478.
XX PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
XX prevention and/or reduction of the severity of neurological conditions.
XX PS Claim 3; Page 73-77; 80pp; English.
XX CC This invention describes a novel recombinantly produced human patched-2
XX (ptc-2) polypeptide which has notropic, neuroprotective, cardiant,
XX antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
XX protein is a hedgehog receptor and is therefore capable of modulating
XX hedgehog signalling, and so affect a number of hedgehog-mediated
XX biological activities. The human patched-2 (ptc-2) protein can be used to
XX screen for modulators, antagonists and agonists, which are likely to play
XX an important role in the modulation of cellular proliferation and
XX maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
XX tissues during disease states. Modulators of ptc-2 protein can be used
XX for in vivo reformation of tissue; to improve grafting and morphology of
XX transplanted tissue; for the treatment, prevention and/or reduction of
XX the severity of neurological conditions deriving from: injury to the
XX nervous system including traumatic injury, chemical injury, vascular injury
XX and deficits (such as ischemia resulting from stroke), together with
XX infectious/inflammatory and tumor-induced injury; ageing of the nervous
XX system including Alzheimer's disease; chronic neurodegenerative diseases
XX of the nervous system including Parkinson's disease, Huntington's chorea,
XX and chronic immunological sclerosis, as well as spinocerebellar degenerations;
XX amyotrophic lateral sclerosis, as well as multiple sclerosis.
XX Multiple sclerosis, ptc-2 therapeutics can also be used in the treatment
XX of autonomic disorders of the peripheral nervous system, including
XX disorders affecting the innervation of smooth muscle and endocrine
XX tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
XX Antagonists of ptc-2 protein can be used to prevent differentiation of
XX cells in culture, as well as for treatment of chronic pain syndromes.
XX Agonists may be used to rescue neurons from lesion-induced death as well
XX as neuron regeneration, in diseases such CNS trauma infarction, (viral)

CC infection, metabolic disease, nutritional deficiency, toxic agents, and
CC so on. ptc-2 therapeutics may also be used for the repair of central and
CC peripheral nerve damage, for repair and regeneration of non-neuronal
CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
CC for generation of prosthetic cartilage devices, and to induce
CC spermatogenesis and as fertility enhancers. This sequence represents the
CC human ptc-2 protein described in the invention
XX
XX SQ Sequence 1203 AA;
Query Match 99.6%; Score 6248; DB 2; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTRSPRLRLPSYPPARTAPQIILAGSKAPLMRAYFOGLFSLGGCIQRHCGKVLV 60
DB 1 MTRSPRLRLPSYPPARTAPQIILAGSKAPLMRAYFOGLFSLGGCIQRHCGKVLV 60
QY 61 LGLLAFGALALGLRMAIETNLEQLWVEGVSQELHYTKELGHEAAYSQMLIQTAR 120
DB 61 LGLLAFGALALGLRMAIETNLEQLWVEGVSQELHYTKELGHEAAYSQMLIQTAR 120
QY 121 QEGENILTPBALGLHLQAALTASKVQVSLYKGSNDLNKI CYKSGVPLIENGMIENIEKL 180
DB 121 QEGENILTPBALGLHLQAALTASKVQVSLYKGSNDLNKI CYKSGVPLIENGMIENIEKL 180
QY 181 FPCVILTPDLCFWGAKLQGSAYLPGRPDIQWNLDPEQLLELPGFASLEGGFRELDDK 240
DB 181 FPCVILTPDLCFWGAKLQGSAYLPGRPDIQWNLDPEQLLELPGFASLEGGFRELDDK 240
QY 241 AQVQAVYVGRPCLLHPDHLCPSPAPNHHSRAQVNAHLSGCGHGFSGHKNHWEELLG 300
DB 241 AQVQAVYVGRPCLLHPDHLCPSPAPNHHSRAQVNAHLSGCGHGFSGHKNHWEELLG 300
QY 301 GMARDPOGELIRAEALOSTFLLMSPROIYEHFRGDYQTHDIGWSEEOASTVLQAWRRFV 360
DB 301 GMARDPOGELIRAEALOSTFLLMSPROIYEHFRGDYQTHDIGWSEEOASTVLQAWRRFV 360
QY 361 QLAQALPENASQOIHAFFSTTLDLILHAFSEVSAARVVGYYLMLAYACVTMLRWDCAQ 420
DB 361 QLAQALPENASQOIHAFFSTTLDLILHAFSEVSAARVVGYYLMLAYACVTMLRWDCAQ 420
QY 421 SQSVGLAGVLLVALAVASGLICALLGITFNATTVLPALGICVDVDFLLAHAFTE 480
DB 421 SQSVGLAGVLLVALAVASGLICALLGITFNATTVLPALGICVDVDFLLAHAFTE 480
QY 481 ALPGTPIQRMGECLORTGTSVVLTSINNMAAFMAALVPALPAFSAQAIVVGCTFV 540
DB 481 ALPGTPIQRMGECLORTGTSVVLTSINNMAAFMAALVPALPAFSAQAIVVGCTFV 540
QY 541 AVMLVFPAILSLDRLRRHQRDLVLCSSPSCSAQVIQILPOELGDTVPVGIHLTAIV 600
DB 541 AVMLVFPAILSLDRLRRHQRDLVLCSSPSCSAQVIQILPOELGDTVPVGIHLTAIV 600
QY 601 QAFTHCEASSQHVVTLPQAHVLPDPSPGLSELPSPGSGSTRDLGQBEETRQAAKCS 660
DB 601 QAFTHCEASSQHVVTLPQAHVLPDPSPGLSELPSPGSGSTRDLGQBEETRQAAKCS 660
QY 661 LPCAPWLAHFARYOAPFLLQSHAKAIVLVFGALLGLSYGATLVODGLALTVDVPRG 720
DB 661 LPCAPWLAHFARYOAPFLLQSHAKAIVLVFGALLGLSYGATLVODGLALTVDVPRG 720
QY 721 TKEHAFSLAQRYSLSYVALVTGGFDYAHQORALFDLHORFSSKAVLPPPTQAPT 780
DB 721 TKEHAFSLAQRYSLSYVALVTGGFDYAHQORALFDLHORFSSKAVLPPPTQAPT 780
QY 781 WLHYRNWLOGIAAFQDQWASGRITRHSYNGSEGDGALAYKLLIQTGDAQEPDLSOLT 840
DB 781 WLHYRNWLOGIAAFQDQWASGRITRHSYNGSEGDGALAYKLLIQTGDAQEPDLSOLT 840
QY 841 TRKLVDEGLIPPELVYGLTVWVSSDFGLAASQANFYPPPEWLHKYDVTTCENLRIP 900
DB 841 TRKLVDEGLIPPELVYGLTVWVSSDFGLAASQANFYPPPEWLHKYDVTTCENLRIP 900

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Db 841 TRKLVREGILPELFFMGLTVWVSSDPLGLAASQANFYPPPPWHLHDKYDTTGENLRIP 900
 QY 901 PAQPLEFAQPFLLRGHLOKTDADFVEAIEGARAACAEAGAGVHAYPGSGPFLFWEQYVGL 960
 Db 901 PAQPLEFAQPFLLRGHLOKTDADFVEAIEGARAACAEAGAGVHAYPGSGPFLFWEQYVGL 960
 QY 961 RRCFLAVCTLLVCTELVCAALLLNPNWTAGLIVLVLAAMTVFELGIMGFIKLSAIPVV 1020
 Db 961 RRCFLAVCTLLVCTELVCAALLLNPNWTAGLIVLVLAAMTVFELGIMGFIKLSAIPVV 1020
 QY 1021 ILVASGIGVEFVHVALGELTTQGRNLRARAAHLEHTPAVTDGALSTILGLMLAGSH 1080
 Db 1021 ILVASGIGVEFVHVALGELTTQGRNLRARAAHLEHTPAVTDGALSTILGLMLAGSH 1080
 QY 1081 FDFIVRYFFAALTTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
 Db 1081 FDFIVRYFFAALTTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
 QY 1141 LRWGASSLPQSFARVTTSTMTVAIHPPPLPGAVIHPADBPWPSPATSSGNLSRGPQP 1200
 Db 1141 LRWGASSLPQSFARVTTSTMTVAIHPPPLPGAVIHPADBPWPSPATSSGNLSRGPQP 1200
 QY 1201 ATG 1203
 Db 1201 ATG 1203

RESULT 5

AAY92703
 ID AAY92703 standard; protein; 1203 AA.
 AC AAY92703;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human patched 2 (PTCH2) protein splice variant.
 KW Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMM1;
 KW familial adenomatous polyposis; hMcml; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
 XX
 OS Homo sapiens.
 PN WO20020037-AL.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-SE001784.
 XX
 PR 06-OCT-1998; 98SE-00003393.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
 XX Hollingsworth RE;
 XX
 DR WPI; 2000-303645/26.
 DR N-PSDB; AAA09084.
 XX
 XX Isolated human protein capable of participating in human patched
 PT gene/sonic hedgehog pathway during embryonic development is used in
 PT medicament for treatment of condition involving tumors such as basal cell
 PT carcinoma.
 XX
 PS Disclosure; Page; 55pp; English.
 XX
 CC This protein is a splice variant encoded by the novel human patched 2
 CC gene (PTCH2), which has been localised by radiation hybrid mapping to
 CC chromosome 1p32-35 with D1S211 and W1404 as closest flanking markers and
 CC with an estimated localisation 5.5 cR from D1S443. This region is often
 CC lost by LOH in various different tumour types, such as neuroblastoma,

CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour
 CC suppressor gene in this region. It is also a candidate gene for
 CC involvement in familial melanoma CMM1, modifier locus for familial
 CC adenomatous polyposis hMcml and Michelin Tire Baby Syndrome. PTCH2 is
 CC capable of participating in the human patched gene/sonic hedgehog
 CC (PTCH/SHH) pathway during embryonic development and/or carcinogenesis.
 CC The isolated human protein is useful as a medicament for the treatment of
 CC a condition involving tumours such as BCC (basal cell carcinoma). The
 CC nucleic acid is useful in gene therapy, and for use as a probe, primer or
 CC a diagnostic agent. Note: This sequence was constructed using information
 CC from Figure 2B and the protein sequence given on pages 41-44 of the
 CC specification
 XX

SQ Sequence 1203 AA;

Query Match 99.5%; Score 6238; DB 3; Length 1203;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1199; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRSPRLRLPSYTPPARTAAPQILAGSLKAPLMRAYFOGLLPSLGGCIQRHCGKVLF 60
 Db 1 MTRSPRLRLPSYTPPARTAAPQILAGSLKAPLMRAYFOGLLPSLGGCIQRHCGKVLF 60
 QY 61 LGLAFGALALCLRMALITETNLEQLWVEVGRSVSOELHYTKEKLEGEAAYSOMLIQTAR 120
 Db 61 LGLAFGALALCLRMALITETNLEQLWVEVGRSVSOELHYTKEKLEGEAAYSOMLIQTAR 120
 QY 121 QEGENILTPREALGLHQAALTASKVQVSLYKSWDLNLCYKSGVPLIENGMIEMIEKL 180
 Db 121 QEGENILTPREALGLHQAALTASKVQVSLYKSWDLNLCYKSGVPLIENGMIEMIEKL 180
 QY 181 PFCVILTDLDCFWEGAKLOGGSAYLPGRPDIQTWNLDPEOLLEELGPPASLEGPRELDK 240
 Db 181 PFCVILTDLDCFWEGAKLOGGSAYLPGRPDIQTWNLDPEOLLEELGPPASLEGPRELDK 240
 QY 241 AQVGQAVYGRPCLHPDDLHCPPSNHHSROAPNVAHELSCGCHGFSKFNHWEELLG 300
 Db 241 AQVGQAVYGRPCLHPDDLHCPPSNHHSROAPNVAHELSCGCHGFSKFNHWEELLG 300
 QY 301 GMARDPOGELLRAEALQSTFLMSPRQLYEHFRGDYQTHDIGNWSEBOASTVLQAWORRFV 360
 Db 301 GMARDPOGELLRAEALQSTFLMSPRQLYEHFRGDYQTHDIGNWSEBOASTVLQAWORRFV 360
 QY 361 QLAQEALPENASQOIHFASSTTDLDDILHAFSEVSAARVWGGYLLMAYACVTLRWDCAQ 420
 Db 361 QLAQEALPENASQOIHFASSTTDLDDILHAFSEVSAARVWGGYLLMAYACVTLRWDCAQ 420
 QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITVOVLPFLALGIGVDDVFLAHAFTE 480
 Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITVOVLPFLALGIGVDDVFLAHAFTE 480
 QY 481 ALPGTQERMGECLQRTGTSVLTSINNMAALFMAALVPIPALRAFSLQAAIVVGCTFV 540
 Db 481 ALPGTQERMGECLQRTGTSVLTSINNMAALFMAALVPIPALRAFSLQAAIVVGCTFV 540
 QY 541 AVMLVPEAILSLDLRRHRCORLNVLCFSPSCSAQVIQILPQELGDTVPVGAHATATV 600
 Db 541 AVMLVPEAILSLDLRRHRCORLNVLCFSPSCSAQVIQILPQELGDTVPVGAHATATV 600
 QY 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELPSPGSGTDLICOBETQKAAKS 660
 Db 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELPSPGSGTDLICOBETQKAAKS 660
 QY 661 LPCARNLHAHFARYQFAPLLQSHAKAIVLVLFGALLGLSLYCATLVQDGLATDVVRG 720
 Db 661 LPCARNLHAHFARYQFAPLLQSHAKAIVLVLFGALLGLSLYCATLVQDGLATDVVRG 720
 QY 721 TKEHAFSLQRLYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSSLKAVLPPPATQAPT 780
 Db 721 TKEHAFSLQRLYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSSLKAVLPPPATQAPT 780
 QY 781 WLHYENWLGQICAFDQDQWASGRITRHSYRNGSEGALAYKLLIQTGAQBPPLFSQUT 840

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:01 ; Search time 5460 Seconds

(without alignments)

8028.754 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

-Q=/cgn2_1/USPTO_spool/US0990046/runat_21112004_130919_18544/app_query.fasta_1.1351

-DB=EST -QMT=FASTAP -SUFFIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US0990046@cgn_1_1_3361@runat_21112004_130919_18544 -NCPU=6 -ICPU=3

-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2724	43.4	3868	9 AY415485	AY415485 Homo sapi
2	2708	43.2	3871	9 AY415487	AY415487 Mus muscu
3	2362	37.7	3950	9 AY415486	AY415486 Pan trogl
4	1097.5	17.5	711	7 CF733501	CF733501 UI-M-HB0
5	1071	17.1	708	7 CK830937	CK830937 4054508 B
6	1043	16.6	662	7 CF531700	CF531700 UI-M-FY0
7	1032	16.5	603	7 CN671167	CN671167 A0902E10-
8	1005	16.0	571	4 BM105989	BM105989 509593 MA
9	998	15.9	600	6 CA528868	CA528868 8091-13 M

10	988	15.8	625	7	CN676164
11	970	15.5	911	5	BX844270
12	959	15.3	974	5	BQ964086
13	905	14.4	639	2	BB612664
14	891	14.2	573	2	BE234509
15	884	14.1	778	7	CK639185
16	883	14.1	506	4	BG384338
17	881	14.0	796	7	CN537294
18	865	13.8	788	6	CB723145
19	863.5	13.6	832	7	CN536865
20	853.5	13.6	814	7	CN532855
21	844	13.5	633	4	BJ038661
22	839.5	13.4	590	7	CK388757
23	837.5	13.4	746	7	CF741492
24	834.5	13.3	736	1	AU125183
25	827	13.2	637	4	BJ029994
26	823	13.1	770	7	CK639136
27	818.5	13.1	761	7	CF744664
28	811.5	12.9	711	7	CN535086
29	810.5	12.9	789	6	CB723783
30	805.5	12.9	723	7	CK636036
31	805.5	12.8	812	7	CF745394
32	751.5	12.0	465	5	BQ557141
33	749	11.9	702	7	CF735093
34	734.5	11.7	637	6	BY727737
35	732.5	11.7	731	7	CK781271
36	730.5	11.6	659	6	CB722633
37	726.5	11.6	736	7	CN536823
38	712	11.4	589	4	BJ067833
39	711	11.3	477	6	CA530713
40	701.5	11.2	649	7	CN534794
41	701	11.2	751	7	CN535375
42	695	11.1	742	6	CB526181
43	691	11.0	626	7	CO432549
44	679.5	10.8	733	7	CR586364
45	678	10.8	727	6	CA749673

ALIGNMENTS

RESULT 1	AY415485	3868 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY415485	Homo sapiens PTCH gene, VIRTUAL TRANSCRIPT, partial sequence, Genomic survey sequence.			
DEFINITION	AY415485	GI:39771444			
ACCESSION	AY415485				
VERSION	AY415485.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3868)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 3868)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
	1..3868				

1680 GTCA^{||||}CCAG^{||||}-GACA^{||||}ACCT^{||||}CGAGT^{||||}GCAGAGT^{||||}CCCGAGAGCACCAGCT^{||||}CTACCGAGGACCT 1738

645 uLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaAr 665

1739 GCTCTCCAGAGT^{||||}CTCAGACTCC^{||||}-----AGCTCCACTGCCTCGAGCCCCCTGCACCAA 1792

665 gT^{||||}rAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAl 685

1793 GTGAGACTCT^{||||}CTTCGTTTGAGAGAGCACTATGCTCTTCCTCTCTCTGAAACCCAAAGC 1852

685 aLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaTh 705

1853 CAAGTGTGTGTAAT^{||||}CTCTTTCTGGGCTCTCTGGGGGTGAGCCCTTATGGAGCCAC 1912

705 rLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAl 725

1913 CCGAGTCAGAGACGGGTGGACCTTCACGGCACTGTTCCTCCCGGAAACACAGAAATATGA 1972

725 aPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGl 745

1973 CTTCATAGCTGCCAGGTTCAGTACTTCTCTTCTCAACATGTATATAGTACCCAGAA 2032

745 yGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSe 765

2033 AGCA---GACTACCCGAATATCCAGCACCTACTTTAGCACCTTCATAGAGTTTCAGCAA 2089

765 rLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTr 785

2090 TGTGAAGTATGTCTATGCTGGAGGAGAACAGCAACTTCCCAAAATGTGGCTGCACACTT 2149

785 rArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIl 805

2150 TAGAGCTGGCTTCAGGACTTTCAGGATGCATTTGACGTGACTGGGAACTGGGAGGAT 2209

805 eThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIl 825

2210 CATGCCAAACAATTATATAAATGGATCAGATGACGGGGTCTCGCTTACAAACTCTCGTGT 2269

825 eGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVa 845

2270 GCAGACTGGCAGCCGAGACAAGCCATCGACATTAGTCAGTTGACTTAACAGCGTCTGT 2329

845 lAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValse 865

2330 AGACGAGATGGCATCATTAATCCGACGCTTTCTATCTACTCTACCTGACCGCTGGGTGAG 2389

865 rSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTr 885

2390 CAACGACCTGTAGCTTACGCTCTCCAGGCCAACATCCGGCTCTACCGCCGGAGTG 2449

885 pLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPr 904

2450 GSTCCATGACAAAGCCGACTACATGCCAGAGACCAGGCTGAGAAATCCAGCAGCAGAGCC 2509

904 oLeuGlnPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheVa 924

2510 CATCGAGTAGCTCAGTCTCCCTTTCTACCTCAACGCCCTACGAGACAGCTCAGACTTGT 2569

924 lGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAl 944

2570 GGAAGCCATAGAAAAGTCAGAGTCATCTGTAACTATACGACGCTGGGAGCTGTCCAG 2629

944 aTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPh 964

2630 CTACCCCAATGGCTACCCCTTCTCTGTCTGGGAGCAATATACATCAGCCTGGCCACTGGCT 2689

964 eLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLe 984

2690 GTGTCTATCATCAGCGGTGGTCTGGCCTGCAAGTTTCTAGTGTGCGCAGCTTCTCTCTCT 2749

984 uAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPh 1004

Db	2750	GAA	CCCC	TGG	ACG	CGC	CGG	AT	CT	GT	CA	TG	CT	CG	CT	CT	GA	TG	AC	CG	CT	GA	CG	CT	CT	2809
QY	1004	eGly	Ile	Met	Gly	Phe	Leu	Gly	Ile	Leu	Ser	Ala	Ile	Pro	Val	Val	Ile	Leu	Val	Al						1024
Db	2810	TGG	CA	TG	AT	TGG	CG	CT	CA	T	TGG	AT	CA	AG	CT	GA	GT	GT	GT	GT	GT	GT	GT	GT	GT	2869
QY	1024	aSer	Val	Gly	Ile	Gly	Val	Gl	Phe	Thr	Val	His	Val	Ala	Leu	Gly	Phe	Leu	Thr	Thr	Gl					1044
Db	2870	AT	CT	GT	TGG	CA	TG	AG	TGG	AG	TTC	AC	CG	CT	CA	CG	TG	CG	CT	T	T	T	T	T	T	2929
QY	1044	nGly	Ser	Arg	Asn	Leu	Arg	Ala	Ala	His	Ala	Leu	Gl	His	Thr	Phe	Ala	Pro	Val	Thr	As					1064
Db	2930	TGG	GA	CA	AGA	CA	CA	CG	AG	CT	AT	GT	CT	GT	CT	TGG	AG	CA	AT	GT	T	T	T	T	T	2989
QY	1064	pGly	Ala	Ile	Ser	Thr	Leu	Leu	Gly	Leu	Met	Leu	Ala	Gly	Ser	His	Phe	Asp	Phe	Ile						1084
Db	2990	CG	T	CT	GT	GT	CC	ACT	CT	CT	TGG	T	GT	ACT	GT	GT	T	T	T	T	T	T	T	T	T	3049
QY	1084	eVal																								1085
Db	3050	TGT	CA	GN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	3109
QY	1086																									1102
Db	3110	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	NN	3169
QY	1102	sGly	Leu	Val	Leu	Leu	Pro	Val	Leu	Ser	Ile	Leu	Gly	Pro	Pro	Gl	u	Val	Ile							1121
Db	3170	TGG	CT	TA	AA	CC	GA	T	GC	CA	T															3223
QY	1121																									1121
Db	3224	GTT	TG	CG	T	GC	CT	CT	CG	T	CA	CA	GA	CA	AT	TG	GG	T	CT	CG	ACT	CG	AG	T	CA	3283
QY	1121																									1121
Db	3284	CT	CT	AGA	CA	CG	T	GT	T	GG	CA	T	AG	T	GAG	AG	CT	CAG	CA	AT	AC	GA	AG	CA	CA	3343
QY	1122																									1135
Db	3344	TGC	GG	AG	GG	CC	CT	GC	CA	CA	AG	T	GT	TGG	AG	CC	CA	GA	AA	AC	CT	GT	T	T	T	3403
QY	1135	la	Pro																							1136
Db	3404	GT	CA	CT	GA	CG	CA	AG	CC	AG	CA	CG	CT	CG	AA	GG	AT	CC	CC	CT	AG	AA	AG	GG	CT	3463
QY	1136																									1136
Db	3464	CCC	CC	CT	CA	CAG	AC	CG	CG	CAG	AG	CG	CT	T	T	G	AA	A	T	T	T	CT	AG	AG	GC	3523
QY	1137	--	Gln	Gly	Gly	Leu	Arg																			1146
Db	3524	AG	CA	T	AG	GA	CG</																			

RESULT 3	AY415486	3950 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY415486				
DEFINITION	Pan troglodytes PTCH gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY415486				
VERSION	AY415486.1	GI:39771445			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				


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Db 1560 CATGAAACGACGATTACCATGAGTCCAGCTCCAGCTCCGACGAGTACGACCCCCAC 1619
Qy 610 SerGlnHisValThrIleLeuProGlnAlaHisLeuValProPro----- 627
Db 1620 AGCAGCTGTACTACACCGCTGAGCGCGCTCCGAGATCTCTGTGCGAGCCGCTACC 1679
Qy 628 -----SerAspProLeuGlySerGlnLeuPheSerProGlyGlySerThrArgAspLeu 645
Db 1680 GTGACACAGGACACCTCAGCTGCCAGGCCAGAGACACGAGTCCACAGGAGACCTG 1739
Qy 646 LeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArg 665
Db 1740 CTCCTCCAGTCTCCGACTCCAGCCTCCAGCCTCCAGCCTCCAGCCTCCAGCCTCCAG 1793
Qy 666 TrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHisAla 685
Db 1794 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1853
Qy 686 LysAlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThr 705
Db 1854 NNNNGTAGTGGTATCTCTCTTTCTGGGCTTGTGGGGTCTGAGCTTTATGGGACAC 1913
Qy 706 LeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHisAla 725
Db 1914 CGAGTGAGAGAGCGGCTGAGCTTACGGACATTTGACCTCGGGAACACAGAGATATGAC 1973
Qy 726 PheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGly 745
Db 1974 TTTATGTGTCACAAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2033
Qy 746 GlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSer 765
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Qy 766 LeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 785
Db 2091 GTGAAGTATGTCTGTTGGAGAAACAAACAGCTTCCCAAAATGTGGCTGCATCTTC 2150
Qy 786 ArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlyAlaLeuAlaTyrLysLeuLeu 825
Db 2151 AGAGCTGGCTTACGGACCTTCAGNATGCAATTCACAGCGACTGGGAAACCGGAAATC 2210
Qy 806 ThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 825
Db 2211 ATGCCAAACAAATACAGAAATGATCAGACATGAGTCTTGTCTACAACTCCTGGT 2270
Qy 826 GlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuVal 845
Db 2271 CAAACCGGCGAGNCGATNGCCATCGACATCAGCCAGTTGACTAAACACAGCGTCTGG 2330
Qy 846 AspArgGluGlyLeuIleProGluLeuPheTyrMetGlyLeuThrValTrpValSer 865
Db 2331 GATGCAGATGGCATTAATCCAGCGCTTCTACATCTACCTGACGGCTTGGGTGACG 2390
Qy 866 SerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTrp 885
Db 2391 AACGACCCCTCGGTATGTCTGCCCTCCAGGCCACATCCGGCCACACCCAGCAGATGG 2450
Qy 886 LeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnPro 904
Db 2451 GTCCAGACAAACCGCACTACATCGCTGAAACAGGCTGAGAAATCCCGGCGAGAGGCC 2510
Qy 905 LeuGluPheAlaGlnPheProPheLeuArgGlyLeuGlnLysThrAlaAppPheVal 924
Db 2511 ATNNNGTATGCCAGTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2570
Qy 925 GluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAla 944
Db 2571 GAGGCAATGAAAAAGTAAGACCATCTGCAGCAACTATACAGACCTGGGGCTGTCCAGT 2630
Qy 945 TyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgCysPhe 964
Db 2631 TACCCCAACGGCTACCCCTTCTCTTCTGGGAGCAGTACATCGGCTCCGCCCTCCGCC 2690
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Qy      1170 ProGlyAlaTyrIleHisPro 1176
Db      3765 CCTGGGCTGGGGCGGAACCC 3785

RESULT 4
LOCUS   CF733501
DEFINITION  UI-M-HB0-ckb-n-01-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
VERSION  IMAGE:30608088 5', mRNA sequence.
ACCESSION  CF733501
KEYWORDS   CF733501.1 GI:37629834
SOURCE     EST.
ORGANISM   Mus musculus (house mouse)

REFERENCE  1
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL    NIH-MGC http://mgi.nci.nih.gov/.
COMMENT    National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-remail.nih.gov
           Tissue Procurement: Dr. James Lin University of Iowa
           cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Distribution information can be found at
           http://genome.uiowa.edu/distribution/mousefl.html
           This clone was contributed by the Brain Molecular Anatomy Project
           (BMAP)

Seq primer: PYX-5.
FEATURES             Location/Qualifiers
     source           1..711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57Bl/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30608088"
                     /tissue_type="whole eye"
                     /dev_stage="embryo 12.5,13.5,14.5 dpc"
                     /lab_host="DHI0B (T1 phase resistant)"
                     /clone_lib="NTH BMAP_HB0"
                     /note="Organ: Eye; Vector: PYX- Asc; Site 1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into PYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is TTATGTAAGT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)".

ORIGIN
Alignment Scores:
Pred. No.:      2,51e-87      Length:      711
Score:          1097.50      Matches:      214
Percent Similarity: 91.14%      Conservative: 2
Best local Similarity: 90.30%      Mismatches: 12
Query Match:    17.50%      Indels:      9
DB:              7          Gaps:      1

US-09-990-046-2 (1-1203) x CF733501 (1-711)

Qy      178 GluIysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaIlys 197
Db      3 GAGAAGCTTTCCCTGTGTGATCCACCCCGCTTGACTGCTCTTCGGAGAGGACAAA 62
Qy      198 LeuGlnGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217

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Db      63 CTCACAGGGGCTCTGCTACTTGGCGGGCCGCTGATATCCAGTGGACCAACCTGGAC 122
Qy      218 ProGluGlnLeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeu 237
Db      123 CCTCAGCAGTGTCTCGAGGAGCTGGGCCCTTTGCTCTCTGGAGGGCTTCGCGGAACGTG 182
Qy      238 LeuAspIysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAsp 257
Db      183 CTAGATAAGGCACAGGTGGGCGCAGCCTATGTGGGGGAGCCCTGTCTGGACCCCTGATGAC 242
Qy      258 LeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHis 277
Db      243 CCCCACTGTCCACCTAGTGTCTCCACCGGCACAGCAGGAGGCTCCCAATGTGGCTCAG 302
Qy      278 GluLeuSerGlyGlyCysHisGlyPheSerHisIshysPheMetHisTrpGlnGluLeu 297
Db      303 GAGCTGAGTGGGGGCTGCCATGGCTTCTCCACAAAGTTTCATGCATCGCAGGAGGAGAACTG 362
Qy      298 LeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArg----- 312
Db      363 CTACTAGGGGCAAGCAGCAGAGATCTCAAGGACAGCTGCTGAGGTGGGCTCCCTGG 422
Qy      313 -----AlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrG1 330
Db      423 GACTTGGGCAGAGGCTTGCAGAGCAGCCTTCTCTGCTCATGAGTCCCGCTCAGCTGTACGA 482
Qy      330 uHisPheArgGlyAspTyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerTh 350
Db      483 GCACCTTCGGGGGCACTACCAACAGCAGATGATCGGCTGGAGGAGGAGGAGGAGCCAGAT 542
Qy      350 rValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAs 370
Db      543 GGTGCTGAGGCTGGGAGAGGCGCTTTGTGCAGCTAGCCAGGAGGCTCTGCGGCGCAA 602
Qy      370 nAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeu-AspAspIleLeuHisAlaP 390
Db      603 CGGCTGCAGCAGATCCATGCTTCTCTCCACCAACCCCTNGGATGACATCCTGCGCGGT 662
Qy      390 heSerGluValSerAlaAlaArgValGlyGlyTyrLeuLeuMet 405
Db      663 TCTCTGAAGTCAGCACCCACCGCTGGGTANGAGGCTATCTGCTTATG 709

RESULT 5
CK830937 708 bp mRNA linear EST 04-MAR-2004
LOCUS 4054508 BARC 8BOV Bos taurus cDNA clone 8BOV_18P22 5', mRNA
DEFINITION sequence.
ACCESSION CK830937
VERSION CK830937.1 GI:45056596
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 708)
AUTHORS  Baumann,R.G.; Baldwin,R.L.; Sonstegard,T.S.; Van Tassel,C.P. and
          Matukumalli,L.K.
TITLE Construction and Analysis of a cDNA Library Generated From
JOURNAL Intestinal Muscle and Epithelial Tissues of Holstein Cattle
COMMENT Unpublished (2004)
          Contact: Richard G. Baumann
          Bovine Functional Genomics Lab
          ANRI
          BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
          Tel: 3015048604
          Fax: 3015048744
          Email: rbaumann@auri.barc.usda.gov
          Single pass sequencing. Bases called and trimmed with phred
          0.000925 using options -trim alt - -trim fasta. Vector identified
          by cross_match using options -mismatch 12 -mismatch 12
          Plate: 18 row: P column: 22

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Plate: A0902 row: E column: 10
Seq primer: M13 Reverse
High quality sequence stop: 603
POLYA=No.

FEATURES
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1.603
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/BvTac"
/db_xref="nlaEST:A0902E10-5"
/db_xref="taxon:10090"
/clone="NIA:A0902E10 IMAGE:30767001"
/sex="Male"
/tissue type="Embryonic Stem Cell"
/cell_line="DHI0B"
/lab_host="129.3 ES cells"
/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. ES cells were plated at density 3x10⁴/cm², on gelatin-coated plates and cultured for 48 hrs at 37 °C, 5% CO₂. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 1000 U/ml LIF, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGCGGCCGCTTTT-3'] from purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao."

ORIGIN
Alignment Scores:
Pred. No.: 1.38e-81 Length: 603
Score: 1032.00 Matches: 190
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 95.00% Mismatches: 8
Query Match: 16.45% Indels: 0
DB: 7 Gaps: 0
US-09-990-046-2 (1-1203) x CN671167 (1-603)

QY 156 LeuAenLysIleCysTyrIleValProLeuLeuGluAasnGlyMetileGluTrp 175
Db 3 TTGAACAAGATCTGTACAAATCAGGGGTTCCTTTATGAAATGGGATGATCGAGCGG 62
QY 176 MetileGluLysLeuPheProCysValIleLeuThrProLeuAaspCysPheTrpGluGly 195
Db 63 ATGATTGAGAAGCTGTTCCCTGTGTGATCCTCACCCTGCTGACTGCTCTCTGGGAAGGA 122
QY 196 AlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArgProAaspIleGlnTrpThrAsn 215
Db 123 GCCAAATCTCAAGGGGGCTCTGCCTACTTGCCTGCGGGCGCCCTGATATCAGTGGAGCAAC 182
QY 216 LeuAaspProGluGlnLeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArg 235
Db 183 CTGGACCTCAGCAGCTGTCTCGAGGAGCTGGGCCCCCTTGGCCTCTCTGGAGGGCTTCCGG 242

593 IleAlaHisLeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSerGlnHis 612
Db 2 ATTGCCACCTGACTGCGACCGTGCAGACCTTACCACCTGCGAAGCCAGCAGCCAGCAT 61
613 ValValThrIleLeuProGlnAlaHisLeuValProProSerAspProLeuGly 632
Db 62 GTAGTCAACATTTTGGCTCTCAAGCCACCTGCTGTCTCCAGTCTTCCACCTGGGC 121
633 SerGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThr 652
Db 122 TCCGAATCTATACCTCTGGAGGCTTACACGGGACCTTCTCACTCAGGAGGGGAGCA 181
653 ArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAla 672
Db 182 GGGCCACAGCGGGCTGCGAGCCCTGCTGTGTGCCCACTGGACTCTCGCCCATTTTGGC 241
673 ArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeu 692
Db 242 CGCTATCAGTTTGACCTTTTACTGCTCCAGACACGAGCCAGGCGCTGGTGTCTGTTC 301
693 PheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAla 712
Db 302 TTTGGGCTCTTTTGGGCTGAGCTCTATGAGCCACCTTGTACAGATGGCTGGCC 361
713 LeuThrAspValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArg 732
Db 362 CTGACAGATGTGTCTAGGGGACCAAGGAACATGCTTTCCTGAGCGCCAGCTCAGG 421
733 TyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSer 752
Db 422 TACTTCTCCCTGTAGAGGTGCTCTAGTGACAGGGTGGCTTGTACTACGCCACTCC 481
753 GlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro 772
Db 541 CAACGGCGCTCTTTGATCTGACACGCGCTTCAGCTCCCTCAGAGCTGTGTGCCCCCA 541
773 ProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIle 792
Db 542 CCTGCAACCCAGCCACCGCCACCTTGGCTTCACTACTCCGAGCTGGCTCAGGGGTATC 601
793 GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsn 812
Db 602 CAGGCTGCATTTGACCAAGACTGGGCTTCTGGGCGCATCAGCTGCCACTTACCGCAAC 661

RESULT 7
CN671167
LOCUS
DEFINITION
A0902E10-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0902E10 IMAGE:30767001 5', mRNA sequence.
CN671167
CN671167.1 GI:47437618
EST.
Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
Sharov A.A., Piao Y., Matoba R., Dudekula D.B., Qian Y., VanBuren V., Falco G., Martin P.R., Stagg C.A., Bassey U.C., Wang Y., Carter M.G., Hamatani T., Aiba K., Akutsu H., Sharova L., Tanaka T.S., Kimber W.L., Yoshikawa T., Jaradat S.A., Pantano S., Nagaraja R., Boheler K.R., Taub D., Hodes R.J., Longo D.L., Schlensing D., Kellier J., Klotz E., Keisoe G., Umezawa A., Vescovi A.L., Rossant J., Kunath T., Hogan B.L., Curci A., D'Urso M., Keisoe J., Hide W. and Ko M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun.grc.nia.nih.gov

593 IleAlaHisLeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSerGlnHis 612
Db 2 ATTGCCACCTGACTGCGACCGTGCAGACCTTACCACCTGCGAAGCCAGCAGCCAGCAT 61
613 ValValThrIleLeuProGlnAlaHisLeuValProProSerAspProLeuGly 632
Db 62 GTAGTCAACATTTTGGCTCTCAAGCCACCTGCTGTCTCCAGTCTTCCACCTGGGC 121
633 SerGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThr 652
Db 122 TCCGAATCTATACCTCTGGAGGCTTACACGGGACCTTCTCACTCAGGAGGGGAGCA 181
653 ArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAla 672
Db 182 GGGCCACAGCGGGCTGCGAGCCCTGCTGTGTGCCCACTGGACTCTCGCCCATTTTGGC 241
673 ArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeu 692
Db 242 CGCTATCAGTTTGACCTTTTACTGCTCCAGACACGAGCCAGGCGCTGGTGTCTGTTC 301
693 PheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAla 712
Db 302 TTTGGGCTCTTTTGGGCTGAGCTCTATGAGCCACCTTGTACAGATGGCTGGCC 361
713 LeuThrAspValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArg 732
Db 362 CTGACAGATGTGTCTAGGGGACCAAGGAACATGCTTTCCTGAGCGCCAGCTCAGG 421
733 TyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSer 752
Db 422 TACTTCTCCCTGTAGAGGTGCTCTAGTGACAGGGTGGCTTGTACTACGCCACTCC 481
753 GlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro 772
Db 541 CAACGGCGCTCTTTGATCTGACACGCGCTTCAGCTCCCTCAGAGCTGTGTGCCCCCA 541
773 ProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIle 792
Db 542 CCTGCAACCCAGCCACCGCCACCTTGGCTTCACTACTCCGAGCTGGCTCAGGGGTATC 601
793 GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsn 812
Db 602 CAGGCTGCATTTGACCAAGACTGGGCTTCTGGGCGCATCAGCTGCCACTTACCGCAAC 661

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QY 236 GluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisPro 255
Db 243 GAACCTGCTAGATAAGGACACAGGTGGGCCCTATGTGGGGGAGCCCTGTCTGGACCCCT 302
QY 256 AspAspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnVal 275
Db 303 GATGACCCCCACTGTCCACTAGTGTCTCCCAACCGGCACAGCAGGAGGCTCCCAATGTG 362
QY 276 AlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu 295
Db 363 GCTCAGGAGCTAGTGGGGGCTGCCATGGCTTCTCCCAAGTTCATGACATGGCAGGAG 422
QY 296 GluLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlnLeuLeuArgAlaGluAla 315
Db 423 GAACCTGCTACTAGGGGGGCACAGCAGAGATCTCCAGAGCAGCTGTGTAGGGCAGAGGCC 482
QY 316 LeuGlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAsp 335
Db 483 TTGCAGAGACCTTCTGCTCATGAGTCCCGCTCAGCTGTACGAGCAGCTTCCGGGGCGAG 542
QY 336 TyrGlnThrHisAspIleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrp 355
Db 543 TACCAGACACATGATCGGCTGGAGCGAGGAGCAGCCAGCATGTGTGCTGAGGCGCTGG 602

RESULT 8
BM105989
LOCUS 571 bp mRNA linear EST 21-NOV-2001
DEFINITION 509593 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM105989
VERSION BM105989.1 GI:17037059
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 571)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 102 row: B column: 18
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1 . 571
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

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ORIGIN

Alignment Scores:

Pred. No.: 3,29e-79 Length: 571
 Score: 1005.00 Matches: 184
 Percent Similarity: 98.95% Conservatives: 4
 Best Local Similarity: 96.84% Mismatches: 2
 Query Match: 16.02% Indels: 0
 DB: 4 Gaps: 0

US-09-990-046-2 (1-1203) x BM105989 (1-571)

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QY 770 LeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeu 789
Db 1 CTGCCCCCACCAGCCGACCCAGCAGCTGGCTGCTACTTACCGCAGCTGGCTA 60
QY 790 GlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSer 809
Db 61 CAGGGAAATCCAGGCTGCAATTGACCAGGACTGGGCTTCTGGGGCGCATCACCGCCACTCA 120
QY 810 TyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAsp 829
Db 121 TACCGCAATGGCTCTGAGGATGGGCCCTGGCATACAGCTGCTGTCAGACCCGGGAT 180
QY 830 AlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGly 849
Db 181 GCCCCAGGAGCCTCTAGATTTTCAGCCAGCTGACCAACAAGAGCTGGTGACAAAGAGG 240
QY 850 LeuIleProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeu 869
Db 241 CTGATCCCAACCGAGCTCTTTACATGGGGTGACCGGTGGGTGAGCAGTACACCCCTG 300
QY 870 GlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGluTrpLeuHisAspLys 889
Db 301 GGTCTGGCAGCTCACAGGCCAACTTCTATCCCCACCTCTGAGTGGCTGCATGACCAAG 360
QY 890 TyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAlaGln 909
Db 361 TATGACACCAACCGGGGAGAACTTTCGATCCCGCGCGCCAGCCCTTGGAGTTTGCCCA 420
QY 910 PheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGly 929
Db 421 TTCCTCTTCCTCGCGCGGCTCCAGAAGACTCGAGACTTTCGTGGAGGCCATTGAGGGG 480
QY 930 AlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySer 949
Db 481 GCCCGGGCAGCGTGTGCTGAGGCCAGCCAGCGGGGTGCATGCTACCCCGAGCGGCTCC 540
QY 950 ProPheLeuPheTrpGluGlnTyrLeuGly 959
Db 541 CCCTTCCTCTTCTGGGAGCAGTACCTGGGC 570

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RESULT 9

CA528868

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CA528868 8091-13 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
 mRNA sequence.
 CA528868
 CA528868.1 GI:25042932
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 500)
 Mu X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
 White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
 Gene expression in the developing mouse retina by EST sequencing
 and microarray analysis
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)
 21671825
 11812828
 Contact: Klein WH

Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES

Location/Qualifiers
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

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Score: 998.00 Matches: 190
Percent Similarity: 97.49% Conservativeness: 4
Best Local Similarity: 95.48% Mismatches: 5
Query Match: 15.91% Indels: 0
DB: 6 Gaps: 0

US-09-990-046-2 (1-1203) x CA528868 (1-600)

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QY 829 AspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLyLeuValAspArgGlu 848
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Db 3 AATGCCAGGAGCCTCTGATTTACGCCAGCTGACCAAGAAACTGGTGACCAAGGAG 62

QY 849 GlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTyrValSerSerAspPro 868
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 63 GGACTCAATTCCTCCCGAGCTCTTACATGGGGCTTACCGTGTGGGTGAGCAGCAGCCCC 122

QY 869 LeuGlyLeuAlaAlaSerGlnAlaAsnPhetYrProProProGluTyrTrpLeuHisAsp 888
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 123 CTGGCCCTCGCAGCTCTCAGGCCAACTTCTACCCCCCACTCCAGAGTGGCTTACGAC 182

QY 889 LysTyrAspThrThrGlyGluAsnLeuArgIleProProAlaGlnProLeuGluPheAla 908
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 183 AAATATGATACCACCGGGGAGAACCTTGCATCCCGCAGCCCTGGAGTTGGC 242

QY 909 GlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGlu 928
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 243 CAGTTCCCTTCTCTGTCATGACTCTCAGAGACTGACAGACTGTCAGACTTGTAGAGCCATCGA 302

QY 929 GlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGly 948
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Db 303 GGGCCAGGGGGCATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 362

QY 949 SerProPheLeuPheTyrGluGlnTyrLeuGlyLeuArgCysPheLeuLeuAlaVal 968
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 363 TCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 422

QY 969 CysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTyrThr 988
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 423 TGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482

QY 989 AlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGly 1008
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Db 483 GCTGGCCTCATAGTCTGGTCTGGCAATGATGACTGTGGAGCTCTTGTGTATCATGGGA 542

QY 1009 PheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSerValGly 1027
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Db 543 TTCTTGGGATCAAACTAGTGTGATCTCCCGTGGNAATCTCGNGCCCTCTATAGGC 599

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RESULT 10

LOCUS CN676164 625 bp mRNA linear EST 17-MAY-2004
DEFINITION A0976A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:A0976A07
IMAGE:30774054 5', mRNA sequence.
ACCESSION CN676164
VERSION CN676164.1 GI:47442615

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)

REFERENCE

AUTHORS
Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Basse, U.C.,
Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,
Tanaka, I.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,
Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A.,
Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,
D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

TITLE

Transcriptome analysis of mouse stem cells and early embryos

JOURNAL

PLoS Biol. 1 (3), 410-419 (2003)

COMMENT

Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: A0976 row: A column: 07
Seq primer: M13 Reverse
High quality sequence stop: 625
POLYA-No.

FEATURES

source

Location/Qualifiers

1..625
/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="niaEST:A0976A07-5"
/db_xref="taxon:10090"
/clone="NIA:A0976A07 IMAGE:30774054"
/sex="Male"
/tissue_type="Embryonic Stem Cell"
/cell_line="129.3 ES cells"
/lab_host="DH10B"

/clone_lib="NIA Mouse Embryonic Stem (ES) cell (Lif+, 48 h, high density) cDNA library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [pMID: 11544199]). ES
cells were plated at density 3x10⁴/cm² on gelatin-coated
plates and cultured for 48 hrs at 37 °C, 5% CO₂. Culture
medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine,
0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM
beta-mercaptoethanol, 1000 U/ml Lif, 100 U/ml penicillin,
and 100 ug/ml streptomycin. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to ligo-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.7 kb. The library was
constructed by Yulan Piao."

ORIGIN

Alignment Scores:
Pred. No.: 1,26e-77 Length: 625
Score: 998.00 Matches: 194
Percent Similarity: 96.63% Conservativeness: 7
Best Local Similarity: 93.27% Mismatches: 7


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Db      568 CAAGTGTCTATGATGAAATCTTGGAGCTGAATCAAAATCTCTTAAATCTGGAGTT 627
Qy      166 ProLeuLeuGluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValile 185
Db      628 CCAATTATGAAATGCAATGATTTGAGAGGATGATTGAGAACTTTTCCCTTGTGTAATA 687
Qy      186 LeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrIleu 205
Db      688 ATTACACCTCTGGACTGTTTTTGGGAAGATCCCAAGCTTCAAGGTGGCTCTGSCATATCTA 747
Qy      206 ProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGluLeu 225
Db      748 CCAGGAAGAGCTGACATTCATGAGACCACTAGATCCCATCAAGTTCATGGAAGAGCTT 807
Qy      226 GlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGln 245
Db      808 GGTCACTTCCAGCTCTTGATGGCTTCAAGGAATGCTGGACAAGGCTGAAGTAGGACAG 867
Qy      246 AlaTyrValGlyArgProCysLeuHisProAspAsp 257
Db      868 GGATATATGGAACGACCTTGTCTGGACCTACAGAC 903

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RESULT 12
 BQ964086
 LOCUS
 DEFINITION AGENCOURT 10054944 NIH_MGC_134 Mus musculus cDNA clone
 IMAGE:6509228 5', mRNA sequence.

ACCESSION BQ964086
 VERSION BQ964086.1 GI:22379564

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 974)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLNMI4076 row: c column: 21

High quality sequence stop: 689.

Location/Qualifiers

FEATURES

source

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    /clone_lib="NIH_MGC_134"
    /notes="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
    Cloned unidirectionally. Primer: Oligo dT. Average insert
    size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
    this is a NIH_MGC library."

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ORIGIN

Alignment Scores: 1,01e-74 Length: 974
 Pred. No.: 959.00 Matches: 199
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 Percent Similarity: 57.02% Mismatches: 76
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 Query Match: 5 Gaps: 4
 DB:

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US-09-990-046-2 (1-1203) x BQ964086 (1-974)
Qy      848 GluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAsp 867
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Qy      868 ProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpIleuHis 887
Db      88 CCTGTAGCTTACGCTGCTCCAGGCCAACATCCGGCTCACCGCGCGGAGTGGTCCAT 147
Qy      888 AspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGlu 906
Db      148 GACAAAGCCGACTACATGCTCCAGAGACCCAGGCTGAGAATCCAGAGCAGAGCCATCCAG 207
Qy      907 PheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAla 926
Db      208 TACGCTCAGTTCCCTTCTTACCTCAAGGCCCTACAGACACCTCAGACTTTTGTGGAAGCC 267
Qy      927 IleGluGlyAlaAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrPro 946
Db      268 ATAGAAAAGTGAGAGTCATCTGTAAACAATATACAGCCTGGGACTGTCCAGCTTACC 327
Qy      947 SerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeu 966
Db      328 AATGGCTACCCCTTCTCTTCTGGAGCAGTACATCAGCCTGGCCACTGGCTGCTGCTA 387
Qy      967 AlaValCysIleLeuLeuValCysThrPheLeuValCysAlaAlaLeuLeuLeuAsnPro 986
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Qy      987 TrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGlyIle 1006
Db      448 TGGAGCGCGGGATCATTTGTCATGCTGCTGTGATGACCGTTGAGCTCTTTGGCATG 507
Qy      1007 MetGlyPheLeuGlyIleLysLeuSerAlaIleProValIleLeuValAlaSerVal 1026
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Qy      1027 GlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySer 1046
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Qy      1067 IleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArg 1086
Db      688 GTGTCCACTCTCTGGGTGTACTGTGCTGAGGTCGCGGTCGAAATTGATTTCAATGTCAGA 747
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Qy      1107 LeuProValLeuLeuSerIleLeuGlyProProProGluValIleGlnMetTyrLysGlu 1126
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Db      844 -----TGAGGGGTCTCC 855
Qy      1147 SerSerLeuProGlnSerPheAlaArgValThrSerMetThrValAlaIleHis-Pr 1166
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Qy      1166 oProProLeuProGlyAlaTyrIleHisProAlaProAspGluProProTrpSerPro--- 1185
Db      886 TTGCGCTGAGCCGCCGCCCGGCGGTGTCGCGGGTTTGGCGGTGCTCTTGGTCAACCGGA 945
Qy      1186 -----AlaAlaThrSerSerGly 1191
Db      946 AAAAAAGGNTCGGATTTCTTCCCGA 970

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ACCESSION BE234509
 VERSION BE234509.1 GI:9019227
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 573)
 Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
 Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,
 Quackenbush, J., and Keefe, J.W.
 Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly
 Mamm. Genome 13 (8), 475-478 (2002)
 22213789
 12226715
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
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 Seq primer: ATTAGGTGACACTAG.
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 library made from pooled tissue from day 11, 13, 15, 20,
 and 30 embryos."
 ORIGIN
 Alignment Scores: Length: 573
 Pred. No.: 173
 Score: 891.00
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 Best Local Similarity: 90.58%
 Query Match: 14.21%
 DB: 2
 Gaps: 0
 US-09-990-046-2 (1-1203) x BE234509 (1-573)
 QY 502 ValValLeuThrSerLeuAsnMetAlaAlaPheLeuMetAlaAlaLeuValProLeu 521
 Db 1 GTGCGCTCAGTCCATCAACATGTTGGCTTTTATGCGCGCTCGTGGCCATC 60
 QY 522 ProAlaLeuArgAlaPheSerLeuGlnAlaAlaLeuValValGlyCysThrPheValAla 541
 Db 61 CCTGCCCTCGGCGCTTCTCTTGCAGCGCGCCATAGTGTGCTGCACTTCGCAGCC 120
 QY 542 ValMetLeuValPheProAlaLeuLeuSerLeuAspLeuArgArgHisCysGlnArg 561
 Db 121 GTGATGTTGTCTTCGCGCGCTCTCAGCTGAGCTGACCGCGCGCTGCGCGCGC 180
 QY 562 LeuAspValLeuCysCysPheSerProCysSerAlaGlnValIleGlnLeuPro 581
 Db 181 CTTGATGTCTGTCTGCTTTCGACGCGCTGCTGCTGCGGTGATTCAGATTGCGCC 240
 QY 582 GlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisIleuThrAlaThrValGln 601
 Db 241 CAGGAGCTGGGGATGGAGCAGTACCGCTGGGCATTGCCCGCTTGAAGTCCACCGTTCAA 300

QY 602 AlaPheThrHisCysGluAlaSerSerGlnHisValValThrLeuLeuProGlnAla 621
 Db 301 GCCTTGGCCACTGTGAAGCCAGCAGCAGCATGTGCTCACCATCTCCCTCCCAACC 360
 QY 622 HisLeuValProProSerAppProLeuGlySerGluLeuPheSerProGlyGlySer 641
 Db 361 CACCTGTGCCCCCACCCTTCTGACCTCTGCGCTCTGAGCTTTCAGCCCCGGAGGTCC 420
 QY 642 ThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeu 661
 Db 421 ACAGGGAGCTTCTAGGCCAGAGAGGAGGACAGCGAGGAGCGCTGCAAGTCCCTG 480
 QY 662 ProCysAlaAlaArgTyrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 681
 Db 481 TCCTGTGCCCACTGGAATCTTGCCCAATTCGCCGCTCTCAGTTTGCACCTTGTGCTC 540
 QY 682 GlnSerHisAlaLysAlaLeuValLeuValLeu 692
 Db 541 CAACCCATGCCAAGGCCATGCTGTGTAATT 573
 RESULT 15
 CK639185
 LOCUS
 DEFINITION
 CK639185.1 GI:41365051
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
 1 (bases 1 to 778)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyX-5.
 Location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6"
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 /clone="IMAGE:30638069"
 /tissue_type="Upper Head"
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 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_H00"
 /note="Organ: Head; Vector: pyX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to the protocol of B. Doolittle, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAAGTCAAT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH)."
 ORIGIN

Alignment Scores:

Pred. No.:	3.56e-68	Length:	778
Score:	884.00	Matches:	165
Percent Similarity:	83.72%	Conservative:	51
Best Local Similarity:	63.95%	Mismatches:	38
Query Match:	14.09%	Indels:	4
DB:	7	Gaps:	3

US-09-990-046-2 (1-1203) x CK639185 (1-778)

```

QY 279 LeuSerGlyGlyCysHisGlyPheSerHisPheMethIstRpGlnGluLeuLeu 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 TTGAATGGTGGATGTCAGGTTTATCCAGGAAGTATATGATCGCAGGAGGATTGATT 66

QY 299 LeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSer 318
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 GTGGTGGTACCGTCAAGAAATGCCACTGGAAATCTTGTCAGCGCTCACGCCCTGCAAAAC 126

QY 319 ThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---AspTyrGln 337
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 ATGTTCCAGTTAATGACTCCACAGCAATGTATGACACTTCAGGGCTACGACTATGTC 186

QY 338 ThrHisAspIleGlyTrpSerGluGlnGlnAlaSerThrValLeuGlnAlaTrpGlnArg 357
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 TCTCAC---ATCAACTGGAATGAAGACAGGCGCAGCCCATCTCGAGGCTCGCAGAGG 243

QY 358 ArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAla 377
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 ACTTAGCTGGAGGTGTTTCATCAAGGTGCGCCCAAACTCCACTCAAAAGGTTCTTCCC 303

QY 378 PheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArg 397
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 TTCACAAACACGACCCCTGGACGACATCCTAAATCCTTCTTGATGTAGTGTATCCGA 363

QY 398 ValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAsp 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 GTGGCCAGCGGTACTACTGATGCTTGCTATGCTGTTTAAACCATGCTGGCTGGGAC 423

QY 418 CysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaVal 437
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 TGCTCCAGTCCAGGTCGCGTGGGGCTGGCTGGCTGCTGTTGGTTCGCTGCAGTG 483

QY 438 AlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGln 457
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 GCTGCAGGATTGGGCTCTGCTCCTTGATGGCATTTCTTTAATGCTGCGACAACCTAG 543

QY 458 ValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAla 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 GTTTTGGCGTTTCTTGCTCTTGCTGTTGGTGGATGATGCTCTCTCTGGCCCATGCA 603

QY 478 PheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGluCysLeu 495
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 604 TTCAGTGAACACAGACAGAAATAAGAGGATTCATTTGAGGACAGGACTGGGAGTGCCTC 663

QY 496 GlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMet 515
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 664 AAGCGACCCGAGCGAGCGTGGCCCTCACCCTCCATCAGCAATGTCACCGCCTTCTTCATG 723

QY 516 AlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle 533
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 724 GNCGATTGATCCCTATCCCTGCGCTGGAGGTTCTCCCTCCAGGCTGCTGTG 777

```

Search completed: November 22, 2004, 12:06:09
 Job time : 5506 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:43:25 ; Search time 25 Seconds

Title: US-09-990-046-2

Perfect score: 6272
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSRRGPGPATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5599	89.3	1182	2 T13952	membrane protein p
2	4042.5	64.5	1220	2 T18291	patched protein -
3	3340	53.3	1442	2 T18538	transmembrane prot
4	3337	53.2	1434	2 T30172	membrane protein p
5	1961.5	31.3	1299	1 S06119	hypothetical prote
6	1708.5	27.2	1405	2 T27969	hypothetical prote
7	992	15.8	714	2 T16126	hypothetical prote
8	603.5	9.6	1278	2 T30188	Niemann-Pick C dis
9	514	8.2	1055	2 T05663	hypothetical prote
10	465.5	7.4	955	2 T21612	hypothetical prote
11	444	7.1	933	2 T25600	hypothetical prote
12	444	7.1	1003	2 T26746	hypothetical prote
13	430.5	6.9	1015	2 T15830	hypothetical prote
14	416.5	6.6	889	2 T29590	hypothetical prote
15	389.5	6.2	936	2 T26521	hypothetical prote
16	386.5	6.2	956	2 A89153	hypothetical prote
17	380.5	6.1	1170	2 S92525	protein C24B5.3 [i
18	343.5	5.5	845	2 T25657	probable membrane
19	340	5.4	881	2 T31739	hypothetical prote
20	317.5	5.1	800	2 T26683	hypothetical prote
21	314	5.0	877	2 T24097	hypothetical prote
22	309	4.9	820	2 T32908	hypothetical prote
23	300	4.8	983	2 T21213	hypothetical prote
24	293.5	4.7	1456	2 T15961	hypothetical prote
25	291	4.6	840	2 T33217	hypothetical prote
26	275.5	4.4	871	2 T28706	hypothetical prote
27	261.5	4.2	890	2 T22186	hypothetical prote
28	258.5	4.1	690	2 T23359	hypothetical prote
29	188	3.0	1276	2 T18526	SREBP cleavage act

ALIGNMENTS

RESULT 1

T13952

membrane protein ptch2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13952

R:Motoyama, J.; Takabatake, T.; Takeshima, K.; Hui, C.

A:Title: Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog.

A:Reference number: Z17830; MUID:98122566; PMID:9462734

A:Accession: T13952

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1182 <MOT>

A:Cross-references: UNIPROT:O35595; EMBL:AB010833; PIDN:BAA24691.1

A:Experimental source: strain BALB/cCrSlc

C:Genetics:

A:Gene: ptch2

C:Superfamily: Drosophila membrane protein patched

C:Keywords: transmembrane protein

Query Match 89.3%; Score 5599; DB 2; Length 1182;

Best Local Similarity 90.9%; Pred. No. 0;

Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

Qy 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFOGLAFSLGCGIQRHCGKVL 60

Db 1 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFOGLLFSLGCRIQKCGKVL 60

Qy 61 LGLAFGALALGLRMAIETNLEQLWVEGSRVSOQLHYTKEKLGEAAAYTSQMLIQTA 120

Db 61 LGLVAFGALALGLRVAVIETDLEQLWVEGSRVSOQLHYTKEKLGEAAAYTSQMLIQTA 120

Qy 121 QEGENIITPALGLHQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL 180

Db 121 QEGGNVITPEALDLHLQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL 180

Qy 181 FPCVILTPDLDFEGAKLQGSAYLPCRPDIQTNLDPEQLLELGFASLEGRELLDK 240

Db 181 FPCVILTPDLDFEGAKLQGSAYLPCRPDIQTNLDPEQLLELGFASLEGRELLDK 240

Qy 241 AQVQAYVGRPCILHCPDPPSAPNHHRSQAPNVAHELSCGGCHGFKHFWHQEELLG 300

Db 241 AQVQAYVGRPCILHCPDPPSAPNHHRSQAPNVAHELSCGGCHGFKHFWHQEELLG 300

Qy 301 GMARDPQGLLRABALQSTFLMSPOLYEHFRGDIYQTHDIGWSEBOASTVLQAWQRFF 360

Db 301 GTARDLQGLLRABALQSTFLMSPOLYEHFRGDIYQTHDIGWSEBOASTVLQAWQRFF 360

Qy 361 QLAQEAALPENASQIIHAFSSTLLDDILLHAFSEVSAARVVGYLMLLAYACVTMLRWDC 420

Db 361 QLAQEAALPENASQIIHAFSSTLLDDILLHAFSEVSTTRVVGYYLLMLLAYACVTMLRWDC 420

probable efflux tr
transport protein
acriflavine resist
F09G8.3 protein -
hypothetical prote
probable antibioti
hypothetical prote
related to SREBP c
probable multi-dru
acriflavine resista
probable RND efflu
probable export pr
conserved hypothet
hypothetical membr
hypothetical prote

Qy	421	SQSGVLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFIILAHAFTE	480
Db	421	SQAGVGLGAVLLVALAVASGLGICALLGITNAATQVLPALAGIGVDDVFIILAHAFTE	480
Qy	481	ALPGTFLQRMGECLORTGTSWLTSTINNAAFALMAALVPIPALRAFSLQAAIVVGCFTV	540
Db	481	APDPTPLPERMGECLRTSTGTSVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFA	540
Qy	541	AVMLVFPAILSLDLRRRCORLDVLCFSPSCSAQVIQILPQELGDDGTVVPGIAHLTATV	600
Db	541	AVMLVFPAILSLDLRRRRQRDLVLCFSPSCSAQVIQMLPQELGDRVAVPGIAHLTATV	600
Qy	601	QAFTHCEASSOHVTVILPQAHLLVPPSPDPLGSELFPSPGGSTRDLGQEBETROKAACKS	660
Db	601	QAFTHCEASSOHVTVILPQAHLLSPASDPLGSELYSPGGSTRDLGQEBEGTPQAACRP	660
Qy	661	LPCARWNLAHAFYQAFAPLLQSHAKATVILVFLGALLGLSLYGATLVODGALATDVVPRG	720
Db	661	LLCAHWTLAHFARQFAPLLQTRAKALVILFFGALLGLSLYGATLVODGALATDVVPRG	720
Qy	721	TKEHAFSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPTQAPRT	780
Db	721	TKEHAFSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPTQAPRT	780
Qy	781	WLHYRNWLOGIOAFDQDQWASGRITRHSYRNGSEGDGALAYKLLIOTGDAQEPLDFSQIT	840
Db	781	WLHYRNWLOGIOAFDQDQWASGRITRHSYRNGSEGDGALAYKLLIOTGDAQEPLDFSQIT	840
Qy	841	TRKLVDRGLLPELFPYMGTLVWSSDPLGLAASQANFVPPPEWHLKDYDTTGNLRIP	900
Db	841	TRKLVDRGLLPELFPYMGTLVWSSDPLGLAASQANFVPPPEWHLKDYDTTGNLRIP	900
Qy	901	PAQPLEFAQFPFLLEGLOKTDVFAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYGL	960
Db	901	AAQPLEFAQFPFLLEGLOKTDVFAIEGARAACAEAGQAGVHAYPSGSPFLFWEQYGL	960
Qy	961	RRCFLAVLCILLVCTFLVCAILLNPNWTAGLIVILVAMTWELFGIMFLGKLSAIPV	1020
Db	961	RRCFLAVLCILLVCTFLVCAILLNPNWTAGLIVILVAMTWELFGIMFLGKLSAIPV	1020
Qy	1021	ILVASVIGTVEFTVHVALGFTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLMLAGSH	1080
Db	1021	ILVASIGTVEFTVHVALGFTTSHGSRNLRAASALEQIFAPVTDGAVSTLLGLMLAGSN	1080
Qy	1081	EDFVRYFFAALTVLTLGLHLGLVLLPVLSILGPPPEVIOYKESPEILSPPAQGGG	1140
Db	1081	EDFVRYFFVVLTVLTLGLHLGLLPLVLSILGPPPVQVQYKESPTLNSAAPQGGG	1140
Qy	1141	LWNGASSLPQSFAFVTTSMVAIHPPPLPGAYIHPADPEP	1181
Db	1141	LWDRPPTLQSFARVTTSMVALHPPLPGAYVHPASEP	1181
RESULT 2			
T18291			
patched protein - zebra fish			
C:Species: brachydanio rerio (zebra fish)			
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004			
C:Accession: T18291			
R:Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;			
Development 122, 2835-2846, 1996			
A:Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic			
A:Reference number: Z18860; MUID:96379744; PMID:8787757			
A:Accession: T18291			
A>Status: preliminary; translated from GB/EMBL/DDBJ			
A:Molecule type: mRNA			
A:Residues: 1-1220 <CON>			
A:Cross-references: UNIPROT:Q98864; EMBL:X98863; PIDN:CAA67386.1			
C:Genetics:			
A:Gene: ptc1			
C:Superfamily: Drosophila membrane protein patched			
Query Match 64.5%; Score 4042.5; DB 2; Length 1220;			
Best Local Similarity 64.6%; Pred. No. 2.8e-272;			
Matches 775; Conservative 156; Mismatches 224; Indels 44; Gaps 8;			
Qy	2	TRSPPP-----LRELPPSYTPPARTAQAIIAGSL---KAPLWIRAYFQGLLFLSLGCGIQ	52
Db	23	TRSPPPVNSDLRR--PSYC-HAFAALKQISGKAVGQKAPLWIRARFQAFFLSLGCHIQ	79
Qy	53	RHCQKVLFLGLLALGALALGLRMAIETNLNLFQWVEGSRVSOELHYTKELGEBEAAVTS	112
Db	80	RHCQKVLFIGLIVFGALSVGLRVAAIETDIEKLWVEAGSRVSKELRYTKEQEBSVETS	139
Qy	113	QMLQOTARQECENILTPREALGLHQAALTASKQVSLYKGSWDLNKKICYKSGVPLIENGM	172
Db	140	QMLQOTPKQEGTNILTQEAALLHLEALSASKQVSLYKGSWDLNKKICFKSGVPIENVM	199
Qy	173	IEWMIKFLPCVITLPLDPCFWEGAKLQGGSAIYLPGRPDIOWTNLDPEOLLBELGPFASLE	232
Db	200	IERMIDKLPFCMIVTFLDPCFWEGSKLQGGSAIYLPQMPDIQWNLDPLKMBELSOFTSLE	259
Qy	233	GFRELLDKAOGVQAVVGRPCLHDDHCPSPAPNHHSRQAPNVAHELSGGCHGFSGKPMH	292
Db	260	GFREMLDKAQVGHAYMNRPCLDPSDTCFHSAPNKPQVNPNIABELQGGCHGFSGKPMH	319
Qy	293	WQELLGGMARDPQCELLRAEALQSTFLMSPRLQYEHFRGDYQTHDIGWSEQAQSTVL	352
Db	320	WQELLGGERVKDQNALQSAEALQTMFLMSPKQLYEHFKDDYEHIDINWNEKATAIL	379
Qy	353	QAWQRRFVQLAQEALPENASQOIHAFTSTTDDIILHAFSEVSAARVGGYLLMLAYCVT	412
Db	380	ESWQKFEVHVHSGIPQNSSNVVAFSTTILNDIMKSFSDSVIRVAGGYLLMLAYCVT	439
Qy	413	MLRWDCAQSGVGLAGVLLVALAVASGLGICALLGITNAATTOVLPLFALGIGVDVDF	472
Db	440	MLRWDCAKSGVGLAGVLLVALSVAGLGLCSLLGLSFLNAATTOVLPLFALGIGVDVDF	499
Qy	473	LLAHAFTEALPGTFLQERMGECLQRTGTSVLTSTINNAAFALMAALVPIPALRAFSLQAA	532
Db	500	LLGHSFTETRSNIPFKERTGDCLRGTGTSVALTSVNNMIAFFMAALVPIPALRAFSLQAA	559
Qy	533	IWVGCTFVAVMLVFPAILSLDLRRRCORLDVLCFSPSCSAQVIQILPQELGDDG	586
Db	560	VVWFENFAMALLIFPAILSLDLRRREDKRLDILCCFYSPCSRVQIQPQELSDANDNHQ	619
Qy	587	-----GTVPGVGIHLTATVQAFTHCEASSOHVTVILPPOAHL-VPPPS-----	628
Db	620	RAPATPTVTGTSITTTSTHTTTVQAFTHCEASSOHVTVILPPOAHL-VPPPS-----	679
Qy	629	--DPLGSELFPGGSTRDLGQEBETROKAACKSLPCARWNLAHAFYQFAPLQLQSHAK	686
Db	680	TTDPYGSQVFTTSSSTRDLGQEBETROKAACKSLPCARWNLAHAFYQFAPLQLQSHAK	739
Qy	687	ATVLVFLGALLGLSLYGATLVODGALATDVVPRGTYKHAFLSAQRYPSLYEVALVTQGG	746
Db	740	TVVWVVFVALLSLSLYGTMTVHDGLYLTIVPRDQYEFITAQYKFSFYNNVILVMDG	799
Qy	747	FDYAHSQRALFDLHQRFSSLKAVLPPPTQAPRTWHLHYRNWLOGIOAFDQDQWASGRIT	806
Db	800	FDYAHSQRALFDLHQRFSSLKAVLPPPTQAPRTWHLHYRNWLOGIOAFDQDQWASGRIT	859
Qy	807	RHSYRNGSEGDGALAYKLLIOTGDAQEPLDFSQITTRKLVDRGLLPELFPYMGTLVWSS	866
Db	860	YDSYRNGSEGDGALAYKLLIOTGSKKEPNYSQTSRLVDGGLIFPEVFYIYLVWVSN	919
Qy	867	DPLGLAASQANFYPPPPWHLKDYDTTGENLHIPPAPLEFAQFPFLLEGLOKTDVFA	926
Db	920	DPLGYAASQANFYPPPREWIHDKYDTTGENLHIPPAPLEFAQFPFLLEGLOKTDVFA	979
Qy	927	IEGARAACAEAGQAGVHAYPSGSPFLFWEQYGLRRCFLVAVLCILLVCTFLVCAILLNPN	986
Db	980	IESVRTICEEFMRQGIKNYPNGYPPFLFWEQYGLRHHWFLLSISVVLACTFLVCAILLNPN	1039
Qy	987	WTAGLIVLVLAMTWELFGIMFLGKLSAIPVILVASVIGTVEFTVHVALGFTTQGS	1046

D6	1040	WTAGVVFILPMMTVELFGMLGFKLSAIPVVLIVASVGIGVEFTVHIALGFLTAIGD	1099
QY	1047	RNLRAAHALEHTFAPVDTDGAISTLLGLMLAGSHFDIVRYFFFAALTVLTLLGLLHGVL	1106
D6	1100	RNTRSAVAMEHPAPVIDGAISTLLGVLMLAGSEDFIMRYFFFAVALITLLGLINGLVL	1159
QY	1107	LPVLLSTLGGPPPEVI-----QMYSKSPILLSPPAOGGGLRWGASSLLPQSFARVTTTS	1159
D6	1160	LPVLLSLMGPPAEVVVPANNANHHQLSQSPPEMPPEPMNHGHGYAGHIPKAHQASSETSDS	1218

RESULT 3
Tl8538
patched protein - chicken
C:Species: Gallus gallus (chicken)
C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: Tl8538
R:Marigo, V.; Scott, M.P.; Johnson, R.L.; Goodrich, L.V.; Tabin, C.
Development 122, 1245-1233, 1996
A:title: Conservation in hedgehog signaling: induction of a chicken patched homolog by S
A:Reference number: Z18958; MUID:96205046; PMID:8620849
A:Accession: Tl8538
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1442 <MAR>
A:Cross-references: UNIPROT:Q90693; EMBL:U40074; NID:gl335850; PID:gl335851; PIDN:AAC598
C:Genetics:
A:Gene: PTC
C:Superfamily: Drosophila membrane protein patched
C:Keywords: transmembrane protein

Query Match	53.3%;	Score 3340;	DB 2;	Length 1442;
Best Local Similarity	54.3%;	Pred. No. 2.1e-223;		
Matches	663;	Conservative 204;	Mismatches 234;	Indels 50;
Gaps	17			
QY	12	PSYTPPANTAAPQILAG--	SLKAPLMRAVFGQLLESLGGCIGRCHGKVLFIHLAPCA	68
DB	54	PSYC--DAAPALEQIAKGRATGRAPLMIRAKFQLLFNLGCGYQKNGKPLVWGLL--YSA	111	
QY	69	LALGLRMAIIFETNLEQLMVEVGSRSVQSELHYTEKLGEEAAYTSQMLIOTAROGENIIT	128	
DB	112	FAVGLRAANLETNVEELMVEVGGVRSRELNVTRQKIGEEAMFNPQMLIQTPQEDGTVILT	171	
QY	129	PEALGLHLOAALTASKQVSVLYGKSWDLNKICYKSVGLPILENGMIEMWTEKLPFPCVILNP	188	
DB	172	TEARLQHULDSALQSRVHVYMYNMQWLEKLYCHYKSELITEAGYMQDIIIEYLYPCLIIITP	231	
QY	189	LDCFMEGAKLQGGSAIYFGRPDIOQTMLDPLEQILLEELGPF--ASLGEFRELLDKAOGVQAY	247	
DB	232	LDCFMEGAKLQSGTAYLLGKPELQWINFDPLEFLEELKKINYQVESWEMLNKAIEVGHGY	291	
QY	248	VGRPCLIHPDDLHCPSPAPNHHISROAPNVAHELGGCHGFSHKPMHWQEBELLGGWMARDPQ	307	
DB	292	MDRPCLNPADEPDCITAPNKNSTKPLDVALVLSGGCYGLSRKYMHWQEBELLTGGTVKSS	351	
QY	308	CELLARAEALQSTFLMSPROLYEHRFG--DYOTHDIGWSEEQASTVLQANQRFRVQLAQEA	366	
DB	352	GKLVSQAQLQTMFQMLTPKQMYEHRFGYEVVSH--INWNEDKAAIIIEAWQRMVYEVVHQ	410	
QY	367	LPENASQIHAFSSTTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQGGSGV	426	
DB	411	VAQNSTQKVSFTTTTLLDLDILKSPSDVSIVRASGYLLMLAYACVTMLRWDCAKSQGAVG	470	
QY	427	LAGVLVVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVDFLLAHATEALPG--	484	
DB	471	LAGVLVVALSVAGSLGICSGISFNAAATQVLPFLALGVGVDDVDFLLAHAFSETQGNKR	530	
QY	485	TPLOERMGECHQRTGTSWLTSTNNMAAFUAAALVPIPALRAFSLOAAIVTGCSTFVAVML	544	
DB	531	IPFEDRTGECIKRTGASVALTSTNTVAFMAALIFIPALRAFSLOAAVVVFNFAVILL	590	
QY	545	VFPAILSLDLRRRHCBQBLDVLCCFSPCSAQVITQLPQELGD-----GTVPVGTIAH---	595	

[illegible]

RESULT 4
T30172

C;Species: Mus musculus (house mouse)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T30172
 R;Goodrich, L.V.; Johnson, R.L.; Milenkovic, L.; McMahon, J.A.; Scott, M.P.
 Genes Dev. 10, 301-312, 1996
 A;Title: Conservation of the hedgehog/patched signaling pathway from flies
 A;Reference number: Z20752; MUID:96176226; PMID:8595881
 A;Accession: T30172
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1434 <GO>
 A;Cross-references: UNIPROT:O61115; EMBL:U46155; NID:g1181884; PID:g1181885
 A;Experimental source: clone M2, M9
 C;Superfamily: Drosophila membrane protein patched

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Query Match      53.2%; Score 3337; DB 2; Length 1434;
Best Local Similarity 53.1%; Pred.No. 3.4e-223;
Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;

CY 3 RSPPLREL--PPYTPPTAAPQIAGSL---KAPLWLKRAYFGCLLFSLGCGIQRHCGK 57
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 28 RAAPDRDYLRHPSYC-DAAFALQISGKGATGKRAPLWLKAKFORLLFKLGICYTKNCGK 86

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QY 58 VLFGLLAFGALGLRMAIETNLEQLVVEGSRVSOELHYTKELGEEAAYTSOMLQ 117
Db 87 FLVVGILLIFGAVGLKAANTETNVEELWVEGGRVSRVETNROKIGEEAMFNQMLQ 146
QY 118 TAROGENILPEALGLHQAALTASKQVQSVLYGKSWDLNKICYKSGVPLIENGMEIWI 177
Db 147 TPKEGANVLTTEALQLHDLGALQSRVHVVMYNRQWKLEHLCYKSGBLITETGYMDQII 206
QY 178 EKLEPCVILTPIDCFWEKAGLQGGSAIYLPGRPDIOIWNLDPEQLLEELGPF-ASLEGPRE 236
Db 207 EYLXPCLIITPIDCFWEKAGLQSGTAYLLGKPEPLRWTFNFDPLFLEELCKINYQVDSWEE 266
QY 237 LLDKAOVGQAVGRPCILHCPSPAPNHHRSQAPNVAHLSGCGHGFSGHFKFWQEE 296
Db 267 MLNKAEGVGHYMDRPLCPADPCATAPNKNSTKPLDVALVINGCCQLSKRYMHWQEE 326
QY 297 LLLGGMARDPOCELLRAEALQSTFLMGPRQLYEYHFRG-DYOTHIDIGNSEEQASVLOAW 355
Db 327 LIVGTVKNATKLSNAHALQTMFQMTPKQMYEHRGYDYVSH-INWNEDRAAAILLAW 385
QY 356 QRRFYQLAQEALPENASQIHAFSSTLDDILHAFSEVSAARVWGYYLLMLAYCTMUR 415
Db 386 QRTYVEVHQSVAWPNSTOKVLPFTTTLLDILKSFSDSVIRVASGYLLMLAYACTMUR 445
QY 416 WDCASQSGVLGAVLLVALAVASGLGICALLGIFENATTOVLFPFALGIGVDDVFLLA 475
Db 446 WDCSKSQAGVLAGVLLVALSVAAAGLGLCSLIGSFNAATTOVLFPFALGIGVDDVFLLA 505
QY 476 HAFTEALPG--TPLOERMECELCRTGTSVULTSINNMAFLMAALVPPIPALRAFSLOAAI 533
Db 506 HAFSTGQNKRIIPFEDRTGECLKRTGASVALTISINVTAFMAALIPPIPALRAFSLOAAV 565
QY 534 VVGCTFVAVMLVFPAILSLDRLRRRCORLDVLCFSPSCSAQVQIQLPQELGD----- 586
Db 566 VVVENFAMVLLIFPAILSMVLRREDRLDIFCCFTSPCVSRVIOVEPQAYTEPHSNTRY 625
QY 587 GTVPVGIH-----LTATVQAFTHCEASSQHVTTILPQAHVLPVP-----SDPLGS 633
Db 626 SPPTPTYSHFAETHITMQSTVQLRTEYDPTHVYVYTAEPSEISVQFVTVTQNLSC 685
QY 634 ELFPGSGSRDLGLGEEETROKAAKSLPCAENLAHFAHYOFAPLILLSHAKAIVLVLF 693
Db 686 QSEPTSTRDLLSQFSDS--SLHCLPECTKTWTSSFAEKHYAPPELLPKAKVWVILF 743
QY 694 GALLGLSLYGATLVQDGLALTDVWRGTHKEHAPLSAQLRYFSLYEVALVTQGGFOYAHQ 753
Db 744 LGLGLSVLYGTVRVRDGLDLDIVPRETREYDFIAAQFKYFSGFYNNYIYVTKA-DYPNTQ 802
QY 754 RALFDLHORFSSIKAVLPPATCAPRTWLHYVYRNMLQGTQAAFDQDQWASGRITRHSYRG 813
Db 803 HLLYDLHKFSNVKYVLMENKQLPQWMLHYFRDLQGLQDADFSDWETGRIMPNYKNG 862
QY 814 SEDGALAYKLLIQTGDAQEPDLPFSQLTTRKLVDRGLIPPELFYMGTLVWVSSDPLGLAA 873
Db 863 SDGVLAYKLLVQTSRDRPDIISQLTKQLVDADGILNPSAFYIYLTAVSNDPVAYAA 922
QY 874 SQANFYPPPEMHLKDYDTGE-NURIPPAQPLEPAQFPFLRGLQKTDADFVEAIEGARA 932
Db 923 SQANTRPHRPEWHDKADYMPETRLIPAAEPIEYAQFPFYLNGRLDTSDFVEAIEKVRV 982
QY 933 ACAEAGQAGVHAPSSGFLWEQYGLRCFELIACVILLVCTFLCALLELNPWTAGLI 992
Db 983 ICNNYTSGLSSYPNGYFLFWEQYISLRHWLLSISVVLACTFLVCAVELNPNWTAGII 1042
QY 993 VLVAMMTVELFGIMGFLGILKLSAIPWVILVASVGIGVEFTVHVALGFLTTOGSRNLRAA 1052
Db 1043 VMVALMTVELGMMGLIGLKSAPVFPVILIASVGIGVEFTVHVALAFLTAIGDKNHRAM 1102
QY 1053 HALEHTFAPVTDGAI STLGLMLAGSHFPFIVRYFFAALTVTTLGLHLGLVLLPVLLS 1112
Db 1103 LALEHMFAPVLDGAVSTLLGVMLAGSEFDFIVRYFFAVAILTILVLGVLNGLVLLPVLLS 1162
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QY 1113 ILGPPEVI-----QMYKESPEILSP-----APQGGGLRWGASSSLPQSFARVTT-- 1159
Db 1163 FFGCPPEVSPANGLNRJLTPSPE--PPSVVRFAVPPGHTNNGSDSSDEYSSQITVSGI 1220
QY 1160 -----MTVAIHPPPLPGAYTHP-APDEPPWSPAA---TSSGMLS 1194
Db 1221 SEELRQYEAQQAGGPAHQVIVEATENPVFASTVWHPDSRHRQPLTPRQOFLHDSGSL 1280
QY 1195 SRPG 1199
Db 1281 ---PG 1282

RESULT 5
S06119
membrane protein patched - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: S06119; A33468
R:Nakano, Y.; Guerrero, I.; Hidalgo, A.; Taylor, A.; Whittle, J.R.S.; Ingham, P.W.
Nature 341, 508-513, 1989
A:Title: A protein with several possible membrane-spanning domains encoded by the Drosop
A:Reference number: S06119; MUID:90015164; PMID:2797178
A:Accession: S06119
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1299 <NAK>
A:Cross-references: UNIPROT:P18502; GB:X17558; NID:g8389; PIDN:CAA35591.1; PID:g8390
R:Hooper, J.E.; Scott, M.P.
Cell 59, 751-765, 1989
A:Title: The Drosophila patched gene encodes a putative membrane protein required for se
A:Reference number: A33468; MUID:90058658; PMID:2582494
A:Accession: A33468
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-110,'R',112-273,'G',275-331,'R',333-635,'P',637-861,'DVF',878,'Y',890-1299
A:Cross-references: GB:M28418; GB:M28999; NID:g552097; PID:g552099
C:Genetics:
A:Gene: FlyBase:ptc
A:Cross-references: FlyBase:FBgn0003892
A:Map position: 2 44D3-D4
C:Superfamily: Drosophila membrane protein patched
C:Keywords: glycoprotein; transmembrane protein
F:74-92/Domain: transmembrane #status predicted <TM01>
F:427-448/Domain: transmembrane #status predicted <TM02>
F:456-503/Domain: transmembrane #status predicted <TM03>
F:529-555/Domain: transmembrane #status predicted <TM04>
F:557-585/Domain: transmembrane #status predicted <TM05>
F:677-699/Domain: transmembrane #status predicted <TM06>
F:967-1017/Domain: transmembrane #status predicted <TM07>
F:1019-1047/Domain: transmembrane #status predicted <TM08>
F:1061-1086/Domain: transmembrane #status predicted <TM09>
F:1093-1121/Domain: transmembrane #status predicted <TM10>
F:142,298,335,388,807,861,1194,1271/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 31.3%; Score 1961.5; DB 1; Length 1299;
Best Local Similarity 37.0%; Pred. No. 9.3e-128;
Matches 429; Conservative 225; Mismatches 412; Indels 93; Gaps 21;
QY 18 ARTAAPQILAGSL---KAPLWLRVYQGLLFLSLGGCIQRHCKVLFLGLLAFGALALGR 74
Db 34 AQVALDQIDKGARGSRTAIYLRVFSQSHLETGLGSSVQKHAGKVLVAILVLSTFCVGLK 93
QY 75 MAILTNEQLVVEGSRVSOELHYTKELGEEAAYTSOMLIQTARQEGENILTPREALGL 134
Db 94 SAQIHSKHVQLMIQEGGGLAEALAYTQKTIGDEGATHQLLIQTTHDPNASVLHPALLA 153
QY 135 HLAALTASKQVQSVLYGKSWDLNKICYKSGVPLIEN-GMIEMIEKLFPCVILTPDPCFW 193
Db 154 HLEVLVKATAVKLVHLYDTEWGLRDMCNMPSSTPSFEGIYVIEQILRELIPCSIITPLDCFW 213
QY 194 EGAKLQG--GSAYLPG-RPDIQWNLDP-----EQLEELGPFALEGFRELLDKAQ 242
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Db 214 EGSQLLGPESAVVPCINQLRLWTLINPASVMQYMKQKMBEEKISF-DFETVEQYMKRAA 272

QY 243 VQAYVGRCLHPDDLHCPSPAPNHSRQAPNVVAHELSGGCHGFSKFMHWOEILLGQM 302

Db 273 TASGWEKPCLNPNCPDTPAKNKTSTPPDVGAILSGGCYGYAAKMHWPFEELIVGGA 332

QY 303 ARDPQELRLAEALSTFLLMSPROLYEHFRGDYDTHDVGWSEBOASTVLQAWORRFVOL 362

Db 333 KNRSGHLRKAQALQSVQLMTEKEMYQDQYKVVHGLGTQEKAAEVLNWAQRNFSRE 392

QY 363 AQEALPENAAAA--SQIHAFSSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRW-D 417

Db 393 VBQLLRKOSRIATNYDIYVFSSAALDDILAKESHPALSIVIGVAVTVLYAFCTLLWRD 452

QY 418 CAQSGSVGLAGVILVALAVASSGLGALLGTENAAATVQLPFLALGIVGDDVFLAHA 477

Db 453 FVRGSSVGVAGVLLMCFSTAGLGLSALLGIVFNAASTQVVPFLALGIVGDDHIFMLTAA 512

QY 478 FTEALPGTLPQRMGECIQRTGTSTVLTSSINMAAFMAALVPIPALRAFSLOAAIVGVC 537

Db 513 YAE-----SNRQETKLLKKGPSILFSACSTAGSFFAAAFIPVPAKVCLOAAIWMCS 568

QY 538 TFVAVMLVFPALSLDLRRRHQRDLVLCFSSPCSAQ---VQILPQELGDTVPVGTA 594

Db 569 NLAAALLVFPAMISLDLRRRTAGRADIFCCCPVWKEQPKVAPPVPLNNNG----- 621

QY 595 HLTATVQAFTHCEASSQHVVTILPQAHLVPPSPDLGSELSPGSGSTRDLGQBEETRQ 654

Db 622 -----RGARHPKSCNNRVAL-----PAQNPLEQRADIPGSSHSL----- 657

QY 655 KAAKSLPCARWLAHAFARYOFAPLLQSHAKAIVLVLFGLLGLSYGATLVQDGLALT 714

Db 658 -----ASFSLATFAFYHTPLMRSWKFLTWGFLAALISLYASTRLQGLDII 708

QY 715 DVVRGTKEHAFSLAQRYFSLYEVALVTQGFYAHSQRALFDLHQRFSSIKAVLPPPA 774

Db 709 DLVPKDSNEHKFLDAQTRLFQFYSYAVTQGNFEYPTQQLRDYHDSFVRVPHVIXNDN 768

QY 775 TQAPRTWLYHYNNMLOGTQAFDQDQWASGRITRHS-YNGSEDGALAYKLLIQTGDAQEP 833

Db 769 GGLPDLFWLLLFSEMLGNLQKIFDEYRGRITKECFWENASSDAILAYKLIQVTHGVNDP 828

QY 834 LDFSQLTRKLVDRGELIPPELFYVGLTVWV--SSDPLGL-----AASQANFYP 880

Db 829 VDKEVLVTLNRLVNSDGIINQAFYNLSAWATNASSPTELIRANCIRNANGASQKLYP 888

QY 881 PPPWLH--DKYDTGGENLRIPPAQLEFAQFPFLRLGLQKTADFVEAIEGARAAACBAG 938

Db 889 EPROYFHQNEYD-----LKIPKSLPLVYAQMPFYLHGLTDTQIKTLIGHIRDLVSKYE 943

QY 939 QAGVHAYPGSPPLFWEOYGLRRCF-LLAVALIVCTFLVCALLINPWTAGLIVLVA 997

Db 944 GFGLPNVPSPGPFIFWEQYMLRSLAMLACVILLALV-LV-SLLLSVMAAVLVLSVL 1002

QY 998 MMTVELFCIMGFLGKLSAIPWVILVASVGVIBFTVHVHVLGFLTTQGSRLRAAHLEH 1057

Db 1003 ASLAQIFGAMTLLGKLSAIPAVILLSVGMMLCFNVLSIGFTSVGNRRVQLSNQM 1062

QY 1058 TFAPVTGATSLTGLMLAGSHDFIVRYFAALTVLTLGLHLGLVLLPVLVLSILGPP 1117

Db 1063 SLGLPVLHGLTSGVAVFMLSTSPFEFVIRHFCWLLLVLCVGCACNSLLVPFILLSMVGE 1122

QY 1118 PEVLQMYKESPEILSPAP 1136

Db 1123 AELVPL--EHPDRISTPSP 1139

RESULT 6

T27969

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27969

R.Sims, M.
submitted to the EMBL Data Library, November 1994
A:Reference number: Z20448
A:Accession: T27969
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1405 <WIL>
A:Cross-references: UNIPROT:O09614; EMBL:Z46812; PIDN:CAA86843.1; GSPDB:GN00020; CESP:ZK
A:Experimental source: clone ZK675
C:Genetics:
A:Gene: CESP:ZK675.1
A:Map position: 2
A:Introns: 31/3; 59/3; 100/3; 244/2; 485/1; 950/2; 1298/2; 1335/3
C:Superfamily: Drosophila membrane protein patched

Query Match 27.2%; Score 1708.5; DB 2; Length 1405;
Best Local Similarity 31.5%; Pred. No. 3.8e-110;
Matches 433; Conservative 203; Mismatches 440; Indels 299; Gaps 31;

QY 34 LWRAYFGCLLPSLGGCQIRHCGKVFGLGLAFGALGLRMAIETNLQLVWVSGSRV 93

Db 110 LYSRLIQKLLFALGNTVHRNAWSIILAVSMIFAVCCYGLQVYHETDVKLVWAQGGRL 169

QY 94 SOELHY---TKEKL-----GEEAAYTS-----OMLIQTARQGENILTPALGLHLQ 137

Db 170 DEELNLFNIIKEAMNVTGDSGPPELFRENGGLGGYQVLIQTPEYEGDALAAGPLLKHEV 229

QY 138 AALTASKVQVSLYKSWDLNKICVKGVPFI-----ENGMIEMWIKLPCCPVTILTPDCFW 193

Db 230 IMKHIAFNVSVHGVDSLSLDCFKPAPPSVAADSAASGLGVIDKIVPCITWITIDCFW 289

QY 194 EGAKLQGGSAVLP-----GRPIQWNTLDPEQLLEELGPFASLEGFREL 238

Db 290 EGSKALGPHPLPKSSSLGPLGMLSSLSDDGMIRWSDFDPIAVIDEIHRSFNLSGHTFF 349

QY 239 DKAQVQAYVGRPCPLHDPDLHCPSPAPNH----- 267

Db 350 ERAGVSHGYMDRPCIDPLDPECPWMAKNFYDVCPHIDRVRIAKKYGTELEEEKKDSGY 409

QY 268 -----HSRQA---PNVAH----- 277

Db 410 SFFDFLGRKKEAGDQPKMIHPAQADSIPTIEDAVPAQVPVSTAPIPTTTTILSPPEARA 469

QY 278 ----- 285

Db 470 AEEKEKKQARELKDYCKSYKSAFEMLKKNKDKWPEVMSNNYPQNVDAEMTGGCG 529

QY 286 FSHKFMHWEELLGGMARDPQ-CELLRAEALQSTFLLMSPRLYEHP-----RGDIYOTH 339

Db 530 FASNVLWNPEDMILGNPRRAKKGKLSGADALQSVFLVSPADVFLPKQKPGRNSMKTG 589

QY 340 -DI-GWSEEQASTVLQAWRRFVQ-----LAQEALPENASQOIHAFASTTLDLIIHAFSE 392

Db 590 LMDAMNETAAEQVLQAWQRNFTKSLYNHKNANVEDDGNERTLHPLASTSIADMLEFECQ 649

QY 393 VSAARVVGYYLLMAYACVTMLRW-----CAQSGSVGLAGVLLVALVASGLGALLG 448

Db 650 FNYTIILAGVLMAYAIQVQARFNDCLPATSSMGLALAGLVVTVFASVAGLGLATWFG 709

QY 449 ITENAAATVQVLPFLALGIVGDDVFLAHATEALPGTFLQRMCECLORTGTSVVLTSIN 508

Db 710 IEFNAATQIVPFLTIGIVNDPMFLHNRDVVKLAGHAEMLMRETGMTSILTSIN 769

QY 509 NMAAFMAALVPIPALRAFSLOAAIVVGCITFVAVMLVFPALSLDLRRRHQRDLVLCCE 568

Db 770 NILSFLTGTLPIPALRSFCAQSILLTFNFIALITYPAISIDLRKKAQRDLVCCCL 829

QY 569 SSPCSAQVIOILPQELGDTVPVGIAHLTATVQAFTHCEASSQHVVTILPQAHLVPPPS 628

Db 830 -----YGD-----TREESYS-----MISKPK 845

QY 629 DPLGSELSPGSGSTRDLGQBEETRQKACKSILPCARWLAHAFARYOFAPLLQSHAKAI 688

Db 354 IIPFSLAFITVCSGLVQVTTNPVELMSAPHSQARLEKEYFDKHF--PPFRTQLII 411
QY 118 TARQEGENILTEALG-----LHLOALTASKVOVSLYKSWDLNKTIC 160
Db 412 QAPNTSVHIYEPYAGADVFPGLPNKEILHQLVNLQIAI--ESITASYNNETVTLQDIC 469
QY 161 YKSGVPLIENGMEIWMIEKLPFCVILTPLDCEWAGAKLOGGAYLPGRPDIQWNTLNDPEQ 220
Db 470 VAPLSFYNNK-----CTMSVLYNF-----QNSHVAL----- 496
QY 221 LLEELGPPASLEGFRELDDKAQVQYVGRPCLLHPDDLHC--PPSAPNHSRQAPNVAHE 278
Db 497 -----DSQGGDDFYIYADVHTFLYCVRAPASLNDTSL----- 529
QY 279 LSGGCHG-FSHKFMHQBELLLGGWARDPOGELLRAELQSLFLLMSPOLYEHFRGDVQ 337
Db 530 LHGPCLCGTFGGVPFW--LVJGGY--DDQ--NYYNATALVITFPV-----NYYNDTE 576
QY 338 THDIGWSEEQASTVLQAMORRVQLAQEALPENASQOIHAFSSTLDDILHAFSEVSAAR 397
Db 577 RLQRAW-----ANEKEFISFVKVY--KNPNLTISFTAESIEDELNRESNDVPT 624
QY 398 VVGGLMLAY-----ACVTMLRWDCAOSQSGVGLAGVLLVALAVASGLGLCALIG 448
Db 625 VLIISYVVMFLYISLALGHITQSCRLL-----VDSKISLGIAGILIVLSSVACSLGIFSYMG 680
QY 449 ITFNAATTQVLPFLALGIGVDVDFLLAHAF--TEALPGTFLQERNGECLQRTGTSVVLTS 506
Db 681 MPLTLIVIEVLPFLVLAGVDNIFILVQTYQDERLQEBETLDDQQLGRILGEVAPTFWFLSS 740
QY 507 INNMAAFIPALVPIPALRAFSLQAAIVVCGTCFVAVMLVFPAILSLDLRRHRCQLDLVLC 566
Db 741 FSETSAFFGALSSNPVHTSLFAGMVLIDFLQITCFVSLGLDGRKQKNHLDILC 800
QY 567 CFSPSCSAQVIOILPQELGDTGVPVGVIAHLTATVQAFTHCEASSQHVVTILPPQAHLVPP 626
Db 801 C-----VRGADDGQGS-----HASESY----- 817
QY 627 PSDPLGSELFPFGSGTRDLLGQEEBETROKAAACKSLPCARWNLAHFARYQPAPLLLOSNAK 686
Db 818 -----LRFREKNYFAPLKLKDWLR 836
QY 687 AIVLVFGALLGLSLYGATLVQDGLALTDVVPRGTGKEHAFSLAQURLYFSLY-----EVAL 741
Db 837 PIWAVFVGLVSFAVNVKVDIIGLQSLSP-----NDSYVIANFKSLAQVLHSGPPVYF 892
QY 742 VTQGGFYA--HSQALFD-----LHQRFSLSKAVLPPPPATQAPRTWLHYRNWLQ 790
Db 893 VLEEGYNSRKGQNMVCGMGCONDSLVOQIFNAAEELDTVTVGVFAPSSMIDDYFDWVS 952
QY 791 GIQAADFQDMSAGRI--TRHSYRNGSEDGALAYKLLIQTGDAQEPDLPSQLTTRKLVDRE 848
Db 953 PQSSCC-----RLYNVTHQFCNAS-----VMDPTCVRCRPLTP-E 986
QY 849 GLIPPE--LFTVGLTVMVSSDPLGLAASQANFYPPPPPEWLHDXY-----DTTGENLRIPPA 902
Db 987 GKQEPQGEKFKLPMFLSDNP-----NPKCGKGHAAVGSANVIGDITYIGAT 1036
QY 903 QPLEFAQFPFLRLGLQKTADVEAIEGARACABAGQ-----AGVHAYPSGSPFLFEWQ 956
Db 1037 YFMTYHTI-----LKTSDADYDAMKARLIASNITETMRSGSDYRVFPYSVFVVFYEQ 1090
QY 957 YLGRRCFLLAVALCILLVCTELVACALL--LNPWTAGLVVLVLAAMTVLFGIMFLGKLS 1015
Db 1091 YLTIIDDTFNLVSLGSIIFLTVLVGLCELMASAVIMCITAMILVNMFGVMWMLWGISLN 1150
QY 1016 AIPVVILVASVIGVGVTHVVALGF-LTQGSRLNRAHAHLHTFAPVTDCAITLL-GL 1073
Db 1151 AVSLVNLVMSGSISEVFCSHITRAFTMTSGSRVSRABEALAHMGSVFSGITLTKFGGI 1210
QY 1074 LMLAGSHDFIVRYFFFAALTVTLGLLGHGLVLLFVLLSILGP 1116
Db 1211 VVLAFAKSQIFEIYFRMYLAMVLLGATHGLIFLFPVLLSYIGP 1253

RESULT 9

T05663

Hypothetical protein F22I13.120 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05663

R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420

A:Accession: T05663

A:Molecule type: DNA

A:Residues: 1-1055 <BEV>

A:Cross-references: UNIPROT:Q9SVF0; EMBL:AL035539

A:Experimental source: cultivar Columbia; BAC clone F22I13

C:Genetics:

A:Map position: 4

A:Introns: 24/3; 60/3; 99/3; 150/1; 193/1; 216/3; 278/3; 297/2; 336/3; 364/3; 396/3; 419/026/3

A:Note: F22I13.120

Query Match

Best Local Similarity 8.2%; Score 514; DB 2; Length 1055;

Matches 238; Conservative 137; Mismatches 328; Indels 424; Gaps 35;

QY	36	LRAYPQGLLFSLGGCIQRHCGKVLFLGLLAFGALGALGRMAITETNLEQLWVEVGSRSVQ	95
Db	288	VQRYMAKFRSVSGSWIARNPSILVFMVAIVLALCSGLYNFKVETRPKLVGPESKAAE	347
QY	96	ELHYTEKLGEEAAYTSQMLTQTARQE-----GENILTEALGLHLQAALTASKVQVSLY	150
Db	348	EKKFPDTHL--SPFYRIEQLLILATVPDKSGRAPSVITDENIL-----	389
QY	151	GKSWDLNLCYK-----SGVPLIENGMIENMIEKLPFCVILTPLDCFWEGAKLOGG	201
Db	390	--LFDIQKYFMDSGTDFDYGGVEHAECYQHYTSSETCLSAFOAPVD--PSAVLGGF	444
QY	202	SAYLPGRPDIOWTNDLPEQLLEELGFPASLEGFRELDDKAQVQYVGRPCLLHPDDLHCP	261
Db	445	SG-----NNYSEVMVSELG-----CSVPD-----	464
QY	262	PSAPNHSRQAPNVNAHELSGGCHGFHKFMHQBELLLGGWARDPOGELLRAELQSTFL	321
Db	465	-----CYS-----DVKRTLFQATAFVVTYP	484
QY	322	LMSPRQLYHEPRGDYQTHDIGWSEEQASTVLQAMORRVQLA-CEALPENASQOIH-AFS	379
Db	485	V-----NNVIGDS-----SNENARAV--AWEKSFQLAKBELLPMVRSKNLSUSFS	528
QY	380	S-TTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ-----SOGSVGLAGVL	431
Db	529	SESSIEBELKRESTDVITTAASVLMFVYISVTL--GDAPQFYTFYISSKVLGLSGVV	586
QY	432	LVALAVASGLGLCALLGITFNAATQVLPFLALGIGVDVDFLLAHAFTEALPGTFLQERM	491
Db	587	LVLVSLVLSGVGVFSLGKSTLIIMEVIFPLVAVGVDNMCIILVHAKROPREVSLQRI	646
QY	492	GECLQRTGTSVLTSLINNMAAFMAALVPIPALRAFSLQAAIVVCGTCFVAVMLVFPALLS	551
Db	647	SSALVEVGPSITLASLSEVLAFAVGAVPMPFACRFISMFAALIMLDFFLQITAFVALIV	706
QY	552	LDLRRHRCQBLDVLCCFSSPCSAQVIQILPQELGDDGTVPVGVIAHLTATVQAFTHCEASSQ	611
Db	707	FDCKRSADNRIDCFPCIKVFPSS-----RESVEG-----	735
QY	612	HVVTILPPQAHLVPPSDPLGSELFPFGSGTRDLLGQEEBETROKAAACKSLPCARWNLAHF	671
Db	736	-----GRE-----PG-----FLERY	745
QY	672	ARYQFAPLLAQSHAKAIVLVFLGALLGLSLYGATLVQDGLALTDVPRGTGKEHAFSLAQ	731
Db	746	MKEVHAPVLGLMGVGMVVAVVFA-----FALASIIISRASQ-----	781

QY 732 RYFSLYEVALVTGGFDYAHQSORALFDLHQRFSSLKAVLPBPATCAPRTWLHYRNWLOG 791
DB 782 -----ASDTSYIAKPAA-----SWLD- 797
QY 792 IQAAPDQDASGRITRHSYRNGSEGDALAYKLLIQTGAQBPDFSQLTTRKLVDRGLI 851
DB 798 -----DF----- 799
QY 852 PPELFYMGITVWSSDPLGLAASQAN-FYPPPPPEWLHKYDTGTGNLRIPPAQPLEFAQF 910
DB 800 -----LWLSPEAFGCCRKFTNGSYCPDDQCFRHSDLVQD--RPTAQPRE--KL 846
QY 911 PPLRLGLQKTADFEA-----IEGARACAEAGQ-----AGWAYSGSPFF 951
DB 847 PWFNLAL-PSADCAKGGHGYATNSVDLKGYESGVQASEFRTHYHTPLNTQIDIFFYSVFY 905
QY 952 LFWEQYGLRRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMGFLG 1011
DB 906 IFFEQY-----LNWTVALTNLATAI-----VG 928
QY 1012 IKLSAIPVILVASGIGVEFVHVVALGFLTTQGSRNLRRAHALEHTFAPVTDG-AISTL 1070
DB 929 IQLNAVSVVNLIMSGIAVEFCVHTSHAFMLSSGDRHREAREALETMGASVFGITLTKL 988
QY 1071 LGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLSILGPP 1117
DB 989 VGVIVLCFARSEIFVYVYFQMYLALVIGFLHGLVFLPVILSLAGPP 1035

RESULT 10
T21612
Hypothetical protein F31F6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21612
R:Percy, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19449
A:Accession: T21612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-955 <WIL>
A:Cross-references: UNIPROT:Q19945; EMBL:Z69884; PIDN:CAA93751.1; GSPDB:GN00028; CESP:F31F6
A:Experimental source: clone F31F6
C:Genetics:
A:Gene: CESP:F31F6.5
A:Map position: X
A:Introns: 64/2; 141/3; 255/3; 308/1; 409/1; 435/3; 484/2; 579/1; 632/2; 715/3; 777/3; 8

Query Match 7.4%; Score 465.5; DB 2; Length 955;
Best Local Similarity 21.2%; Pred. No. 4.5e-24;
Matches 230; Conservative 176; Mismatches 414; Indels 267; Gaps 45;

QY 166 PLIENGMIW-----MIKLF-----PCVILTPLDCEWE 194
DB 8 PLVRNA-FEWYGPVVRWVWFCEISPLFLTLACSVGFRTMELRVDDPSVYVTPSDAM- 65
QY 195 GAKLOGGSAYLPGRPDIOWTN-----LDPEQLLEELGPFASLEG--FRELLDKAQVQAVY 248
DB 66 -----RREISVFENWVPLDENKFL-----PGKSFEAKRFVNVILIRAKDGGSIM 108
QY 249 GRPCLH-----PDDLH-----CPPSAPHNH-----SRQA 272
DB 109 RDNVLHEILNQWIMNNTSIPTDDLKFNLTVDCLCLSYDWC---GANEHTQMLRRND 165
QY 273 ENVAHEL---SGCGHGFHKFMHWQBELLLIGMARDPQ---GELLRAEALQSTFLMSP 325
DB 166 VNQILDHFRGGTK-----DTPVYLGIGFDGVQFPNGTLDSDAKLTQLFYELKQD 216
QY 326 ROLYEHFRGDYQTHIGWEEQASTVLQAWQRFVQLAQBALPENASQOIHAFSSTLDD 385
DB 217 QKMVEEYSSKFSVALETFLNQVYSSDVITLSFAHYQSLEDGLDENAK---AF-----VFN 268

QY 386 ILHAFSEVSAARVYGGYLLMLAYACVTMLRWDCAQSGSVGLAGVLLVALAVASGLGCA 445
DB 269 FVVSFFVLMYALVSSFTLKSSA--TKIDW--ISSKEWLAAGMFSIVLSIISAFGLF 324
QY 446 LLGITFNAATQVLFPFLALG-----IGVDDVFLLAHAATEALPGTFLQER 490
DB 325 ILGVRYNVINT-IIPFLIIGEFQSKWMEKQIIPAIGIDDMFLMNACWDQTSKLSVPER 383
QY 491 MGECLQRTGTSVLTSTINMAAFMAALVPALRAFSLQAAIVGCTFVAVMLVFPAIL 550
DB 384 MSKTLSHAGVAVTITNVDVMSFAIGCTIDPGIQCFCIYACSVAFSYFYQLTFFSGAM 443
QY 551 SL-----DLRRHC-----ORLDVLCFSSPCSAQVQIILPQELGDGTPVPGIAHLTAT 599
DB 444 AIMGEVEREKHCHLFFYRTFOVDI-----SKMNEEADSKLQIKSRASAPFNYLSS 498
QY 600 VQAFTHCEASSQHVVTILPQOAHVPPSPDPLGSELPSPGGSTRDLLQOEBETROKACK 659
DB 499 NSSFSDSDSFSSKXTI-----PAEPAWKEQSQSPNS--LSKKSXDRE----- 540
QY 660 SLPCARNWLAHFARYQFAPALLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVR 719
DB 541 -----KDRIVHFHIGKIYGPFFILSNVRIFSGLIFVVIATAIWYGCYNFREGLNPNLV-- 593
QY 720 GTKEHAFLSAQLRYFSLYEVALVTGGFDYAHQSORALFDLHQRFSSLKAVLPBPATCAPR 779
DB 594 -TNDHYI-----AKYFS-----DIKHFWEIGALH-----VAVLNP-----PN 625
QY 780 TWLHYRNWLOGIQAAFPQ-DWASGRITRHSYRNGSEGDALAYKLLIQTGAQBPDFSQ 838
DB 626 LTISENRNELLKVSASFENTQVTLGR-----EGTVPFLL-----EYLVLS 666
QY 839 LTRKLVDRGLIPPEL-----FYWGLTVWYSS-----DPLGLAASQANFYPPPP 883
DB 667 ELNAEVEDTERLWKTKLNSWLKYTCGSTQWASNLKINKITDGSQFAFRFOIAUKNFVEP-- 724
QY 884 EWLHDKYDTGTGNLR-IPPAQPLEFAQFPFLRLGLQKTA-DFVEAIEGARACAEAGQAG 941
DB 725 -----NDHKHAQALLRDIADHQFPNVVHVHVSFGNRKILNDFISS-----HSCYAQKNIP 775
QY 942 VHAYPSGSPFLFWEQYGLRRCFLLAACILLVCTFLVCALLLNPNWTAGLIVLV-LAMMT 1000
DB 776 KLAFF-----FADQVLIILPATIQNVVISLILC-MAVVSFLLVPSLPSCGFVFVSIVSN 828
QY 1001 VELFGIMGFLGKLKLSAIPVILVASGIGVEFVHVVALGFLTTQGSRNLRRAHALEHTFA 1060
DB 829 IGVFGYMTLWGVNLDVAVSMISIIIMSGFAVDLSAHTIYAFVTSHGDTKORVIGALETLGW 888
QY 1061 PVTGCAISTLLGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLSILGSPPEV 1120
DB 889 PIFQASSTIAGISILY-TVDAYIILVFPKTIWLTWLTWLTWLTWLTWLTWLTWLTWLTW 945
QY 1121 IQMYKES 1127
DB 946 FRIPKSS 952

RESULT 11
T25600
Hypothetical protein C32E8.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25600
R:Gatung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid C32E8.
A:Reference number: Z20056
A:Accession: T25600
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-933 <GAT>
A:Cross-references: UNIPROT:P91129; EMBL:U88308; PIDN:AAB42325.1; GSPDB:GN00019; CESP:C3

A:Experimental source: strain Bristol N2; clone C32E8

C:Genetics:

A:Gene: CESP:C32E8.8

A:Map position: 1

A:Introns: 145/1; 177/2; 385/1; 418/3; 833/3; 878/3

```
Query Match          7.1%; Score 444; DB 2; Length 933;
Best Local Similarity 21.4%; Pred. No. 1.4e-22;
Matches 217; Conservative 170; Mismatches 398; Indels 228; Gaps 37;

QY 204 YLPGRP-----DIQWNL--DPQLLEELGPPASLEGFRELIDKAQV---GOAYVGRP-C 252
DB 81 YIPGRAVTSQREITQVLTALAENDSNILDPKFANAVQLDKYIOTRVLHNGHYYSYKNL 140

QY 253 LHDDDLHCPSPAPNHSRQAPNAHLSGCGCF--SHKFMWQEBLLGGHWARDPQGL 310
DB 141 LQYKNGGCSNKHVHLSLHN-----HGFNITYPYFRFGSE---GGYIGSSLGV 188

QY 311 LRABALQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRVQLAQEALPEN 370
DB 189 TWKMGNETDILASAKAM-----FMVHLKXHPHPEMSYISGEWELELGRMLTQ-YPED 240

QY 371 ASQIHAFSTTLLDILHAFSEVSAARVVGGLMLAYACVTMLRW-----DCAQSOG 423
DB 241 PYISITYFHSQTLADELKENADTLIPRFIISITLLIVFSTLCSLFDGFSIDWLSKP 300

QY 424 SVGLAGVLLVALAVASGLGLCALGTITENNAATQVLPALGIGVDDVPELLAHAFTEALP 483
DB 301 ILSILGVMSAGAILUTGVFLSMGPYN-DIVGNPFVLVAVGVDNFMELMAVAVRRTSR 359

QY 484 GTPLOERMECEQRTGTSVVLTSINMAAFMAALVPALRAFSLQAAIVVGCTFVAMV 543
DB 360 THTVHERMGECLADAASVILITSDVLSFGVGAITTPAVGICVYTGVAIFPAFIYQI 419

QY 544 LVFPALSLDLRRRCORLDVLCFSSPCSAQVQILPOELGD-GTVPGVIAHLTATVQA 602
DB 420 TFFAACALAMKHEASGRNSLFLI EAVSAEKKTSLSLTFQFLNLSVP-----467

QY 603 FTHCASSOHVVTILPPQAHVLPPSPDPLGSELPFGSGSTRDLLQEBETROKAAKSLP 662
DB 468 ----DHSASHV-----KQPLTSRFF-----484

QY 663 CARWNLAFARYQFAPLLQSHAKAIVLVFGA-LLGLSLYGATLVQDGLALTDVVRGT 721
DB 485 -GEW-----YAPVLMHPVVRGIAWVFIYLLGAS-YGCSRIKGLGEPNVLVDS 533

QY 722 KEHAFSLQALYFSLY--EVALVTGGDFDYAHSQRALFDLHQRFSSLKAVLPPPPATQAPR 779
DB 534 YAIPIHYRLLEKRYFKYGOQVQIVINNAPDLRN-----HTRDRVHAMVLDPATSKHA 585

QY 780 TWLHYRNWLQGIQAAFPQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQ 839
DB 586 IGMESVQFWLFEMERYOKELEVQIIDSSFY-----GLLHHFLASKT-----627

QY 840 TTRKLVDREGLIPPELFYMTGLTWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRI 899
DB 628 -----NNPL-----AEDIYWGMPD-----DDNGTWVK- 650

QY 900 PPAQPLEFAQPFLL--RGLQKTADFVAISGARAACAAGVHAYPSGSP-FLWEQ 956
DB 651 -----SFRILGMKDLVTTMDQTDATMSFEVAARWPEFNVTTF---MPIWMFTDQ 698

QY 957 YLGRRCFLLAVCTLLVCTFLVCAILLNP-----WTAGLIVLVLAMMTVELFGIMGLF-- 1010
DB 699 YIIIPNTVQNIITALLVMIVIAVLFPQPMCSLWVA-----LACASID-FGVIGYMTL 751

QY 1011 -GIKLSAIPVVILVASVIGVEFTVHVALGELTT--QGSRNLRAAHALEHTFAPYTDGAIS 1068
DB 752 WGVNLDALSMITITMSIGFSDYSAHAYGVVSRDTAAGRVEALSGALNPLSQGMS 811

QY 1069 TLLGLLMLAGSHDFIVRYFAALTUTLGLLHGLVLLPVLISL-----GP 1116
DB 812 TIIAVSLADIAPYMIWT-FEKTWVLSISLGLHGLVFLPVLISIFVRCGCIIPSSPHG 870
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QY 1117 PPEV-----TQMYKESPEILSPAPQGGGLRWGASSSLPQSFARVTTMTV 1162
DB 871 PSAQKIEKQIRIAAISSSPLDLRTVAP-----LRASSPIGFPHRLEVTDESPTV 919
```

RESULT 12

T26746

hypothetical protein Y39A1B.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26746

R:Wall, M.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z20258

A:Accession: T26746

A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: DNA

A:Residues: 1-1003 <WIL>

A:Cross-references: UNIPROT:Q9XXR9; EMBL:AL021482; PIDN:CAA16339.1; GSPDB:GN00021; CESP:

A:Experimental source: clone Y39A1B

C:Genetics:

A:Gene: CESP:Y39A1B.2

A:Map position: 3

A:Introns: 89/2; 126/3; 167/2; 194/2; 232/1; 266/3; 295/2; 323/2; 363/1; 519/3; 696/3; 7

Query Match

Best Local Similarity 21.6%; Pred. No. 1.5e-22;

Matches 214; Conservative 131; Mismatches 333; Indels 312; Gaps 34;

QY 285 GFSHKFMWQEBLLGGHWARDPQGLLRABALQSTFLMSPRQLYEHFRGDYQTHDIGMS 344

DB 214 GNTH-----LLGGVTLDDDKRIAGAKAMLLPYALR-----HSSDDEW- 251

QY 345 BEQASTVLQAWORRVQLAQEALPENASQOIHAFSTTLLDILHAFSEVSAARVVGGLL 404

DB 252 -----VAEKWE--VRLA-DFLQYDSPIIRA-SWYTIETLA---AESARDRLQLIHML 297

QY 405 MLAYACVTMLRWDC-----QSQSGVGLAGVLLVALAVASGLGLCALGTITFNATQV 458

DB 298 LPCFVCVSIFTIACCCVFSWRSPWLAIGGVISAAMAIASAVGILLAGVMTSVAYS- 356

QY 459 LPFLALGIGVDDVLLAHAFTEALPGTPOERMCEIQTGTSTVVLTSINMAAFMAAL 518

DB 357 MEFTVFSVGVNDVFIILSAMRSTSTETLEHRMKEETADAASVITVSLTDLISFGVCA 416

QY 519 VPIPALRAFSLQAAIVGCTFVAVMLVFPALISLDLR-----RHCORLDVLCFSSPCSA 574

DB 417 TPFVSQVQFCAVAAVIFTIYIQTFFAAVVMVTNRREINNRHC-----461

QY 575 QVIQILPOELGDTVPVVGIAHLTATVOAFTHCEASSQHVVVTILPPQAHVLPSPDPLGSE 634

DB 462 ----IFFHKLKDDTLPEKIA-----477

QY 635 LFSFGSTRDLLGQEBETROKAAKSLPCARWNLAHFARYQFAPLLQSHAKAIVLVLF 694

DB 478 -----AQGDRSFENNTI-----LAQFFRTTYSDFLLNPLVRIVLVTF 516

QY 695 ALLGLSLYGATLVQDGLALTDVVRGTEKEHAFSLAQRLYFSLYEVALVTQGFYAHQS 754

DB 517 VYLGVASYGCTKVKLGLPEPNDLLPENSGKRTLMMAEKYFS--DYGS-- 562

QY 755 ALFDLHQRFSSLKAVLPPPPATQAPRTWLYHYRNWLQGIQAADFODW-----ASGRITRHSY 810

DB 563 -----LHVWYNLSEVDVAPRKIWNVLEKEVELYEHT 595

QY 811 RNSGEDGALAYKLLIQTGDAQEPLDFSQLTRKLVDREG-LIPELF-YMGLTVMVSSDP 868

DB 596 FTASSDSWLR-----TFLAFVKQAGLLITPENFVILKNVFLSQ-- 634

QY 869 LGLAASQANFYPPPEWLHDKYDTT---GENLRIPPAQPLEFAQPFPLRGLQKTDADV 924

DB 635 -----POFAKYNRQDVLTEDGEH-----LEASRIPVQLR-----HV 665

Db 161 KLAGDNGENIIVEA--TAWLLIYQLKYPEN-----EISVSGLWEREFK 203
QY 361 QLAQALPENASQIIHAFSTLDDILHAFSEVSAARVVGYYLLMAYACVTML-----414
Db 204 NKDEYKQAKYISITYFTSOTLSDELNRAERLAPKFIGAFVILVCFSLCSIVTIKGS 263
QY 415 -RWDCAQSGVGLAGVLLVALAVASGLGICALLGITTENAAATTVQLPFLALGIVDDVFL 473
Db 264 GYIDWVVTKPIILSVLGVSNAGIASAGMLYLEIQYNDITA--VMPFLVAVGTNMF 322
QY 474 LAHAFTALPGTLPQRMGECIQTGTSVVLTSINNMAAFMAALVPIIPALRAFSIQAAI 533
Db 323 MVASLKRITDRNLKYDORIAECMAADAASLITALTALDALSFGVGTITIPAVQIFCIYTC 382
QY 534 VVGCTFVAVMLVFPALISLDRRRHQRDLVLCFSSPCSAQVIQILPQELGDTVPVGI 593
Db 383 ALLLTAYQUTFFCALVY-----401
QY 594 AHLTATVQAFTHCEASSQHWVTILPQAHVLPSPDPLGSELFSPG-----G 640
Db 402 -----YTRIEOGLHSIMLRPAVY---SSTSLNVKLVFWSQKQPLPSCGTVS 449
QY 641 STRDLGQEEETROKAAKSLPCARWNLAHFARYQFAPILLQSHAKAIIVLVFGALLGLS 700
Db 450 STSSVSTWTSQATSPASKLHCA---ATSPFNWYAPVLMQPIWIRATAGLWYLYLGLS 506
QY 701 LYGATLVQDGLALTQV---PRGTKEHAFSLAQBYFSLEYVALYTOGGFDYAHNS-ORAL 756
Db 507 YGCTHLKEGLEPANLLVDDSDVATPHYRVLEKHYHYGA-SLQIVVSNPPDLRDPVERIN 565
QY 757 FD-LHQRFSSSLKAVLPPATQAPRTWLVHYRNWLOGIQAAFPQDQWASGRITRHSYRNGSE 815
Db 566 MDKMASTFANCAIGDSDVQF-----WLREMQ-----VSEIHKIQYDN---605
QY 816 DGALAYKLLIQTDGAQEPDLSQLTRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQ 875
Db 606 -----EKFYDHAQAQYIYSD-----MSQ 622
QY 876 ANFYPPPEWLHD-KYDTTGENLRTPPAQLEFAQFPFLRLGLOQTADFEVIEGARAC 934
Db 623 -----PWVVDVWVGRRNNSERI-----IKTRFMIGMRDISITTKQTEATNTFREIA 669
QY 935 AEAGQAGVHAYPGSGP-FLFWEQYGLRRCFLAVCILLVCTFLVALLNPNWTAGLIV 993
Db 670 SRFEQYNTTY---MPLWLFDOYALVVPNTMQDIIVAVACMLVLSALLIOPQVCSFWVA 726
QY 994 LVLAMTVELGIMGFLGKLSAIPVILVASVGIGVEFTVHVALGF-LTTQGSNLRRAA 1052
Db 727 VTIGSIDGLVGLFMTLWNVNLDASMITIIMSFGPSVDYSAHITVAYVISKESTTSARVC 786
QY 1053 HALBHTTAPVTDGAISTLLGLLMLAGSHFDIVRYF---PAALTVLTLGLLHGLVLLPV 1109
Db 787 DALGDLGWPAQGAWSITLAVSLVSDVPAYMIVTFFKTVFLAISI---GFLHGLVFLPL 842
QY 1110 LLSI 1113
Db 843 MLSV 846

RESULT 15
T26521
hypothetical protein Y18D10A.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26521
R;Harris, B.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z20226
A;Accession: T26521
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-936 <WIL>
A;Cross-references: UNIPROT:Q9XW22; EMBL:AL034393; PIDN:CAA22312.1; CESP:Y18D10A.7

A;Experimental source: clone Y18D10A

C;Genetics:

A;Gene: CESP:Y18D10A.7

A;Introns: 11/1; 44/2; 106/1; 166/3; 289/2; 373/1; 396/3; 485/1; 573/3; 615/3; 644/3; 68/

Query Match 6.2%; Score 389.5; DB 2; Length 936;
Best Local Similarity 20.1%; Pred. No. 8.4e-19;

Matches 186; Conservative 152; Mismatches 339; Indels 247; Gaps 33;

QY 279 LSGGCHGFSGHK--FMHWQBELLLGGWARDPOCELLR---AEALQSTFLMSPLQVLEHPR 333
Db 149 LLSAGRIPTYKDVCLHFQNDCF-----SNPHAKLLANIYKSHQNSMFNIT---YPIIR 199
QY 334 GYQTHDIGWSE-----EQASTVL-----QAWQ---RRFVQ-LAQEALPEN 370
Db 200 STYATEPIDISKLVGNVSLDYDGHVENASAWLILYQKNEKWLSDRDPEDGLAEKIQSGE 259
QY 371 ASQQ---THAFSTTILDDILHAFSEVSAARVVGYYLLMAYACVT-----412
Db 260 APSELNLYYFHSATFDQELEKENRRLTPKFSITFSVLIIIPAIMTFTTIKFMKFKTENG 319
QY 413 ---MLRWDCAQSGSVGLAGVLLVALAVASGLGICALLGITTENAAATTVQLPFLALGIV 468
Db 320 NQYPVIDW--VLSKPLLGICGVLTMCALISTGLMLFNVTVDVDMCT--VMPFLSLTIGI 376
QY 469 DDVFLLAHAFTALPGTLPQRMGECIQTGTSVVLTSINNMAAFMAALVPIIPALRAFS 528
Db 377 DDTFLMLAAWTHETDRNLPYKRIEKAMRHAASVISITSLDALAFILGSIAPLPAVIYFC 436
QY 529 LQAAIVVGCCTFVAVMLVFPALISLDRRRHQRDLVLCFSSPCSAQVIQILPQELGDT 588
Db 437 YSSAAILFIPLYLTMFVAVLALQGRREEDKHSV-----TGMKT 477
QY 589 VPVGIAHLTAVQAFTHCEASSQHWVTILPQAHVLPSPDPLGSELFSPGSTRDILGQ 648
Db 478 IDLSDYETATR-----QLLLKMSRVSVKAD 505
QY 649 BEETROK-----AACKSLPCARWNLAHFARYQFAPILLQSHAKAIIVLVFGALLGLSLY 703
Db 506 ENNNNNNEKSIENIKIDNMW-YQRFEDQYAFFINSKISILSLIYLAAYLAAAFVG 564
QY 704 ATLVDQD-----LALTVDVPGTKEHAFSLAQRYF-----SLYEVALVYQ 744
Db 565 VKHLKIGDFVTVVLTITIKYKVLQINIVQEDSASRVLEVRQLEFPEDTKLMDIAVMS 624
QY 745 GGFQYAHQSORALFDLHQRFSSSLKAVLPPATQAPRTWLVHYRNWLOGIQAAFDQDQWASGR 804
Db 625 PNFNSPEER---FNFMEVLSEFESTWCSEGSTQFWFFENQKYLSD--GFGGDLTK--677
QY 805 ITRHSYRNGSEDGALAYKLLIQTG-----DAQEPDLSQLTRKLVDRGLIPPELFYMG 859
Db 678 -TMNSERKLSQ-----SKTFLMSHEKFGYDVLSDKQFRLSTRLKNVETD---EEMFNCA 728
QY 860 LTVWVSDPLGLAASQANF--YPPPEPW-LHDKYDVTGTGENLRIPPAQLEFAQFPFLLRG 916
Db 729 RTM-----RKLQKHANYSIITYSPLWNTADEYD-----757
QY 917 LQKTADFEATEGARAACAAGQAGVHAYPGSGPFLFWEQYGLRRCFLAVCILLVCTF 976
Db 758 -----INWPQTM---QDIYISIAVWNP---776
QY 977 LVCALLLNPNWTAGLIVLVLAMTVELGIMGFLGKLSAIPVILVASVGIGVEFTVHV 1036
Db 777 -VALLFIQPLCSVIIIGLNIASTAFVIGTMSFLGVSLDATSMITVAMSVGFSVDFAAHV 835
QY 1037 ALGFLTTQGSR-----NLRAAHLEHTPAPVTDGAISTLLGL--LMLAGSHFDIVRY 1087
Db 836 SYAMTESGAQIPKSAIYSRFRCHTGTICWPVTQASVSVLLGVSSLYLSDS---YVQOT 892
QY 1088 FFAALTVLTLGLLHGLVLLPVLL 1111
Db 893 CFRTVVLVILFGTTHALVFLPLL 916

Search completed: November 22, 2004, 07:58:08
Job time : 32 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: November 22, 2004, 10:37:41 ; Search time 914 Seconds
(without alignments)
7112.209 Million cell updates/sec

Title: US-09-990-046-2
Perfect score: 6272
Sequence: 1 MTRSPRLRLPSYTPPART.....SPAATSSGNLSRGPGPAG 1203

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US0990046/runat_21112004_130921_18649/app_query.fasta_1.1351
-DB=Published Applications NA -QMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -USER=US0990046 @CGN_1_1_511 @runat_21112004_130921_18649
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
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- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6272	100.0	4030	9	US-09-990-046-1	Sequence 1, Appli
2	6248	99.6	4391	9	US-09-909-280A-1	Sequence 1, Appli
3	3955	63.1	4004	9	US-09-990-046-8	Sequence 8, Appli
4	3387	54.0	2082	9	US-09-990-046-9	Sequence 9, Appli
5	3349	53.4	5288	8	US-08-954-701A-18	Sequence 18, Appl
6	3349	53.4	5288	10	US-09-754-032-18	Sequence 18, Appl
7	3349	53.4	5288	15	US-10-421-446-18	Sequence 18, Appl
8	3337	53.2	5187	8	US-08-954-701A-3	Sequence 3, Appli
9	3337	53.2	5187	8	US-08-954-701A-9	Sequence 3, Appli
10	3337	53.2	5187	10	US-09-754-032-3	Sequence 3, Appli
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13	3337	53.2	5187	15	US-10-421-446-9	Sequence 3, Appli
14	3336	53.2	6568	15	US-10-302-279-1	Sequence 1, Appli
15	3329	53.1	6568	9	US-09-964-824A-266	Sequence 266, App
16	1972.5	31.4	3900	8	US-08-954-771-42	Sequence 42, Appl
17	1972.5	31.4	3900	8	US-08-462-386D-42	Sequence 42, Appl
18	1972.5	31.4	3900	10	US-09-736-476-42	Sequence 42, Appl
19	1972.5	31.4	3900	18	US-10-647-654-42	Sequence 42, Appl
20	1956	31.2	4434	8	US-08-954-701A-5	Sequence 5, Appli
21	1956	31.2	4434	10	US-09-754-032-5	Sequence 5, Appli
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23	640	10.2	4550	14	US-10-208-731-1	Sequence 1, Appli
24	640	10.2	4673	15	US-10-172-118-459	Sequence 459, App
25	640	10.2	4673	16	US-10-342-887-459	Sequence 459, App
26	640	10.2	4673	17	US-10-776-827-100	Sequence 100, App
27	631	10.1	4814	10	US-09-971-392-103	Sequence 103, App
28	627	10.0	3996	16	US-10-621-758A-1	Sequence 1, Appli
29	627	10.0	3996	17	US-10-663-208A-1	Sequence 1, Appli
30	627	10.0	3996	17	US-10-646-301A-1	Sequence 1, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-046-1

Alignment Scores:

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US-09-990-046-2 (1-1203) x US-09-990-046-1 (1-4030)

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DB	293	GCAGCACCCAGATCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTCTACTTC	352
QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe	60
DB	353	CAGGSCCTGCTCTCTCTCTGGGATGCGGATCCAGAGACATTTGGCMAAGTGTCTTT	412
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr	80
DB	413	CTGGGACTGTTGGCCCTTTGGGCGCCCTGGCATTAGGCTCTCCGCATGGCCATTATGAGACA	472
QY	81	AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr	100
DB	473	AACTTTGGAAACAGCTCTGGGTAGAACTGGGACCGCGGTGAGCCAGGAGCTGCATTACACCC	532
QY	101	LysGluLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
DB	533	AAGGAGAGCTGGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGACCGCAGCC	592
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu	140
DB	593	CAGGAGGAGAGAACATCTCACCCGGAAGCACCTTGGCTCCACCTCCAGGAGCCCTC	652
QY	141	ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys	160
DB	653	ACTGCCAGTAAAGTCCAGTATCACTCTATGGGAAGTCTCTGGATTGGAACAAATCTGC	712
QY	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu	180
DB	713	TACAACTCAGGAGTTCCTTATGAAATGGAATGATTGAGTGGATGATTGAGAAGCTG	772
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200
DB	773	TTTCCGTGCTGATCCTACCCCGCCCTCGACTGCTTCTGGGAGGAGCCAAACTCCAAAGG	832
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220
DB	833	GGCTCCGCTACTCTGCCCGCGCGCCGGATATCCAGTGACCAACCTGGATCCAGAGCAG	892
QY	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
DB	893	CTGCTGGAGAGAGCTGGGTCCCTTTGCTCCCTTGAGGGCTTCGGGAGCTGTAGACAAG	952
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisPheProAspLeuHisCys	260
DB	953	GCACAGTGGCGCAGGCTACGTGGGCGCGCCCTGTCTGCACCCCTGATGACCTCCACTGC	1012
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
DB	1013	CCACCTAGTGGCCCCAACCATACAGCAGGAGGCTCCCAATGTGGCTCAGAGCTGAGT	1072
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly	300
DB	1073	GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACCTGGCAGGAGGAATTTGCTGTGGA	1132
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
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DB	1313	CAGCTGGCCCGAGGAGGCTCCCTGAGAACCTTCCCAGCAGATCCATGCTCTTCTCCCTCC	1372
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
DB	1373	ACCACCTGGATGACATCTGCATGGCTTCTCTGAAGTCAGTGTGCCGCTGTGTGGGA	1432
QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
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QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440
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QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrGlnValLeuPro	460
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QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
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QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
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QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660
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Db 2333 CTCTACGGAGCCACCTTGGTGCAGAGCGGCTGGCCCTGACGATGTGTGCTCGGGGC 2392
QY 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
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QY 881 ProProGluTrpLeuHisAspLysTyrAspThrThrGlyLeuAsnLeuArgIlePro 900
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QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnThr 920
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Db 2993 GCAGACTTTGTGGAGGCCATCGAGGGGCGCGGCGAGCATGCGCAGAGCGCGCCAGGCT 3052
QY 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
Db 3053 GGGGTGACGCTACCCCGAGGGCTCCCTCTCTCTTCTGGGAACAGTATCTGGGCGCTG 3112
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QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
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QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
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RESULT 2

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; Sequence 1, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297) .. (3905)
US-09-909-280A-1
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Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 5 Gaps: 0
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US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)

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QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe	60
DB	417	CAGGCGCTGCTCTCTCTGGATGCGGGATCCAGAGACATTGGCAAGTGTCTTT	476
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleLeuThr	80
DB	477	CTGGGACTGTTGGGCGCTTGGGCGCTGGCATTAGGTCTCCGCTAGCCCATATTAGACAC	536
QY	81	AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnLeuLeuIstYrThr	100
DB	537	AACTTGGAAACAGCTCTGGGTAGAGTGGGAGCGCGGTGAGCGAGCTGATTAACACC	596
QY	101	IysGluIysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
DB	597	AAGGAGAGCTGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGCCGACGC	656
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisIstLeuGlnAlaLeu	140
DB	657	CAGGAGGAGAGACATCTCACCCGAGACACTTGGCTCCACCTCCAGGCGAGCCCTC	716
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QY	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluIysLeu	180
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QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200
DB	837	TTTCCGTGGTGATCTCTACCCCTCGACTGCTCTGGGAGGAGGCCAACTCCCAAGG	896
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DB	897	GGCTCGGCTACCTGCCCGCGCGCGGATATCCAGTGACCAACCTGGATCCAGAGCAG	956
QY	221	LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
DB	957	CTGCTGGAGAGCTGGGTCCCTTTGGCTTCCTTTGAGGGCTTCGCGGAGCTGTAGACAAG	1016
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys	260
DB	1017	GCACAGTGGCCAGGCGCTAGGTGGGGGCGGCTGTCTGCACCTGATGACCTCCACTGC	1076
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
DB	1077	CCACCTAGTGCCCGCCCAACATCA CAGCAGCAGGCTCCCAATGTGGCTCAGAGCTGAGT	1136
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly	300
DB	1137	GGGGGTGCATGGCTTCTCCCAAAATTATGCATGCGCAGAGGAAATTGCTGCTGGGA	1196
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
DB	1197	GGCATGGCCAGACACCCCAAGGAGAGCTGCTGAGGGCAGAGGCGCTTCAGAGCACCTTC	1256
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340
DB	1257	TTGCTGATAGTCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATACAGACATGAC	1316
QY	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPhePheVal	360
DB	1317	ATTGGCTGGAGTGAGGAGCAGGCAGACAGTGTCTACAGCCTGGCAGCGCGCTTTGTG	1376
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380
DB	1377	CAGCTGGCCAGGAGGCGCTGCCTGAGACGCTTCCAGCAGATCCATGCTCTCTCTCC	1436
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
DB	1437	ACCACCCCTGGATGACATCTGCAATGCGTTCCTGAAGTCAGTGTGCCGTGTGTGGGA	1496
QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
DB	1497	GGCTATCTGCTCATGCTGGCTGTATGCTGTGTGACCATGCTGCGGTGGAGCTGCGCCAG	1556
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValaSerGly	440
DB	1557	TCCCAAGGTTCCGTGGGCTTTCGCGGGTACTGCTGGTGGCCCTGGCGGTGCCTCAGGC	1616
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460
DB	1617	CTTGGGCTCTGTGGCTCTGCTGGCATCACCTTCAATGTGCCACTACCCAGGTGTGCC	1676
QY	461	PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu	480
DB	1677	TTCTTGGCTCTGGGAATCGGCTGTGATGACGTATTCCTGCTGGCGCATGCCCTTCACAG	1736
QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500
DB	1737	GCTCTGCCCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCGCAGGCC	1796
QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520
DB	1797	AGTGTGCTACTCACATCCATCAACAACATGGCGGCTTCTCATGGCTGCCCTCGTTCC	1856
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
DB	1857	ATCCCTCGCTCGAGCGCTTCTCCCTACAGCGCGCATAGTGTGTGGCTGGCACTTTGTA	1916
QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
DB	1917	GCGGTGATGCTGTCTGTCTGCTTCCCGCCATCTCAGCTTGAGATTACGGCGCGCCACTGCC	1976
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
DB	1977	CGCCTTGATGCTGTCTGTCTGCTTCCAGTCCCTGCTGCTCAGGTGATTAGATCCTG	2036
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
DB	2037	CCCCAGGAGCTGGGAGCGGACAGTACCAGTGGGCAATTGCCACCTCTCATGCGCACGTT	2096
QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
DB	2097	CAGGCTTTACCCACTGTGAGCGCAGCAGCCAGCATGTGTCACCATCTGCTGCCCTCCCAA	2156
QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
DB	2157	GCCACCTGGTGGCCCCCCTTCTGACCCACTGGGCTCTGAGCTCTTCCAGCCCTGGAGGG	2216
QY	641	SerThrArgAspLeuLeuGlnGluGluThrArgGlnIysAlaAlaCysLysSer	660
DB	2217	TCCACACGGGACCTTCTAGCGCAGGAGGAGACAAAGCAGAGCAGCTTCCAGTCC	2276
QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
DB	2277	CTGCCCTGTGCCCGCTGGAAATCTTGCCCATTTCCCGCGTATCAGTTTCCCGCTGTGCTG	2336
QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
DB	2337	CTCCAGTCAATGCCAAGGCCATCGTGTGCTCTTTGGTGTCTCTTCTGGGCTGTAGC	2396
QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIleuThrAspValValProArgGly	720
DB	2397	CTCTACGGAGCCACTTGGTGCAGAGCGCTGGCCCTGACGATGTGTGCTGCTCGGGC	2456
QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
DB	2457	ACCAGGAGCATGCTTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGCC	2516
QY	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760

Db 3597 CTCACGTGACTCGTGTCTGCTGCTGTGCTCATCTCTGGGGCCGCCGCCACAGAGTG 3656
 QY 1121 lleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
 Db 3657 ATACAGATGTACAAGAAAGCCACAGATCTCTAGTCCACAGCTCCACAGGAGCGGG 3716
 QY 1141 LeuArgTTPGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
 Db 3717 CTTAGTGGGGGGCATCTCTCTCCCTGCCAGAGCTTTCCAGAGTGACTACTCTCATG 3776
 QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 Db 3777 ACCGTGGGCATCCACCCACCCCTGCTGGTGCTTACATCCATCCAGCCCTGATGAG 3836
 QY 1181 ProProTTPSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 Db 3837 CCCCTTGGTCCCTGCTGCTGCTAGCTCTGGCAACCTCAGTTTCCAGGGGACCAGGTCCA 3896
 QY 1201 AlaThrGly 1203
 Db 3897 GCCACTGGG 3905
 RESULT 3
 US-09-990-046-8
 ; Sequence 8, Application US/09990046
 ; Patent No. US20020156245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: de Sauvage, Frederic
 ; APPLICANT: Carpenter, David A.
 ; TITLE OF INVENTION: Patched-2
 ; FILE REFERENCE: P1405R1
 ; CURRENT APPLICATION NUMBER: US/09/990,046
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
 ; NUMBER OF SEQ ID NOS: 32
 ; SEQ ID NO 8
 ; LENGTH: 4004
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-990-046-8
 Alignment Scores:
 Pred. No.: 0 Length: 4004
 Score: 3955.00 Matches: 847
 Percent Similarity: 65.81% Conservative: 2
 Best Local Similarity: 65.66% Mismatches: 10
 Query Match: 63.06% Indels: 434
 DB: 9 Gaps: 10
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 QY 101 LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
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 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 71 CAGGAGGAGAGAACATCTCACCCGAAGCACCTTGGCTCCACTCCAGCGAGCCCTC 130
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTTPAspLeuAsnIleLysCys 160
 Db 131 ACTGCCAGTAAAGTCCAAGTATCATCTATGGGAAGTCTCTGGATTTGAAACAAATCTGC 190
 QY 161 TyrLysSerGlyValProLeuIleGlnAsnGlyMetIleGluTTPMetIleGluLysLeu 180
 Db 191 TACAAGTCAGAGATTCCCTTATTGAAATGGAATGATTGAGCGGATGATTGAGAAGCTG 250
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTTPGluGlyAlaLysLeuGlnGly 200
 Db 251 TTTCGTGGTGATCTCACCCTCCGACTGCTTCTGGGAGGAGGCCAACTCCAAGGG 310
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTTPThrAsnLeuAspProGluGln 220

Db 311 |||||GGCTCCGCTACCTGCCCT-----330
QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 330 -----330
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 330 -----330
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 331 -----331
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuGly 300
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QY 301 GlyMetAlaArgAspProGlnGlyLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 474
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCGCCGAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC 534
QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db 535 ATTGGCTGAGTGAGGAGCAGGCAGACAGTGTCTACAAGCCTGGCAGCGGGCTTTGTG 594
QY 360 -----360
Db 595 CAGTCCGTATGACAAAGACAGGGGGTGCCCTGAGGCCATTCCTCTCTGCCCCCT 654
QY 361 -----GlnLeuAlaGlnGlnAlaLeuProGluAsnAlaSerGlnG 374
Db 655 CCTATCCACCTGTTTCTCCAGCTGGCCAGGAGGCCCTGCTGAGAACGCTTCCAGCA 714
QY 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCTTCTCTCCACACACCTGGATGACATCTGTGATGCGTTCTCTGAATCAG 774
QY 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet-----405
Db 775 TGCTGCCCTGTGTGGGAGGCTATCTGCTCATGTGGTGGGTCTTGACCTGGCACCTTGCC 834
QY 405 -----405
Db 835 CCACACCCACCTCCAAACAGTGCACCCCTGGGGAGGCCCTGAGACTGCCCTTTCCTCC 894
QY 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCATATGCTGTGTGACCATGCTGCGGTGGGACTGGCGCCAGTCCACAGGGTTC 954
QY 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyCys 444
Db 955 CGTGGGCGCTTGCCGGGGTACTGTGTGTGGCCCTGGGGGTGGGCTTCAGGCGCTTGGGCTG 1014
QY 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr-----456
Db 1015 TGCCCTGTCTGGGATACCTTCAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
QY 457 -----G 457
Db 1075 AGACTCAGTGCAGTCACAGGCTTTCACGGGTCTCTCAGCTGCCCGCTCTCTGCCCTCC 1134
QY 457 lnValLeuProPheLeuAlaGlyIleGlyValAspAspValPheLeuLeuAlaHis 477
Db 1135 AGTGTGCTGCTCTTCTGACTCTGGGAATCGCGGTGGATGATGATATCTCTGCTGGCGATG 1194
QY 477 laPheThrGluAlaLeuProGlyThr-----485

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QY 485 -----485
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QY 485 -----485
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QY 485 -----485
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Db 1495 CAAGTTCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGAGG 1554
QY 486 -----ProLeuGlnGluArgMetGlyCysLeuGlnArgThrGlyT 500
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QY 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTGTGATCATCATCCATCAACATCGCGCCCTTCTCATGGTGCCTCTGTTTC 1673
QY 520 roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaValValGlyCysThrPheV 540
Db 1674 CCATCCCTCGCTGGAGCCTTCTCC-----1699
QY 540 alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTAGCCTGGACCTAGCGGCGCCACTGC 1730
QY 560 GlnArgLeuAspValLeuCysCysPheSer-----569
Db 1731 CAGCGCTTGTGTGTCTGTCTGTCTC-CAGGTACTGCTGGGCCCCAGCCCCCTCCT 1789
QY 569 -----569
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QY 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
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QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGAGCGGACAGTACAGTGGCANTGCCACTCCTCCTGCCACAGTTCAGGCTTATCC 1969
QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal 624
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QY 625 ProProSerSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
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Db 2090 CTTCTAGGCCAGGAGGAGAGACAGGAGAGCCCTGCAAGTCCCTGCTGCTGCTGCTG 2149
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Db 2150 CGCTGGAATCTTGCCTTCTGCGCCGCTATCAGTTTGCCTGCTGCTGCTGCTGCTGCTG 2209
QY 685 AlaIysAlaIleValLeuValLeuPheGlyValLeuLeuGlyLeuSerLeuTyrGlyVal 704
Db 2210 GCCAAGGCCATCGTGTGCTGCTTCTTGTGTGCTTCTTGTGGCCTGAGCCTCTACGGAGCC 2269

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 QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
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 QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer----- 837
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 QY 837 ----- 837
 Db 2690 GGGTCCACTAGTACAGGGGCTGCAGGCTCTCTGGGCCAGGCTTCTGACGCTTCTGCCT 2749
 QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
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 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPhe 952
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 Db 3470 TGACAGTGAACCTCTTTGGTATCATGGTTCCTGGGCATCAAGCTGAGTGCCATCCCCG 3529
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 Db 3530 TGGTGAATCTTGTGGCTCTGTAGGCATTTGGCTTCAGTTCACAGTCCACGTGGCTCTGG 3589
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 US-09-990-046-9
 ; Sequence 9, Application US/09990046
 ; Patent No. US20020156245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: de Sauvage, Frederic
 ; APPLICANT: Carpenter, David A.
 ; TITLE OF INVENTION: Patched-2
 ; FILE REFERENCE: P1405R1
 ; CURRENT APPLICATION NUMBER: US/09/990,046
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
 ; NUMBER OF SEQ ID NOS: 32
 ; SEQ ID NO 9
 ; LENGTH: 2082
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-990-046-9

Alignment Scores:

Pred. No.: 3,350-308 Length: 2082
 Score: 3387.00 Matches: 656
 Percent Similarity: 96.33% Conservative: 1
 Best Local Similarity: 96.13% Mismatches: 3
 Query Match: 54.00% Indels: 23
 DB: 9 Gaps: 2

US-09-990-046-2 (1-1203) x US-09-990-046-9 (1-2082)

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 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
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 QY 61 LeuGlyLeuLeuAlaPheGlyValAlaLeuAlaLeuGlyLeuArgMetAlaIleIleThr 80
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 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 248 AACTTGGAACAGCTCTGGTAGAAGTGGCAGCGCGGTGAGCCAGGAGCTCATACACC 307
 QY 101 LysGlnLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 308 AAGGAGAGCTGGGGGAGGAGGCTGCATACCTCTCAGATGTGTATACAGACCGCAGC 367

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121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
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368 CAGGAGGAGAGAAACATCTCACACCCGAGCACTTGGCTCCACTCCAGGACCCCTC 427
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141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
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161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
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488 TACAGTACAGGAGTCCCTTATTAATAATGAATGATGAGTGATGATGAGAGCTG 547
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548 TTTCCGTGCTGATCTCATCCCTCCCTCGACTGCTTCTGGGAGGAGCCAAACTCCAAAGG 607
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201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
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221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
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668 CTGCTGGAGAGCTGGTCCCTTTGCTTCCCTTGAGGGCTTCCGGGAGCTGTAGACAAG 727
Qy
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261 ProProSerAlaProAsnHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db
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301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
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908 GGCATGCCAGACACCCCAAGGAGAGCTGCTGAGGGCAGAGCCCTGCGAGACACCTTC 967
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321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
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341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
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361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
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381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
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1148 ACCACCTTGATACATCTTCGATCGCTTCTCTCAAGTCACTGCTGCCCTGTGTGGGA 1207
Qy
401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db
1208 GGCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGTGCGGTGGGACTGCGCCAG 1267
Qy
421 SerGlnGlySerValGlyValAlaGlyValLeuLeuValAlaValAlaSerGly 440
Db
1268 TCCAGAGGTTCGCGGGGCTTCCGGGGTACTGTGTGGCCCTGGCGGTGGCTCAGGC 1327
Qy
441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db
1328 CTGGGTCTGTGCGCTTGTGCGGATCACTTCAATGTGCGCACTACCCAGGTGCTGCC 1387
Qy
461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db
1388 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCTCTGTGGCGCATGCTTCCACAG 1447
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481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyThr 500
Db
1448 GCTCTGCTTGGCACCCCTCTCCAGGAGCGCATGGCGAGTGTCTCAGCGCAGCGGACAC 1507
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501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
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1508 AGTGTGCTACTCACATCCATCAACACATGCGCGCTTCTCATGGCTGCGCTCGTTC 1567
Qy
521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db
1568 ATCCCTGCGCTGCGAGCCTTCTCCTTACAGCC----- 1599
Qy
541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db
1600 -----ATCCTCAGCCTGGACCTACGCGCGCCACTGCCAG 1635
Qy
561 ArgLeuAspValLeuCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db
1636 CGCCTTGATGTCTCTGCTGCTTCTCCAGTCCCTGCTCTGCTCAGTGATTCAGATCCTG 1695
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581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db
1696 CCCAGGAGCTGGGGACGGGACAGTACCAGTGGGCAATGCCACCTCCTGCCAGATT 1755
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601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
Db
1756 CAAAGCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGTCACCATCTGCTGCCCAA 1815
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621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
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Qy
641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db
1876 TCCACAGGAGCTTCTAGCCAGGAGGAGACAGCAGCAGCAGCAGCAGCAGCAGCAGTCC 1935
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661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
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1936 CTGCCCCGTGCGCGCTGGAATCTTGGCCAT-----TTCCGCCCGGAATTC 1980
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681 LeuGln 682
Db
1981 CTGCAG 1986

RESULT 5
US-08-954-701A-18
; Sequence 18, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709

SOFTWARE: PatentIn Release #1.0.0, Version #1.30

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APPLICATION NUMBER: US/09/754,032

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/540,406

FILING DATE: 06-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: a60190-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 5288 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-754-032-18

Alignment Scores:

Pred. No.:	4-8e-304	Length:	5288
Score:	3349.00	Matches:	662
Percent Similarity:	70.02%	Conservative:	200
Best Local Similarity:	53.78%	Mismatches:	298
Query Match:	53.40%	Indels:	71
DB:	10	Gaps:	16

US-09-990-046-2 (1-1203) x US-09-754-032-18 (1-5288)

QY	12	ProSerThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu---	30
DB	540	CCAGTACTGC---GACGCGCTCTCGCTCTGAGCAGATTTCCAAAGGGAGGCTACT	596
QY	31	-----LysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly	48
DB	597	GGCCGGAAAGCCCACTGTGGGTGAGAGCGAAGTTTCAGAGACTCTTATTAACTGGGT	656
QY	49	CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuLeuAlaPheGlyAla	68
DB	657	TGTTACATCAAAAACACTGGCGAAGTCTTGGTTGGGGCTCTCTATATTGGGGCC	716
QY	69	LeuAlaLeuGlyLeuArgMetAlaIleIleGluThrAsnLeuGluGlnLeuTrpValGlu	88
DB	717	TTCCGGGTGGGATTAAAGCAGCGAACCTCGAGACCAACGTGGAGAGCTGTGGGTGGAA	776
QY	89	ValGlySerArgValSerGlnGlnLeuHisTyrThrLysGluLysLeuGlyGluAla	108
DB	777	GTGGAGACGAGTAAGTAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	836
QY	109	AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr	128
DB	837	ATGTTTAACTCACTCATGATACAGCCCTAAAGAAAGAGGTCCTAATGCTCTGACC	896
QY	129	ProGluAlaLeuGlyLeuHisLeuGlnAlaLeuAlaLeuThrAlaSerLysValGlnValSer	148
DB	897	ACAGAGCGCTCTCAACACACCTCGACTCGGCACTCCAGGCCAGCGGTCTCATGTATAC	956
QY	149	LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle	168
DB	957	ATGTACACAGCAGCAGTAAATTTGGAATTTGTTGTTTAAATTAATTAATTAATTAAT	1016
QY	169	GluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuTrpPro	188
DB	1017	GAACAGGTATCATGATCATGATATAGATATATCTTTACCTTGTGTTGATTATTAACCT	1076
QY	189	LeuAspCysPheTrpGluGlyValAlaLysLeuGlnGlySerAlaTyrLeuProGlyArg	208

DB	1077	TTGACTGCTTCTGGGAAGGGGGAATAATTACAGTCTGGGACAGCATACCTCTTAGTAAA	1136
QY	209	ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGlyProPhe	228
DB	1137	CCTCCTTTGGGTGGACAAACTTCGACCCCTTGAATTCCTGGAGAGTAAAGAAATA	1196
QY	229	---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr	247
DB	1197	AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGCTGAGGTGGTTCATGTTAC	1256
QY	248	ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis	267
DB	1257	ATGACGCGCCCTCGCTCAATCCGGCGATCCAGACTGCCCCGCCACAGCCCCCAAAA	1316
QY	268	HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer	287
DB	1317	AATTCAACCAAACTCTTGTATATGGCCCTGTTTGAATGGTGATGTCAAGCTTATCC	1376
QY	288	HisLysPheMetHisTrpGlnGluLeuLeuGlyGlyMetAlaArgAspProGln	307
DB	1377	AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGGTGGCACAGCTCAAGAACAGCACT	1436
QY	308	GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln	327
DB	1437	GGAAACTCTGTCAGCGCCATGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCA	1496
QY	328	LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu	346
DB	1497	ATGTACGACACTTCAAGGGGTACGAGTATGCTCACAC---ATCACTGGAAACAGGAG	1553
QY	347	GlnAlaSerThrValLeuGlnAlaTrpGlnArgPheValGlnLeuAlaGlnGluAla	366
DB	1554	AAAGCGGCACCATCTCGAGGCTGGCAGAGACATATGTGAGGTGTTTCATCAGAGT	1613
QY	367	LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspIle	386
DB	1614	GTGCGACAGACTCCACTCAAAAGGTGCTTCTCTACCCACCCAGCCCTGGACGACATC	1673
QY	387	LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyTyrLeuLeuMetLeu	406
DB	1674	CTGAAATCTCTCTGACGTGAGTCTCCGCTGGCCAGCGGTCTTACTCATGCTC	1733
QY	407	AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly	426
DB	1734	GCCTATGCTGTCTAACCATGCTGGCTGGGACTGCTCCCAAGTCCCGAGGTGCCGGGG	1793
QY	427	LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu	446
DB	1794	CTGGCTGGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1853
QY	447	LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle	466
DB	1854	ATCGGAATTCCTTTAAACGTGCAACACTCAGGTTTTTGGCCATTTCTCGCTTGGTGT	1913
QY	467	GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----	484
DB	1914	GGTGTGGATGATGTTTTTCTTCTGGCCCGCTTCAGTGAACAGGACAGATAAAGA	1973
QY	485	ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu	504
DB	1974	ATCCCTTTTGGAGACAGGACCGGGAGGCTCTGAAGCGCAGGAGCCAGGCGTGGCCCTC	2033
QY	505	ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu	524
DB	2034	ACGTCCATCAGCAATGTCCACAGCTCTCTTCATGCGCGGTGTTAATCCCAATTTCCGCTCTG	2093
QY	525	ArgAlaPheSerLeuGlnAlaAlaIleValGlyCysThrPheValAlaValMetLeu	544
DB	2094	CGGGGTCTCTCCCTCCAGGACGCTAGTAGTGGTGTTCATTTTGGCATGCTTCTGCTC	2153
QY	545	ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal	564
DB	2154	ATTTTCTGCAATTCAGCATGATTTTATATCGACGCGAGGACAGGAGACTGGATATT	2213

565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
2214 TTCTGCTGTTTACAAAGCCCTGCGCTACGACAGTGAATTCAGGTTGAACCTCAGCGCTAC 2273
585 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
2274 ACCGACACACAGCAATACCCGCTACAGCCCCACCTCCCTCCACGACGACACAGCTTT 2333
596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
2334 GCCCATGAACGACGATTACCATGTCAGTCCAGCTCCGACGAGTACGACCC 2393
609 SerSerGlnHisValThrIleLeuProGlnAlaHisLeuValProPro----- 627
2394 CACACGACGCTGACTACACACCGCTGAGCGCGCTCCGAGCTCTCTGCGAGCCGTC 2453
628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
2454 ACCGTGACACAGACACCTCAGCTCCGAGCCGACGACGACGACGACGACGAC 2513
645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
2514 CTGCTCTCCAGTCTCCGACTCC-----AGCTCCACTGCTCGAGCCCTCTAGC 2567
665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
2568 AAGTGACACTCTCATCTTTTGTGAGAACGACTATGCTCTTCTCTTGAACCAAAA 2627
685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
2628 GCCAGGTAGTGTGATCTCTCTTTTCTGGGCTTGTGGGCTGAGCTTTATGGCACC 2687
705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
2688 ACCCGAGTGAGACGCGCTGGACCTTACGGACATTGTACTCTCGGAAACACGAGAATAT 2747
725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
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2808 AAGACA---GACTACCGAATATCCACACTTACTTTACACCTTACACGAGATTTCAGT 2864
765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
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785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
2925 TTCAGACACTGGCTTCAGGACTTCAGGATGCAATTTGACAGTACTGGGAAACCGGAAA 2984
805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
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825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
3045 GTGCAACCCGCGACCGCGATAGCCCATCGACATCAGCCAGTGTGACTAAACAGCGTCTG 3104
845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
3105 GTGATGACGATGATGATCAATTAATCCCGCGCTTCTTACATCTACCTGACGGTGTGGTC 3164
865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
3165 AGCAACGACCCCGTCTGCTATGCTGCTCCAGGCCAACATCCCGGCCACACCGACGAA 3224
885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
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904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
3285 CCCATCGAGTATGCCAGTTCCTTTTACCTCAACGGGTTCCGGGACACCTCAGACTTT 3344
924 ValGluAlaIleGluGlyAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
3345 GTGAGGCAATTAAGAAAGTAGGACCATCTCAGCAACTATACGAGCCCTGGGGCTGTC 3404
944 AlaTyrProSerGlySerProPheLeuPheTyrGluGlnTyrLeuGlyLeuArgArgCys 963
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1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
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4143 GTGATCTGGAAGCCACAGAAAACCCCGTCT 4173

RESULT 7
US-10-421-446-18
; Sequence 18, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use


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QY 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGGAGCAGGACCGGGGAGTGCCTGAAGCGCACAGGAGCGAGCCCTG 2033
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Db 2034 AGCTCCATCAGCAATGTACAGCCTTCTTCATGGCCGCTTAATCCCAATCCCGCTCTG 2093
QY 525 ArgAlaPheSerLeuGlnAlaAlaValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTCTCCCTCCAGCAGCGGTAGTAGTGGTTCATTTTGGCCATGTTCTGCTC 2153
QY 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTCTCTGCAATTTCTACGATGATTTATATATCGACGCGAGCAGGAGACTGGATATT 2213
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Db 2214 TTCTGCTGTTTTACAGCCCTCGCTCAGCAGAGTGATTCAGTTGAACCTCAGGCCTAC 2273
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Db 2274 ACCGACACACACAGCAATACCGCTACAGCCGCCACCTCCCTACAGCAGCCACAGCTTT 2333
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Db 2394 CACACGACGTGTACACACCCTGAGCCGCTCCGAGTCTCGAGATCTCTGTGACGCCCTC 2453
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Db 2865 AACGTGAAGTATGTGTCATGTTGGAAAGAAAACAAACAGCTTCCCAAAATGTGGCTGCATC 2924
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Db 2925 TTCAGACTGGCTTTCAGGACTTTCAGGATGCAATTTGACAGTGAATGGGAAACCGGGAAA 2984
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Db 3285 CCCATCGAGTATGCCAGTTCCTTTTACCTCAACGGGTTCGGGACACCTCAGACTTT 3344
QY 924 ValGluAlaIleGlnGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAGTAAGGACCATCTCGACCACTATACGAGCCTGGGGCTGTCC 3404
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QY 1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuHisGly 1103
Db 3825 ATTGTCAAGTATTTCTTGTGCTGGGATCTCACCATCTCGGCTTCTCAATGGG 3884
QY 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTGTCTTCCCGTCTTTTCTTCTTCTTGGACCATATCTCGAGGTGTCTCCAGCC 3944
QY 1123 tTyrLys-----GluSerProGluIleLeuSerProAlaLeuProGlnGlyG 1139
Db 3945 AACGGCTTGAACCGCTGCCACACACCTCCCTCGAGCCACCCCGGCG----- 3993
QY 1139 yGlyLeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSe 1159
Db 3994 -----TGTCGCTTTCGCGATGCCCGCG-----GCCAC 4022
QY 1159 rMetThrValAlaIleHisPro----- 1167
Db 4023 ACGCACAGCGGCTGTATCTCCGACTCGGAGTATAGTTCCACAGACGACAGTGTCAAGC 4082
QY 1168 -----ProLeuProGlyAlaTyrIleHisProAlaProAspG 1180
```

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Db      4083 CTCAGCGAGGAGCTTGGCGACTACAGGCCCCAGCAGCGCGGGAGGCCCTGCCACCAA 4142
Qy      1180 uProProTyrSerProAlaAlaThrSerSer 1190
Db      4143 GTGATCGTGAAGCCACAGAAAACCCCGTCT 4173

RESULT 8
US-08-954-701A-3
; Sequence 3, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-954-701A-3

Alignment Scores:
Pred. No.:      6,28e-303      Length:      5187
Score:          3337.00      Matches:     677
Percent Similarity: 69.5%      Conservative: 204
Best Local Similarity: 53.48%      Mismatches: 306
Query Match:      53.20%      Indels:      80
DB:               8          Gaps:         20

US-09-990-046-2 (1-1203) x US-08-954-701A-3 (1-5187)
Qy      3 ArgSerProProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr 20
Db      178 CGCGCCGCGCGGAGCCGGGACTATCGACCGCGCCGAGTACTGC- --GAGCCGCCCTTC 234
Qy      21 AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTyrLeuArg 37
Db      235 GCTCTGGAGCAGATTTCGAAGGGGAAGGCTACTGCCCGGGAAGCGCGCTGTGGCTGAGA 294
Qy      38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db      295 GCGAAGTTTCAGAGACTCTATTAAACTGGGTGTTTACATTCAAAAGAACTGCCGCAAG 354
Qy      58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77

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436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaIaThr	455	773	oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleG1	793
1492	TCAGTGGCTGCAGAGTGGGCTCTGCTCTTGATTTGGATCTTCTTTAACTCGGACA	1551	2562	GAACAAGCAACTTCCCAAAATGTGGCTGCATCTACTTTAGAGACTGGCTTCAAGGACTTCA	2621
456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475	793	nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnG1	813
1552	ACTCAGTTTTCGCGTTTCTTCTTGGTGTGGTGGATGATGTTCTTCTCTCGGCC	1611	2622	GGATGCATTTGACACAGTACTGGGAACCTGGGAGGATCATGCCAACCAATTATAAAATGG	2681
476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493	813	ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr	833
1612	CATGCATTCAGTGAACACAGCAGACAATAAGAGGATTTCATTTGAGCAGACGACTGGGAG	1671	2682	ATCAGATGACGGGTCTCGCTTACAAACTCTCTGGTGACAGCTGGCAGCCGAGACAAGCC	2741
494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaIaPhe	513	833	oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr	853
1672	TGCCTCAACGCGACCGGACCGCAGCGTGGCCCTCACCTCTCATCAGATGTACCGCCTC	1731	2742	CATCGACATTAGTCAGTTGACTAAACACGCTCTGGTAGACCGAGATGCATTAATATCC	2801
514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaIaIle	533	853	oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaA1	873
1732	TTTCATGGCCGCATTGATCCTATCCTCTGCTCGCTCGAGCGTCTCTCCCTCCAGGCTGTGG	1791	2802	GAGCGCTTCTACATCTACCTGACCGCTTGGTTCAGCAACGACCTGTAGCTTACGCTGC	2861
534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553	873	aSerGlnAlaAsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrTh	893
1792	GTGGTGGTATTCAATTTTGTATGTTCTGCTCATTTTCTTGCATTTCTCAGCATGGAT	1851	2862	CTTCCGAGCCAAACATCCGCGCTCACCGCGGAGTGGTCCCATGACAAAGCCGACTACAT	2921
554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573	893	rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912
1852	TTATACAGCGCTGAGACAGAGATGGATATTTTCTGCTGTTTTCACAGCCCTGTGTC	1911	2922	GCCAGAGACCGAGCTGAGAATCCCGACGACAGAGCCCATCGAGTACGCTCATCTCCCTTT	2981
574	AlaGlnValIleGlnLeuProGlnGluLeuGlyAspGly-ThrValProValGlyI1	593	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932
1912	AGCAGGTTGATTCAAGTTGAGCCACAGGCTCACAGAGCCTCACAGTAACCCCGGTAC	1971	2982	CTACCTCAACGGCTTACGAGACACCTCAGACCTTGTGGAGGCCATAGAAAAAGTGAAGT	3041
593	eAla-----HisLeuThrAlaThrValGln-----	601	932	alaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952
1972	AGCCCCCCCACCATACACACCCACAGCTTCGCCCCACGAAACCCCATATCATATGCAG	2031	3042	CATCTGTAACTACTATACAGCTGGAGCTGTCCAGCTACCCCAATGGCTACCCCTTCT	3101
602	-----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProG1	620	952	uPheTrpGluGlnTyrLeuGlyLeuArgCysPheLeuLeuAlaValCysIleLeuLeu	972
2032	TCCACCGTTTTCAGCTCCGACAGAGATGACCCCTCACAGCAGCTGTACTACACCCGCC	2091	3102	GTTCTGGGAGCAATATCATCAGCTTCGCTGGCTGTCTGTCTATCATCAGCGTGTGTCT	3161
620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633	972	uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuI1	992
2092	GAGCCAGCTCTGAGATCTCTGACAGCTTTTACCGTTCACCCAG-GACAACTCAGCTG	2150	3162	GGCTCTGACGTTTCTAGTGTGGCAGCTTCTCTCTGAAACCCCTGTGACGGCCGGATCAT	3221
633	rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653	992	eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyI1	1012
2151	TCAGAGTCCCGAGAGCACCAAGCTCTACAGGGACCTGCTCTCCAGTTCTTCAGACTCC--	2208	3222	TGTCATGTCCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCTCATTTGGAT	3281
653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673	1012	eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh	1032
2209	----AGCCTCCACTCGCTCGAGCCGCCCTCCACCAAGTGGACACTCTCTGTTTGCAGA	2264	3282	CAAGCTGAGTGTGTGCTGTGGTCTCATCTGTATTCATCTGTGGCATCGAGTGGAGTT	3341
673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh	693	1032	eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl	1052
2265	GAGCAGTATGCTCTTCTCTCTGAAACCCCAAGCCCAAGTTGTGGTATATCTCTTTT	2324	3342	CACCGTCCAGTGTTCGCCCTTCTGACAGCCATTTGGGACACAGAAACACAGGGCTAT	3401
693	eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe	713	1052	aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuG1	1072
2325	CCTGGGCTTGTGGGGTTCAGCTTTATGGACCACCCGAGTGGAGACGGGCTGGACCT	2384	3402	GCTCGCTCTGGAAACATGTTTGTCTCCCGTTCTGGACGGTGTGTGTCTCCTCTGTGGG	3461
713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTly	733	1072	yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe	1092
2385	CACGGACATTTTCCCCGGGAAACACAGAAATATGACTTTCATAGCTCCCGAGTTTCAAGTA	2444	3462	TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTGTGCAGATACTCTTTGCCGCTCT	3521
733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyPheAspTyrAlaHisSerG1	753	1092	uThrValLeuThrLeuLeuGlyLeuHisGlyLeuValLeuLeuProValLeuLeuSe	1112
2445	CTTCTCTTTTACAAATGATATATGTCACCCAGAAAGCA-----GACTACCCGATATCCA	2501	3522	GGCCATTCTCACCGCTTCTGGGGTCTCTCAATGAGACTGGTTCGTCTGCTGCTCTTATC	3581
753	nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr	773	1112	rIleLeuGlyProProGluValIle-----GlnMetTyrLysG1	1126
2502	GCACCTACTTTACGACCTTCATAAGAGTTTCAGCAATGTGAAGTATGTCTGCTGGAGGA	2561	3582	CTTCTTTGGACCGCTGCTGAGGTGTCTCCAGCAATGGCTAAACCGACTGCCACTCC	3641
			1126	uSerProGluIleLeuSerProPro-----AlaProGlnGlyGlyGlyLe	1141

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Db      3642  TCGCCTGAG-----CGCCTCAAGTGTGCTCCGGTTTCGCCTGCTGCTGCACAC 3695
Qy      1141  uArgTTPGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db      3696  GAACAATGGGTCTGATTCCTCCGACTCGGAGTACAGCTCTCAGACCACGGTGTCTGGCAT 3755
Qy      1159  -----
Db      3756  CAGTGAGGAGCTCAGCAATACGAACACACACAGCGGTGCCGAGGCCCTGCCACCAAGT 3815
Qy      1160  ---MetThrValAlaIleHisProProLeuProGlyAlaTyrIleHisPro---Al 1177
Db      3816  GATTGTGAAGCCACAGAAACCCCTGTCTTGTGCCGGTCCACTGTGTCCATCGGACTC 3875
Qy      1177  aProAspGluProProThrSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
Db      3876  CAGACATCAGCTCCCTTGACCCCTCGGCAACAGCCCACTCGGACTCTGGCTCTGTGTC 3935
Qy      1194  rSerArgGlyProGly 1199
Db      3936  C-----CCTGGA 3942

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RESULT 9

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US-08-954-701A-9
; Sequence 9, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-954-701A-9

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Alignment Scores:
Pred. No.: 6.28e-303
Score: 3337.00
Percent Similarity: 69.59%
Best Local Similarity: 53.48%
Query Match: 53.20%
DB: 8
Length: 5187
Matches: 677
Conservative: 204
Mismatch: 306
Indels: 80
Gaps: 20

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US-09-990-046-2 (1-1203) x US-08-954-701A-9 (1-5187)
Qy      3 ArgSerProLeuArgGluLeu-----ProSerTyrThrProProAlaArgThr 20
Db      178  CGCGCCGCGCGGACCGGACTATCTGCACCGGCCAGCTACTGC---GACGCCGCTTC 234
Qy      21 AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTyrPleuArg 37
Db      235  GCTCTGGAGCAGATTTTCAAGGGGAGGCTACTTGGCCGGAAGCGCCGCTGTGGCTGAGA 294
Qy      38 AlaTyrPheGlnGlyLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db      295  GCGAAGTTTCAGAGACTCTTATTAACTGGTGTGTACATTCAAAAGAGACTGCGGCAAG 354
Qy      58 ValLeuPheLeuGlyLeuLeuAlaPheGlyValAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
Db      355  TTTTGGTGTGGGTCTCCTCATATTGGGGCCCTGCTGTGGGATTAAGGAGCGAGCTPAAT 414
Qy      78 IleGluThrAsnLeuGluGlnLeuTyrValGluValGlySerArgValSerGlnGluLeu 97
Db      415  CTCGAGACCAACGTGGAGGAGCTGTGGTGAAGTTGGTGGACGAGTGAGTCGAGAAATTA 474
Qy      98 HisTyrThrLysGluLysLeuGlyGluAlaTyrThrSerGlnMetLeuIleGln 117
Db      475  AATTATACCCGTGAGAAGATAGGAGAGGCTATGTTTAATCTCTCAACTCATGATACAG 534
Qy      118 ThrAlaArgGlnGlyGluAsnIleLeuThrProGlyAlaLeuGlyLeuHisLeuGln 137
Db      535  ACTCCAAAGAGAGCGCTAATGTCTGACACAGAGGCTCTCTGCAACACCTGGAC 594
Qy      138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTyrAspLeuAsn 157
Db      595  TCAGCACTCCAGGCCAGTCTGTGCAGCTCATATGATAACAGGCAATGGAAGTTGGAA 654
Qy      158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle 177
Db      655  CATTTGTCTACAAATCAGGGGAACCTTATCAGGAGACAGGTTTACATGATCAGATAATA 714
Qy      178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheThrPleuGlyAlaLys 197
Db      715  GAATACCTTTACCTTGTCTAATCATTCATCCTTTGGACTGCTCTTGGGAAGGGGCAAG 774
Qy      198 LeuGlnGlySerAlaTyrLeuProGlyArgProAspIleGlnTyrThrAsnLeuAsp 217
Db      775  CTACAGTCGGGACAGCATACCTCTAGTAAGCTCTCTTACGGTGGCAACATTGTGAC 834
Qy      218 ProGluGlnLeuLeuGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db      835  CCTTGGAAATTCCTAGAGAGTTAAAGAAATAAACTACCAAGTGGACAGCTGGGAGGAA 894
Qy      237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db      895  ATGCTGAATAAGCGAAGTTGGCCATGGGTACATGGACCGCCCTTGGCTCAACCCAGCC 954
Qy      257 AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAla 276
Db      955  GACCCAGATTGCCCTGCCACAGCCCTTAACAAAAATTCAACCAACCTCTTGTATGGGCC 1014
Qy      277 HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTyrGlnGluGlu 296
Db      1015  CTTGTTTGAATGTGGATGTCGAAGTTTATCCAGGAAGTATATGTCATTTGGCAGGAGAG 1074
Qy      297 LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeu 316
Db      1075  TTGATTGGGTGGTACCGTCAAGATGCCATGGAAAATTTGTCAGCGCTCAGCCCTG 1134
Qy      317 GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp 335
Db      1135  CAAACCATGTTCCAGTTAATGACTCCCAAGCAAAATGATGAACACTTCAGGGGCTAGCAC 1194
Qy      336 TyrGlnThrHisAspIleGlyTyrSerGluGluGlnAlaSerThrValLeuGlnAlaTyr 355
Db      1195  TATGTCCTCTCAC---ATCAACTGGAATGAAGACAGAGCGGACCGCCATCTCTGGAGCCTGG 1251

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Db 3402 GCTCGCTTGGACACATGTTTGTCTCCGTTCTGGACGGTGTGTCCACTCTCTGG 3461
Qy 1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAla 1092
Db 3462 TGTACTGATGCTTGAGGGTTCGAATTTGATTTCAATTTGTCAGATACTTTCTTGGCGTCT 3521
Qy 1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeu 1112
Db 3522 GGCCATTCTACCGCTTGGGGTTCTCAATGGACTGGTTCTGTGCTGCTGCTCTTATC 3581
Qy 1112 rLeuLeuGlyProProGluValIle-----GlnMetTyrLysG 1126
Db 3582 CTTCTTTGGACCGTGTCTGAGGTCTCTCCAGCAATGGCCTAAACCGACTGCCACTCC 3641
Qy 1126 uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
Db 3642 TTCGCTGAG-----CGCCTCCAGTGTGTGCGGTTCGCGTCCGCTGCTGTCACAC 3695
Qy 1141 uArgTyrGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db 3696 GAACAATGGGTCTGATTCCTCGACTCGAGTACAGCTCTCAGACCAGGTGTCTGCAT 3755
Qy 1159 ----- 1159
Db 3756 CAGTAGAGGCTCAGCAATACGAAGCACAGAGGTGCGCGAGGCCCTGCCACCAAGT 3815
Qy 1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro----Al 1177
Db 3816 GATTGTGAAGCCACAGAAACCTGTCTTTGCGCGTCCACTGTGTGCTCATCGGACTC 3875
Qy 1177 aProAspGluProProTrpSerProAlaAla-----ThrSerGlyAsnLeu 1194
Db 3876 CAGACATCAGCCCTCCCTGACCCTCGGCAACAGCCCACTTGACTCTGGCTCCTTGT 3935
Qy 1194 rSerArgGlyProGly 1199
Db 3936 C-----CCTGGA 3942

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RESULT 10

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US-09-754-032-3
; Sequence 3, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-754-032-3

```

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Alignment Scores:
Pred. No.: 6,28e-303 Length: 5187
Score: 3337.00 Matches: 677
Percent Similarity: 69.59% Conservative: 204
Best Local Similarity: 53.48% Mismatches: 306
Query Match: 53.20% Indels: 80
DB: 10 Gaps: 20

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US-09-990-046-2 (1-1203) x US-09-754-032-3 (1-5187)

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Qy 3 ArgSerProLeuArgGluLeu-----ProSerTyrThrProProAlaArgThr 20
Db 178 CGGCGCGCGCGGACCGGACTATCTGCACCGGCCAGCTACTGC---GACGCGCGCTTC 234
Qy 21 AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTrpLeuArg 37
Db 235 GCTCTGGAGCAGATTTCRAAGGGAGGCTACTGGCCGGAAGCGCCGCTGTGCTCAGA 294
Qy 38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db 295 GCGAAGTTTCAGAGACTCTATTATACTGGGTGTACATTCAAAAGAACTCGGCAAG 354
Qy 58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
Db 355 TTTTGGTGTGGGTCTCTCATATTGGGGCCCTCGCTGTGGGATTAAGAGCAGCTAAT 414
Qy 78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
Db 415 CTCGAGACCAACGTCGAGGAGCTGTGGGTGGAGTTGGTGGAGCTGAGTCGAGAATA 474
Qy 98 HisTyrThrLysGluLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
Db 475 AATTATACCCGTCAGAAATAGAGAGAGGCTATGTTTAACTCCTCACTCATGATACAG 534
Qy 118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisGln 137
Db 535 ACTCCAAAGAAAGAGGCGCTAATGTTCTGACACAGAGGCTCTCTCTGCAACACCTGGAC 594
Qy 138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
Db 595 TCAGCACTCCAGCGCAGTCGTGTCACGCTCTACATGTATACAGCAATGGAAGTGGAA 654
Qy 158 LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleLtrpMetIle 177
Db 655 CATTTGTCTACAAATCAGGGGAACCTTATCCGAGAGACAGGTTTACATGATCAGATAATA 714
Qy 178 GluLysLeuPheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys 197
Db 715 GAATACCTTTACCTTGTCTTAATCATTAACCTTTGGACTGCTTCTGGAAAGGGCAAG 774
Qy 198 LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp 217
Db 775 CTACAGTCCGGGACAGATACCTCTAGTGAAGCCTCTTACGTTGACAAACTTTTAC 834
Qy 218 ProGluGlnLeuLeuGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu 236
Db 835 CCCTTGGAAATTCCTAGAAGAGTTAAAGAAATAAATACTACCAAGTGGACAGCTGGAGAA 894
Qy 237 LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp 256
Db 895 ATGCTGAATAAGCCGAAGTGGCCATGGGTGATGACGCGGCTTGTCTCAACCCAGCC 954

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QY	257	AspLeuHisCysProProSerAlaProLenHisHisSerArgGlnAlaProAsnValala	276
Db	955	GACCCAGATTGGCTGCCACAGCCCTACAAAATTCAAACACCTTCCTGATGTGGCC	1014
QY	277	HisGluLeuSerGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu	296
Db	1015	CTTGTTTCAATGGTGGATGTCAAGGTTCATCCAGAAATGATATGATTCGTCAGGAGGAG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuAlaGluAlaLeu	316
Db	1075	TTGATTGGGGTGGTACCGTCAGAAATGCCATCGGAAACCTGTTCAGCGCTCACGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly	335
Db	1135	CAAACCATGTTCCAGTTAATGACTCCCAAGCAAAATGATGAACACTTCAGGGGCTACGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCTCTCAC---ATCAACTGGAATGAAGACAGGGCAGCGCCCATCTCTGGAGGCTGG	1251
QY	356	GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGGTGGTTCATCAAGTGTGCGCCCAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerSerThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCACACCCAGCACCTCGACGACATCCTAAATCCCTCTCTGATGTCAGTGC	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCGAGTGGCCAGCGCTACTACTGATGCTTGCCTATGCTGCTTTAACCATGCTGCCG	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCCAAAGTCCAGAGTGGCGTGGGCTGGTGGCTCTGTGTGGTGGCTG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTGCAGAAATGGGGCTCTGCTCTTGATTGGCATTTCTTTAATGCTGCAC	1551
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAla	475
Db	1552	ACTCAGGTTTGGCGTTTCTTGCTCTTGGTGTGGTGGATGATGCTCTCTCTCTCTGGCC	1611
QY	476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGATTTCAGTGAACACGACAGAAATGAGAGGATTCATTTGAGGACAGCATGGGGAG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCCTCAGCGCACCGGAGCGAGCGTGGCCCTCACCTCCATCAGCAATGTCAACGGCTTC	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTTCATGGCGCATTCATCCCTATCCCTGCGCTGGAGCGTTCCTCCCTCCAGGCTGTGTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGGGGGTATTCATATTTTGGCTATGGTTCCTGCTCATTTTCTGCAATTCATCAGCATG	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573
Db	1852	TTATACAGCGTGGAGCAGAGAATGGATATTTTCTGCTGTTTCAAGAGCCCTGTGTC	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIle	593
Db	1912	AGCAGGGTGATTCAAGTTTGAGCCACAGCGCTACACAGAGCTTCACAGTAAACCCCGTAC	1971
QY	593	eala-----HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCGCCACCCCATACACAGCCACAGCTTGGCCACGAAACCCATATCACTATGCAG	2031

Qy	602	----	AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProG1	620
Db	2032		TCCACCGTTTCAGCTCGGCACAGAGTATACCCCTCACAGCGCTGACTACACCAACCGCC	2091
Qy	620	nAlaHis-----	LeuValProProProSerAspProLeuGlyse	633
Db	2092	GAGCCACGCTCTGAGATCTCTGTACAGCGCTGTTTACCGTCACCCAG-GACAACCTTCAGCTG	2150	
Qy	633	rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653	
Db	2151	TCAGATGCCGAGAGACACAGCTCTACAGGACCTGCTCTCCAGTCTTCAGACTCC--	2208	
Qy	653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673	
Db	2209	----AGCCTCCACTGCTCGAGCCCTGCACCAAGTGGACACTCTCTTCGTTTGCAGA	2264	
Qy	673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPh	693	
Db	2265	GAAGCACTATGCTCTTCTCTCTGAACCCAAAGCCAAAGTTGTGGTAAATCTCTCTTTT	2324	
Qy	693	eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIle	713	
Db	2325	CCTGGGCTTGTGGGGTTCAGCTTTATGGACACCCTCGAGTGAGAGACGGCTGACCT	2384	
Qy	713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy	733	
Db	2385	CACGGACATTTCCCGCGAAACACAGAAATATGACTTCATAGCTGCCAGTTCAAGTA	2444	
Qy	733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerG1	753	
Db	2445	CTTCTCTTTACAACTATATAGTACCCAGAAAGCA---GACTCCCGAATATCCA	2501	
Qy	753	nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro	773	
Db	2502	GCACCTACTTTACGACCTTCATAGAGTTTCAGCAATGTCAAGTATGTCATGCTGGAGCA	2561	
Qy	773	oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeG1	793	
Db	2562	GAACAAGCAACTTCCCAANTGTGGCTGCCTACTTTAGAGACTGGCTTCAAGGACTTCA	2621	
Qy	793	nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnG1	813	
Db	2622	GGATGCATTTACAGAGTCACTGGGAACCTGGGAGGATCATGCCAAACAATATATAAATGG	2681	
Qy	813	ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr	833	
Db	2682	ATCAGATGACGGGGTCTCGCTTCACAACTCTCTGGTCAGACTGGCAGCGAGACAGCC	2741	
Qy	833	oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProPr	853	
Db	2742	CATCCACATTAGTCAGTTGACTAAACAGCGCTCTGGTAGCGACATGGCATTCATTAATCC	2801	
Qy	853	oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl	873	
Db	2802	GAGCGCTTTCTACATCTACCTGACCGCTTGGGTGAGCAACGACCTCTAGCTTACGCTGC	2861	
Qy	873	aSerGlnAlaAsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrTh	893	
Db	2862	CTCCGAGGCCAATATCCGGCTTCCCGGCGAGTGGGTCCATGACAAAGCCGACTACAT	2921	
Qy	893	rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912	
Db	2922	GCCAGAGACCGGCTGAGAAATCCCGAGCAGCAGAGCCCATCGATCGCTTCAGTTCCCTTT	2981	
Qy	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932	
Db	2982	CTACCTCAACGGCCCTACGAGACACCTCGACTTTGTGGAAAGCCATAGAAAGTGAGAGT	3041	
Qy	932	aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952	
Db	3042	CATCTGTAACTATACGAGCGCTGGACTGTTCAGCTTACCCCAATGCTACCCCTTCCT	3101	
Qy	952	uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe	972	

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Db 3102 GTTCTGGAGCAATACATCAGCGCTGGCCAGCTGGCTGCTATCATCAGCGTGGTCT 3161
QY
Db 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 992
Db 3162 GGCCTGCAGCTTCTAGTGTGGCGAGTCTTCTCTGAACCCCTGGACGGCGGGATCAT 3221
QY
Db 992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyTl 1012
Db 3222 TGTATGCTCTGGCTGTGATGACCGTTGAGCTCTTGGCATGATGGCGCTCATGGGAT 3281
QY
Db 1012 eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032
Db 3282 CAAGCTGAGTGTGGCTGTGGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 3341
QY
Db 1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
Db 3342 CACGCTCCAGCTGTGGCTTGGCTTCTGACAGCCATTGGGACACAGACACACAGGGCTAT 3401
QY
Db 1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuG 1072
Db 3402 GCTCGCTCTGAACACATGTTTGTCCGTTCTCGAGCGTGTGCTGCTGCTGCTGCTGCT 3461
QY
Db 1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092
Db 3462 TGTACTGATGCTGCAGGGTCCGAATTTGATTTCATTGTCAGATACTTCTTTCGCGCTCT 3521
QY
Db 1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuLeuProValLeuLeuSe 1112
Db 3522 GGCAATCTCACGCTGTGGGGTCTCAATGGAGTGGTCTGCTGCTGCTGCTGCTTATC 3581
QY
Db 1112 rLeLeuGlyProProGluValIle-----GlnMetTyrLysG 1126
Db 3582 CTTCTTTGGACCGTGTCTCAGGTGTCTCCAGCCAAATGGCGCTAAACCGACTGCCCACTCC 3641
QY
Db 1126 uSerProGluLeuSerProPro-----AlaProGlnGlyGlyLe 1141
Db 3642 TTGCGCTGAG-----CCGCTCCAAAGTGTGTCGGGTTTTCGGTGTGCTGCTGCTGCTG 3695
QY
Db 1141 uArgTyrGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db 3696 GAACAATGGTGTGATCTCTCCAGTCCGAGTACAGTCTCTCAGACACCGGTGTCTGGCAT 3755
QY
Db 1159 ----- 1159
Db 3756 CAGTGAGGAGCTCAGCAATACGAACACAGCAGGAGTGTGGGAGGCGCTGCCACCAAGT 3815
QY
Db 1160 -----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177
Db 3816 GATTGTGGAGCCACAGAAACCTGTCTTTGCCGCTCCACTGTGTGCTCCATCCGAGCTC 3875
QY
Db 1177 aProAspGluProProTyrSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
Db 3876 CAGACATCAGCTCTCTGACCCCTCGGCAACAGCCCACTGGGACTCTGGGCTCTGTGTC 3935
QY
Db 1194 rSerArgGlyProGly 1199
Db 3936 C-----CCTGA 3942

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RESULT 11

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US-09-754-032-9
; Sequence 9, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco

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; STATE: CA
; COUNTRY: US
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-754-032-9

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Alignment Scores:

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Pred. No.: 6-28e-303 Length: 5187
Score: 3337.00 Matches: 677
Percent Similarity: 69.59% Conservative: 204
Best Local Similarity: 53.48% Mismatches: 306
Query Match: 53.20% Indels: 80
DB: 10 Gaps: 20

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US-09-990-046-2 (1-1203) x US-09-754-032-9 (1-5187)

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QY 3 ArgSerProProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr 20
Db 178 CGCGCGCGCGCGCGCGCGGACTATCTGCACCGCGCCAGTACTGCG---GACGCGCGCTTC 234
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTrpLeuArg 37
Db 235 GCTCTGGAGCAGATTTCGAAGGGGAGGCTACTGGCGGAAAGCGCGCTGTGGCTGAGA 294
QY 38 AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys 57
Db 295 GCGAAGTTCAGAGACTCTTATTAACTGGGTGTTTACATTTCAAAGAAGTTCGCGCAAG 354
QY 58 ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle 77
Db 355 TTTTGGTGTGGGTCTCTCATATTGGGCGCTTCGCTGTGGGATTAAAGCGACTAAT 414
QY 78 IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu 97
Db 415 CTCGAGACCAACGTTGGAGAGCTGTGGTGGAGTTGGTGACGAGTGCAGTGAATA 474
QY 98 HisTyrThrLysGluLysLeuGluGluAlaAlaTyrThrSerGlnMetLeuIleGln 117
Db 475 AATTATACCCGTCAGACATAGAGAGAGGCTATGTTTAACTCTCAACTCATGATACAG 534
QY 118 ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisGln 137
Db 535 ACTCCAAAAGAAGAAGCGCTTAATGTTCTGCACACAGAGGCTCTCTCGAACACCTGCAC 594
QY 138 AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn 157
Db 595 TCAGCACTCCAGGCCAGTCTGTGTGACGCTCTACATGTATTAACAGGCAATGGAAGTTGAA 654

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QY	158	LysileCysTyrLysSerGlyValProLeuileGluAsnGlyMetileGluTrpMetile	177	QY	514	LeuMetAlaLeuValProileProAlaLeuArgAlaPheSerleuGlnAlaile	533
Db	655	CATTGTGCTACAAATCAGGGAACTTATCAGGAGACAGAGGTATACATGGATCAGATAATA	714	Db	1732	TTATGGCGGCATTTGATCCCTATCCCTGCGAGGTTCTCCCTCCAGGCTGCTG	1791
QY	178	GluLysLeuPheProCysValileLeuThrProLeuAspCysPheTrpGluGlyAlaLys	197	QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaileLeuSerLeuAsp	553
Db	715	GAATACCTTTACCTTGTCTTAATCATTTACCTTTGGACTGCTTCTGGGAGGGGCAAG	774	Db	1792	GTGGTGGTATTCAATTTTGGCTATGGTTCTGCTCATTTTCTCGCAATTTCTCAGCATGAT	1851
QY	198	LeuGlnGlySerAlaTyrLeuProGlyArgProAspileGlnTrpThrAsnLeuAsp	217	QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerSerProCysSer	573
Db	775	CTACAGTCCGGGACAGCATACCTCTAGTAGGCTCTCTTACGGTGGGACAACTTTGAC	834	Db	1852	TTATACAGAGCTGAGACAGAGATGGATATTTTCTGCTTTTTCACAGCCCTGTGTC	1911
QY	218	ProGluGlnLeuLeuGluLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu	236	QY	574	AlaGlnValileGlnLeuProGlnGluLeuGlyAspGlyThrValProValGlyL	593
Db	835	CCCTTGAATTCCTAGAGAGTTAAAGAAATAAACTACCAAGTGGACAGCTGGGAGAA	894	Db	1912	AGCAGGCTGATTCAAGTTGAGCCACAGGCTTACACAGAGCCTCACAGTAACCCCGGTAC	1971
QY	237	LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp	256	QY	593	eAla-----HisLeuThrAlaThrValGln-----	601
Db	895	ATGCTGAATAAAGCCGAAGTTGGCCATGGGTACATGGACCGGCTTTCCTCAACCCAGCC	954	Db	1972	AGCCCCCCCCCCCCATACACCGCCACAGCTTCGCCCCAGAAACCATATCATATGCGAG	2031
QY	257	AspLeuHisCysProProSerAlaProCAsnHisHisSerArgGlnAlaProAsnValAla	276	QY	602	---AlaPheThrHisCysGluAlaSerSerGlnHisValValThrileLeuProGln	620
Db	955	GACCCAGATTGCCCTGCCACAGCCCTTACAAATAATTCACCAAACTCTTGATGTGCC	1014	Db	2032	TCACCGTTTCAGTCCGACAGAGTATGACCTTCACAGCAGCTGTACTACACCCGCC	2091
QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296	QY	620	nAlaHis-----LeuValProProProSerAspProLeuGlySe	633
Db	1015	CTTGTGTTGATGGTGGATGTCAGGTTTATCCAGGAAGTATATGATTTGGCAGGAG	1074	Db	2092	GAGCCACGCTCTGAGATCTGTACAGCCTGTTCACCTGTCACCCAG-GACAACTCAGCTG	2150
QY	297	LeuLeuGlyGlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeu	316	QY	633	rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653
Db	1075	TTGATTGTGGTGTACCGTCAAGATGCCACTTGGAAATCTGTACAGGCTCAGCCCTG	1134	Db	2151	TCAGAGTCCCGAGAGCAGCAGCTCTACCGGGACCTGCTCTCCAGTTCTCAGACTCC--	2208
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp	335	QY	653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673
Db	1135	CAACCATGTTCCAGTTAATGACTCCCAAGCAATATGTAACACTTCAGGGGTACGAC	1194	Db	2209	---AGCTCCACTGCTCGAGCCCTCGACCAAGTGGACACTCTCTCTGTTTGAGA	2264
QY	336	TyrGlnThrHisAspileGlyTrpSerGluGluAlaSerThrValLeuGlnAlaTrp	355	QY	673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaileValLeuValLeuPh	693
Db	1195	TATGCTCTCAC---ATCACTGGAATGAAGACAGGCGCCATCTCTGGAGGCTGG	1251	Db	2265	GAAGCACTATGCTCTTCTCTGAAACCCCAAGCCAAAGTTGTGTATCTCTCTTT	2324
QY	356	GlnArgArgPheValGlnLeuAlaGlnAlaLeuProGluAsnAlaSerGlnGlnile	375	QY	693	eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe	713
Db	1252	CAGAGGACTTACGTGGAGTGGTTCATCAAGTGTGCCCCCAAACTCCACTCAAAAGTG	1311	Db	2325	CCTGGCTTGTGGGGTTCAGCTTTATGGGACCCCGAGTGAGAGCGGGCTGGACCT	2384
QY	376	HisAlaPheSerSerThrLeuAspAspileLeuHisAlaPheSerGluValSerAla	395	QY	713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy	733
Db	1312	CTTCCCTTCACACCCAGCCCTGGACGACATCTTAAATCCTTCTCTGATGTCAGTGTC	1371	Db	2385	CACGGACATTTCCCGGGGAACACAGAGAATATGACTTCATAGCTGCCAGTTCAAGTA	2444
QY	396	AlaArgValValGlyGlyLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415	QY	733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl	753
Db	1372	ATCCGAGTGGCCAGCGGCTACTGATGCTTGCCTATGCTGTGTTAACCATGCTGGC	1431	Db	2445	CTTCTCTTTCACAACTATATATAGTACCCAGAAAGCA---GACTACCCGATATATCCA	2501
QY	416	TrpAspCysAlaGlnSerGlnLysSerValGlyLeuAlaGlyValLeuValAlaLeu	435	QY	753	rArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProPro	773
Db	1432	TGGGACTGCTCAAGTCCAGGCTGCGGTGGGCTGGCTGGCTGGCTGGCTGGCTGG	1491	Db	2502	GCACCTACTTACGACCTTCATAAGATTTTCAGCAATGTGAGTATGTCTCATGCTGGAGA	2561
QY	436	AlaValAlaSerGlyLeuLeuCysAlaLeuLeuGlyLileThrPheAsnAlaAlaThr	455	QY	773	oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLileGl	793
Db	1492	TCAGTGGCTGACAGATTGGGCTCTGCTCTTGTATGTCATTTTAAATGCTCGGACA	1551	Db	2562	GAACAGCACTTCCCCAAATGTGGCTGCTACTTTAGAGACTGGCTTCAAGGACTTCA	2621
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyLileGlyValAspAspValPheLeuAla	475	QY	793	nAlaAlaPheAspGlnAspTrpAlaSerGlyArgLileThrArgHisSerTyrArgAsnGl	813
Db	1552	ACTCAGGTTTTCGGCTTCTTCTGCTGGTGGTGGATGCTCTTCTCTGCTGGC	1611	Db	2622	GGATCATTTGACAGTGTGCGGAACTGGGAGGATCATGCCAAATATATAAATATGG	2681
QY	476	HisAlaPheThrGluAlaLeuProGly-----ThrProLeuGlnGluArgMetGlyGlu	493	QY	813	ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuileGlnThrGlyAspAlaGlnGluPr	833
Db	1612	CATGCATTGAGTGAACACAGACAGATAAGAGATTCATTTGAGGACAGGACTGGGAG	1671	Db	2682	ATCAGATGACGGGGTCTCTGCTTACAACTCCTGGTGAGACTGSCAGCCGAGACAAGCC	2741
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerLileAsnAsnMetAlaAlaPhe	513	QY	833	oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuileProPr	853
Db	1672	TGCTTCAAGGCGACCGGACCGCTGGCCCTCACCTCCATCAGCAATGTCACCGCTTC	1731	Db	2742	CATCGACATTAGTCAAGTTGACTTAAACAGCGCTGGGTAGCAGGATGGCATTAATATCC	2801
				QY	853	oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl	873

Db	2802	GAGCGCTTTCTACATCTACCTGACCGCTGGGTGAGCAACGACCTGTAGCTTACGGTGC	2861
QY	873	aSerGlnAlaAsnPhetYrProProProGluTrpLeuHisAspIysTyrAspThrTh	893
Db	2862	CTCCACAGGCCAATCCCGGCTTACCGGCGGAGTGGGTCCATGACAAAGCCGACTACAT	2921
QY	893	rglyGlu---AsnLeuArgilleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912
Db	2922	GCCAGAGACCGCTGAGATCCCAAGCAGCAGAGCCCATCAGTACGCTCAGTTCCTCTT	2981
QY	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932
Db	2982	CTACCTCAACGGCTTACGAGACACCTCAGACTTTGTGAAGCCCATGAAAAGTGAGAGT	3041
QY	932	aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952
Db	3042	CATCTGTAACTATACGACGCTGGGACTGTCAGCTACCCCAATGGCTACCCCTTCCT	3101
QY	952	uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeu	972
Db	3102	GTTCTGGAGCAATACATCAGCTGCGCCTGCTGCTATCCATCAGCGTGGTGCT	3161
QY	972	uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIl	992
Db	3162	GGCTGCAAGCTTTCTAGTGTGCGAGTCTCTCTGAACTGGAGCGCGGGATCAT	3221
QY	992	eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyIl	1012
Db	3222	TGTATGGTCTGGCTCTGATGACCGTTGAGCTCTTTGGCATGATGGGCTCATTTGGAT	3281
QY	1012	eLysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh	1032
Db	3282	CAAGCTCAGTGCTGCTGCTGGTCACTCTGATTCATCTGTGGCATCGAGTGAGGTT	3341
QY	1032	eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl	1052
Db	3342	CACCGTCCAGCTGGCTTTGGCTTTCTGACAGCCATTGGGGACAAGAACCCACAGGCTAT	3401
QY	1052	aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl	1072
Db	3402	GCTCGCTCTCGAACACATGTTGCTCCGCTTCGGACGGTGTGTGTCACCTCTCGTGG	3461
QY	1072	YLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe	1092
Db	3462	TGTACTCATGCTTCAGGGTCCGAATTGATTTCAATTGTACAGACTCTTTGCCGCTCT	3521
QY	1092	uThrValLeuLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe	1112
Db	3522	GGCAITTCACCGTCTGGGGTTCCTCAATGACTGTTCTGCTGCTCTCTCTCTCTATC	3581
QY	1112	rIleLeuGlyProProGluValIle-----GlnMetTyrLysGl	1126
Db	3582	CTTCTTTGGACCGTGTCTGAGTGTCTCCAGCAATGGCTTAAACCGACTGCCCACTCC	3641
QY	1126	uSerProGluIleLeuSerProPro-----AlaProGlnGlyGlyGlyLe	1141
Db	3642	TTGCGCTGAG-----CCGCTCCAAAGTGTGCTCGGTTTGGCGGCTCTCGTGCACAC	3695
QY	1141	uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----	1159
Db	3696	GAACAATGGGTCTGATTCTCTCGACTCGGAGTACAGCTCTCAGACACCGTGTCTGGCAT	3755
QY	1159	-----	1159
Db	3756	CAGTGAGGAGCTCAGGCATACGAAGCACAGCAGGTCGCGAGCGCTGCCCAACCAAGT	3815
QY	1160	----MetThrValAlaIleHisProProLeuProGlyAlaTyrIleHisPro---Al	1177
Db	3816	GATTGTGGAAGCACAGAAACCCCTGTCTTTGCCCGGTCCACTGTGTGTCATCCGACTC	3875
QY	1177	aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe	1194

```

Db      3876 CAGACATCAGCCTCCCTTTGACCCCTCGGAAACAGCCCCACCTGGACTCTGGCTCTTGTC 3933
Qy      1194 rSerArgGlyProGly 1199
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Db      3936 C-----CCTGGA 3942

RESULT 12
US-10-421-446-3
; Sequence 3, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-421-446--3

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Alignment Scores:	
Pred. No.:	6.28e-303
Score:	337.00
Percent Similarity:	69.5%
Best Local Similarity:	53.48%
Query Match:	53.20%
DB:	15
	15
	Gaps:
	20
	Indels:
	80
	Mismatches:
	106
	Conservative:
	204
	Matches:
	677
	Length:
	5187

US-09-990-046-2 (1-1203) x US-10-421-446-3 (1-5187)

QY	3	ArgSerProProLeuArgGluLeu-----ProProSerTyrThrProProAlaArgThr	20
Db	178	CGCGCGCGCGCGACGGAGCTATCTCGACGGCCAGCTACTGC---GACGCGCGCTTC	234
QY	21	AlaAlaProGlnIleLeuAlaGlySerLeu-----LysAlaProLeuTrpLeuArg	37
Db	235	GCTCTGGAGACAGATTCCAGGGGAAGCTACTGGCGGAAACGCGCTGTGGTGTAGA	294

QY	38	AlaTyrPheGlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLys	57
Db	295	CGGAGTTTCAGAGACTCTTAATTAACCTGGGTTGTATCAATCAAAAGAACTGGCGCAG	354
QY	58	ValLeuPheLeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIle	77
Db	355	TTTTTGGTGTGGGCTCTCTATATTTGGGGCTTCGTCTGGGATTAAGGACGCTAAT	414
QY	78	IleGluThrAsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeu	97
Db	415	CTCGAGACCAACGTCGAGAGCTGGGTGGAGTTGGTGGACGAGTGAATCGAGAAATTA	474
QY	98	HisTyrThrLysGluLysLeuGlyGluAlaLeuAlaTyrThrSerGlnMetLeuIleGln	117
Db	475	AATTATACCGCTCAGAAATAGAGAAAGAGGCTATGTTAATCCTCAACTCATGATACAG	534
QY	118	ThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGln	137
Db	535	ACTCCAAAAGAAAGCGCTAATGTTCTGACCAAGAGGCTCTCTCTGCAACACCTGGAC	594
QY	138	AlaAlaLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsn	157
Db	595	TCAGCACTCAGCCAGTCGTGTGCGCTCATCATGATAACAGGCAATGGAAGTTGGAA	654
QY	158	LysIleCysTyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIle	177
Db	655	CATTGTGTCTACAAATCAGGGAACTTATCAGCGAGACAGGTTTACATGATCAGATAATA	714
QY	178	GluLysPhePheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLys	197
Db	715	GAATACCTTTACCTTCTTAATCATTTACACCTTTGGACGTCTCTGGGAGGGGCAAG	774
QY	198	LeuGlnGlyGlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAsp	217
Db	775	CTACAGTCCGGGACAGCACTACCTCTTAGGTAAAGCTCTTACGGTGGCAAACTTTGAC	834
QY	218	ProGluGlnLeuLeuGluGlyLeuGlyProPhe---AlaSerLeuGluGlyPheArgGlu	236
Db	835	CCCTTGGAAATTCCTAGAAGAGTTAAAGAAAATAAATCAACAGTGGACACTGGAGGAA	894
QY	237	LeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAsp	256
Db	895	ATGCTGAATAAAGCGAAGTTGGCCATGGGTACATGACCGCCCTTCCCTCAACCCAGCC	954
QY	257	AspLeuHisCysProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValala	276
Db	955	GACCCAGATTGCCCTGCCACAGCCCTTAACAAAATTCACCAAAACCTCTTGATGTGCC	1014
QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGlu	296
Db	1015	CTTGTTTGAATGTGGATGTCAAGGTTTATCCAGGAAGTATATGCAATTGGCAGAGGAG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeu	316
Db	1075	TTGATGTGGTGGTACCGTCAAGAAATGCCACTGAAAACCTTGTCAGCGCTCAGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly---Asp	335
Db	1135	CAACCATGTTCCAGTTAATGACTCCCAAGCAATGATGAACACTTCAGGGGTATCGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCTCTCAC---ATCAACTGGAATAGACAGGGCAGCGCCATCTGGAGCCCTGG	1251
QY	356	GlnArgArgPheValGlnAlaGlnAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGTGGTTCATCAAGTGTGCGCCCAAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerSerThrThrLeuAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCACAAACCGACCTGGACGACATCTTAAATCTCTCTGATGTCACTGTCT	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCAGTGGCCAGCGGTACTACTGATGCTTGCTATGCTGCTGCTGCTGCTGCTGCTG	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCAAGTCCAGGGTGGCTGGGGCTGGCTGGCTGGCTGGCTGGCTGGCTG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTGGCAGGATGGGCTCTGCTCTGCTGATGATGCTGCTCTCTCTCTCTCT	1551
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475
Db	1552	ACTCAGGTTTGGCGTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1611
QY	476	HisAlaPheThrGluAlaLeuProGly---ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGCAATTCAGTGAACAGGACAGCAATTAAGAGGATTCCTATTGAGGACAGGACTGGG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCTCAAGCGCACCGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTCATGGCCGCTATGCTCTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGCTGTATTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysCysPheSerProCysSer	573
Db	1852	TTATACAGAGCTGAGACAGAGATTTGGATATTTCTGCTGCTGCTGCTGCTGCTGCTG	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly---ThrValProValGlyI	593
Db	1912	AGCAGGTTGATTCAAGTTGACCAAGGCTACACAGAGGCTCACAGTACACCCCGTAC	1971
QY	593	eAla---HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCCCCCCCCATACACCGCCACAGCTTCGCCCAACCCCATATCATCATGACG	2031
QY	602	---AlaPheThrHisCysGluAlaSerSerGlnHisValThrIleLeuProGly	620
Db	2032	TCACCGCTTCCGACAGATGATGACCTCACAGCGCTGCTACTACACCGCC	2091
QY	620	nAlaHis-----LeuValProProSerSerProLeuGlySe	633
Db	2092	GAGCCACGCTCTGAGATCTCTGTACAGCTGTTTACCGCTCACCCAG-GACAACTCAG	2150
QY	633	rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr	653
Db	2151	TCAGAGTCCCGAGACCGAGCTCTACAGGAGCTGCTCTCCAGCTTCTCAGACTCC--	2208
QY	653	gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr	673
Db	2209	---AGCTCCAGTCCCTCGAGCCCCCTGCACCAAGTGGACACTCTCTCTGTTGAGA	2264
QY	673	gTyrGlnPheAlaProLeuLeuGlnSerHisAlaLysAlaIleValLeuValLeuPhe	693
Db	2265	GAAGCACTATGCTCTCTCTCTGAAAACCCCAAGCAAGGTTGTGTAATCTCTCTCT	2324
QY	693	eGlyValAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAla	713
Db	2325	CCTGGCTTGTGGGGTTCAGCTTTATGGACCAACCGAGTGGAGACGGGCTGGACCT	2384
QY	713	uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy	733
Db	2385	CACGACATTTGTTCCCGGAAACAGAGAAATATGACTTTCATAGTGTGCTGCTCAAGTA	2444
QY	733	rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl	753

Db 2445 CTTCTCTTTCTACACATATATATAGTACCCAGAAAGCA---GACTACCCGAATATCCA 2501
 QY 753 nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
 Db 2502 GCACCTACTTTACGACCTTCATAAGAGTTTACAGCAATGTGAAGTATGTCTCGAGGA 2561
 QY 773 oAlaThrGlnAlaProArgThrTIPLeuHisTyrTyrArgAsnTIPLeuGlnGlyLeu 793
 Db 2562 GAACAAGCAACTTCCCAAAATGTGGCTGCACTACTTTAGAGACTGGCTTCAAGGACTTCA 2621
 QY 793 nAlaAlaPheAspGlnAspTIPAlaSerGlyArgIleThrArgHisSerTyrArgAsnG1 813
 Db 2622 GGATGCATTTTCACAGTGTGCTGGAAACTGGAGAGTATGCAACAAATATATAAATGG 2681
 QY 813 ySerGlnuAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
 Db 2682 ATCAGATGACGGGGTCTTCGCTTACAACTCTGTGTGAGACTGGCAGCCGAGACAAGCC 2741
 QY 833 oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGlnGlyLeuIleProPr 853
 Db 2742 CATGCATATTAGTCAGTTGACTAAACAGCGTCTGTGTAGACGCAATGATCAATTATTC 2801
 QY 853 oGluLeuPheTyrMetGlyLeuThrValTIPValSerSerAspProLeuGlyLeuAla 873
 Db 2802 GAGCGCTTTTACATCTACCTGACCGCTTGGGTGAGCAACAGCCCTGTGTAGCTTACGCTGC 2861
 QY 873 aSerGlnAlaAsnPheTyrProProProGluTIPLeuHisAspLysTyrAspThrTh 893
 Db 2862 CTCCAGGCCCAACATCCGGCTCACCGCGCGAGTGGGTGCTGACAAAGCCGACTACAT 2921
 QY 893 rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
 Db 2922 GCCAGACACCGGCTGAGATCCAGCAGCAGAGCCCATCGAGTACGCTCAGTTCCTTT 2981
 QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
 Db 2982 CTACCTCAACGGCTACGACACCTCAGACTTTGTGGAAGCCATAGAAAAGTGAGAGT 3041
 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
 Db 3042 CATCTGTAAACAATATACGAGCGCTGGAGCTGTCAGCTACCCCAATGGCTACCCCTTCT 3101
 QY 952 uPheTIPGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
 Db 3102 GTTCTGGAGCAATATACAGCTGCGCCACTGGCTGCTATCCATCAGCGTGTGTCT 3161
 QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuAsnProTIPThrAlaGlyLeu1 992
 Db 3162 GGCCTGCAGCTTTCTAGTGTGGCAGCTTCTCTCTGAACCCCTGGACGCGCGGATCAT 3221
 QY 992 eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGly1 1012
 Db 3222 TGTATGTGCTCTGCTGTGATACCGCTTGAGCTCTTTGGCATGGGCTCATTTGGAT 3281
 QY 1012 eLysLeuSerAlaIleProValValLeuValAlaSerValGlyIleGlyValGluPh 1032
 Db 3282 CAAGCTGAGTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3341
 QY 1032 eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAla 1052
 Db 3342 CACGCTCCAGTGGCTTTGGCTTTCTGACAGCCATTGGGAGCAAGAACACAGGGCTAT 3401
 QY 1052 aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuG1 1072
 Db 3402 GCTGCTCTGGACACATGTTGCTTCCGCTTCTGACGCTGCTGCTGCTGCTGCTGCTGCT 3461
 QY 1072 yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092
 Db 3462 TGTACTGATGCTGCGAGGTCGGAATTTGATTTCACTGTCAGATACCTTTTGGCGTCT 3521
 QY 1092 uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112

Db 3522 GGCATTTCTCAACCGCTTTGGGGTTCTCAATGCACTGGTTCTGCTGCTGCTCTTATC 3581
 QY 1112 rIleLeuGlyProProGluValIle-----GlnMetTyrIlysG1 1126
 Db 3582 CTTCTTTGGACCGTGTCTGTAGGTGTCTCCAGCCAATGGCTTAAACCGCACTGCCCACTCC 3641
 QY 1126 uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
 Db 3642 TTGCGCTCAG-----CCGCTCCCAAGTGTGTCCGGTTTCCGGTCCCTCTGGTCAACAC 3695
 QY 1141 uArgTIPGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
 Db 3696 GAACAATGGGTCTGATTCCTCCGACTCGAGTACAGCTCTCAGACCAACGGTGTCTGGCAT 3755
 QY 1159 ----- 1159
 Db 3756 CAGTGAGGAGCTCAGGCAATACGAGGACACAGCGGTGCGGAGGCCCTGCCCAAGT 3815
 QY 1160 ----MetThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisPro---Al 1177
 Db 3816 GATTGTGGAAGCCACAGAAACCCCTGTCTTTGCGCGGTCCACTGTGTGCTATCGGACTC 3875
 QY 1177 aProAspGluProProTIPSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
 Db 3876 CAGATACAGCTCCCTTGACCCCTCGGCAACAGCCCAACCTGCGACTCTGCTGCTGCTC 3935
 QY 1194 rSerArgGlyProGly 1199
 Db 3936 C-----CCTGGA 3942

RESULT 13

US-10-421-446-9
 ; Sequence 9, Application US/10421446
 ; Publication No. US20030186309A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; ; GOODRICH, LISA V
 ; ; JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/421,446
 ; FILING DATE: 22-Apr-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/724,631
 ; FILING DATE: 28-No. US20030186309A1-2000
 ; APPLICATION NUMBER: US/08/656,055
 ; FILING DATE: 1996-05-31
 ; APPLICATION NUMBER: 08/540,406
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5187 base pairs

QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296
Db	1015	CTTGTTTGAATGGTGGATGTCAGAGTTTATCCAGGAAGTATATCATTTGGCAGAGGAG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlyLeuLeuArgAlaGluAlaLeu	316
Db	1075	TTGATTTGGTGGTACCGTCAGAAATGCCATCGAAACCTTGTGAGCCCTCAGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly	335
Db	1135	CAAAACCATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTCAGGGGTCACGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCCTCAC--ATCAACTGGAATGAAGACAGCGCAGCCCATCTCTGGAGGCTGG	1251
QY	356	GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGGTGTTCAATCAAGGTGTCGCCCAAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCACACACACGACCTGGACGATCTTAAATCTCTCTGTATGTCAGTGTC	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCGAGTGCCACGCGCTACTTACTGATGCTTGCCTATGCTGCTTAACTGCTGCGC	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCCAAAGTCCCGAGGTGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTGCAGATGGGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1551
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475
Db	1552	ACTCAGGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1611
QY	476	HisAlaPheThrGluAlaLeuProGly--ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGCATTCAGTGAACACGACGAGAAATAGAGGATTCATTTGAGCAGCAGCAGCTGG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCCTCAAGCCACCGGACGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTTCATGGCGCATTTGATCCCTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGGTGATTCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysPheSerSerProCysSer	573
Db	1852	TTATACAGCTGAGGACAGAGATTTGATATTTCTGCTGCTGCTGCTGCTGCTGCTG	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIle	593
Db	1912	AGCAGGGTGAATCAAGTTGAGCCACAGGCTTACAGAGGCTTCAAGTAAACCCGGTAC	1971
QY	593	eala-----HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCCCCACCCTCATACAGGACGACGCTGCGCCACGAAACCATATCATCTATGTCAG	2031
QY	602	-----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	2032	TCCACCGTTACGCTCGGACAGAGTATGACCTTCACGACGCTGCTGCTGCTGCTGCTG	2091
QY	620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633

QY	277	HisGluLeuSerGlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlu	296
Db	1015	CTTGTTTGAATGGTGGATGTCAGAGTTTATCCAGGAAGTATATCATTTGGCAGAGGAG	1074
QY	297	LeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGlyLeuLeuArgAlaGluAlaLeu	316
Db	1075	TTGATTTGGTGGTACCGTCAGAAATGCCATCGAAACCTTGTGAGCCCTCAGCCCTG	1134
QY	317	GlnSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGly	335
Db	1135	CAAAACCATGTTCCAGTTAATGACTCCCAAGCAATGTATGAACACTTCAGGGGTCACGAC	1194
QY	336	TyrGlnThrHisAspIleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrp	355
Db	1195	TATGTCCTCAC--ATCAACTGGAATGAAGACAGCGCAGCCCATCTCTGGAGGCTGG	1251
QY	356	GlnArgArgPheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIle	375
Db	1252	CAGAGGACTTACGTGGAGGTGTTCAATCAAGGTGTCGCCCAAACTCCACTCAAAAGGTG	1311
QY	376	HisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAla	395
Db	1312	CTTCCCTTCACACACACGACCTGGACGATCTTAAATCTCTCTGTATGTCAGTGTC	1371
QY	396	AlaArgValValGlyGlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArg	415
Db	1372	ATCCGAGTGCCACGCGCTACTTACTGATGCTTGCCTATGCTGCTTAACTGCTGCGC	1431
QY	416	TrpAspCysAlaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeu	435
Db	1432	TGGGACTGCTCCAAAGTCCCGAGGTGGCTGGGCTGGCTGGCTGGCTGGCTGGCTGG	1491
QY	436	AlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	455
Db	1492	TCAGTGGCTGCAGATGGGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1551
QY	456	ThrGlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAla	475
Db	1552	ACTCAGGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1611
QY	476	HisAlaPheThrGluAlaLeuProGly--ThrProLeuGlnGluArgMetGlyGlu	493
Db	1612	CATGCATTCAGTGAACACGACGAGAAATAGAGGATTCATTTGAGCAGCAGCAGCTGG	1671
QY	494	CysLeuGlnArgThrGlyThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPhe	513
Db	1672	TGCCTCAAGCCACCGGACGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1731
QY	514	LeuMetAlaAlaLeuValProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIle	533
Db	1732	TTTCATGGCGCATTTGATCCCTATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1791
QY	534	ValValGlyCysThrPheValAlaValMetLeuValPheProAlaIleLeuSerLeuAsp	553
Db	1792	GTGGTGATTCATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1851
QY	554	LeuArgArgArgHisCysGlnArgLeuAspValLeuCysPheSerSerProCysSer	573
Db	1852	TTATACAGCTGAGGACAGAGATTTGATATTTCTGCTGCTGCTGCTGCTGCTGCTG	1911
QY	574	AlaGlnValIleGlnIleLeuProGlnGluLeuGlyAspGly-ThrValProValGlyIle	593
Db	1912	AGCAGGGTGAATCAAGTTGAGCCACAGGCTTACAGAGGCTTCAAGTAAACCCGGTAC	1971
QY	593	eala-----HisLeuThrAlaThrValGln-----	601
Db	1972	AGCCCCCACCCTCATACAGGACGACGCTGCGCCACGAAACCATATCATCTATGTCAG	2031
QY	602	-----AlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	2032	TCCACCGTTACGCTCGGACAGAGTATGACCTTCACGACGCTGCTGCTGCTGCTGCTG	2091
QY	620	nAlaHis-----LeuValProProSerAspProLeuGlySe	633

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-421-446-9

Alignment Scores:
Pred. No.: 6,28e-303 Length: 5187
Score: 3337.00 Matches: 677
Percent Similarity: 69.59% Conservative: 204
Best Local Similarity: 53.48% Mismatches: 306
Query Match: 53.20% Indels: 80
DB: 15 Gaps: 20

US-09-990-046-2 (1-1203) x US-10-421-446-9 (1-5187)


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Db      2092 GAGCCACGCTGTGAGATCTCTGTACAGCGCTGTACCGTCAACCCAG-GACAACTCAGCTG 2150
QY      rGluLeuPheSerProGlyGlySerThrArgAspLeuLeuGlyGlnGluGluThrAr 653
Db      2151 TCAGAGTCCGAGACACAGCTCTACAGGAGACCTGCTCTCCCACTCTCTCAGACTCC-- 2208
QY      gGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrpAsnLeuAlaHisPheAlaAr 673
Db      2209 ----AGCCTCAGCTGCTCGAGCCCTCGACCAAGTGGACACTCTCTCGTTTGGCAGA 2264
QY      gTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLysAlaLilValLeuValLeuPh 693
Db      2265 GAAGCACTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2324
QY      eGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLe 713
Db      2325 CTTGGCTTGTGGGGTCAAGCTTTATGGGACCAACCGAGTGAGAGACGGCTGGACCT 2384
QY      uThrAspValValProArgGlyThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTy 733
Db      2385 CACGGACATTTCTCCCGGAAACCCAGAGATATGACTTCTATAGCTGCCAGTTCAAGTA 2444
QY      rPheSerLeuTyrGluValAlaLeuValThrGlnGlyGlyPheAspTyrAlaHisSerGl 753
Db      2445 CTTCTCTCTTCTACAACATGTATATAGTCAACCAAGCA--GACTACCCGAATATCCA 2501
QY      nArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeuLysAlaValLeuProProPr 773
Db      2502 GCACCTACTTTACGACCTTCATAGAGTTTCAGCAATGTGAAGTATGTATCTGCTGGAGGA 2561
QY      oAlaThrGlnAlaProArgThrTrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyLeGl 793
Db      2562 GAACAAGCAACTTCCCAATATGGCTGCTACTACTTTAGAGCTGGTTCAGAGACTTCA 2621
QY      nAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyrArgAsnGl 813
Db      2622 GGATGCATTTGACAGTGAAGTGGGAAACCTGGAGGATCATGCCAAACAAATATAAATGG 2681
QY      ySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluPr 833
Db      2682 ATCAGATGACGGGTCTCTCGTTACAACTCTGGTGGAGCTGGCAGCGCGAGCAAGCC 2741
QY      oLeuAspPheSerGlnLeuThrThrArgLysLeuValAspArgGluGlyLeuLeuProPr 853
Db      2742 CATCGACATTAGTCAGTTGACTTAAACAGCGTCTGGTAGCGAGATGGCATCAATATCC 2801
QY      oGluLeuPheTyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAl 873
Db      2802 GAGCGCTTTCTATCTACCTGACCGCTTGGGTGAGCAACGACCCCTGTAGCTTACGCTGC 2861
QY      aSerGlnAlaAsnPheTyrProProProProGluTrpLeuHisAspLysTyrAspThrTh 893
Db      2862 CTTCCAGGCCAACATCCCGCCCTCACCGCGGAGTGGTCCATGACAAAGCGGCTATCAT 2921
QY      rGlyGlu---AsnLeuArgIleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
Db      2922 GCCAGAGACCGGCTGAGAAATCCAGCAGCAGCCCATCGAGTACGCTCAGTCTCCCTTT 2981
QY      eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
Db      2982 CTACCTCAACGGCTTACGAGACACCTCAGACTTTGTGGAAGCCATAGAAAAGTGAGAGT 3041
QY      aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db      3042 CATCTGTAAACTATACAGCGCTGGACTGTCAGCTACCCCAATGGCTACCCCTTCTCT 3101
QY      uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
Db      3102 GTTCTGGGAGCAATACATCAGCTCGGCTGGCTGTCTATCCATCAGCGTGGTCT 3161
QY      uValCysThrPheLeuValCysAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 992

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Db      3162 GGCCTGACGTTTCTAGTGTGGCAGTCTTCTCTCTGAACCCCTGGACGGCCGGGATCAT 3221
QY      eValLeuValLeuAlaMetMetThrValGluLeuPheGlyIleMetGlyPheLeuGlyLl 1012
Db      3222 TGTATGCTCTGCTGGCTGTGATGACCGTTGAGCTCTTTGGCATGTGGGCTCATTTGGGAT 3281
QY      elysLeuSerAlaIleProValValIleLeuValAlaSerValGlyIleGlyValGluPh 1032
Db      3282 CAAGCTGAGTCTGCTGCTGTGGTTCATCTGATTGATCTGTTGGCATCGAGTGGAGTT 3341
QY      eThrValHisValAlaLeuGlyPheLeuThrThrGlnGlySerArgAsnLeuArgAlaAl 1052
Db      3342 CACGCTCACGTGCTTTGGCTTTCTGACAGCCATTGGGACCAAGAACACACAGGCTAT 3401
QY      aHisAlaLeuGluHisThrPheAlaProValThrAspGlyAlaIleSerThrLeuLeuGl 1072
Db      3402 GCTCGCTCTGGAACACATGTTTGTCTCCGTTCTCGACGGTCTGTGCTCTGCTCTTATC 3461
QY      yLeuLeuMetLeuAlaGlySerHisPheAspPheIleValArgTyrPhePheAlaAlaLe 1092
Db      3462 TGTACTGATGCTTGCAGGGTCCGAATTTGATTTCATTTGATTCATGTCAGATACTTCTTGGCGCTCT 3521
QY      uThrValLeuThrLeuLeuGlyLeuLeuHisGlyLeuValLeuLeuProValLeuLeuSe 1112
Db      3522 GGCAATTTCTCACGCTCTTGGGGTCTCTCAATGGACTGGTTCTGCTGCTCTCTCTTATC 3581
QY      rIleLeuGlyProProGluValIle-----GlnMetTyrLysGl 1126
Db      3582 CTTCTTTGACCGCTGCTGAGGTGTCTCCAGCAATGGCTTAAACGACTGCCCACTCC 3641
QY      uSerProGluLeuLeuSerProPro-----AlaProGlnGlyGlyLe 1141
Db      3642 TTGCGCTGAG-----CCGCTCCAAAGTGTGCTGGGTTTGGCGTTCCTGCTCTGTCACAC 3695
QY      uArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSer----- 1159
Db      3696 GAACAATGGTCTGATTCTCCGACTCGGAGTACAGCTCTCAGACCAACGCTGCTGSCAT 3755
QY      ----- 1159
Db      3756 CAGTGAGGAGCTCAGCAATACAGACACAGCGGTGGCGGAGGCTGCCCAACAGT 3815
QY      ----MetThrValAlaIleHisProProProProGlyAlaTyrIleHisPro---Al 1177
Db      3816 GATTGTGGAAGCCACAGAAAACCTGTCTTTGCCGGTCCACTGTGTGCTCATCCGACTC 3875
QY      aProAspGluProProTrpSerProAlaAla-----ThrSerSerGlyAsnLeuSe 1194
Db      3876 CAGACATCAGCTCTCCCTTGACCCCTCGGCAACAGCCCACTGGACTCTGCTGCTTGTG 3935
QY      rSerArgGlyProGly 1199
Db      3936 C-----CCTGGA 3942

```

RESULT 14

US-10-302-279-1

; Sequence 1, Application US/10302279

; Publication No. US20030171566A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael Carlton

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; Holmberg-Lindstrom, Erika

; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

us-09-990-046-2.rnpb

91	SerArgValSerGlnGluLeuHisTyrThrLysGlnLysLeuGlyGluGluGluAlaAlaTyr	130
388	GGACGAGTAAGTCGTGAATTAAATTACTCGCCAGAGAATTGGAGAAGAGCGCTATGTTT	447
111	ThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThrProGlu	130
448	AAATCCTCAACTCATGATACAGACCCCTAAAGAAGAAGTGCTATATGTCCTGACCACAGAA	507
131	AlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSerLeuTyr	150
508	GCGCTCCTCAACACCTTGGACTCGGCACCTCAGSCCAGCCGTGTCATGTATACATGTAC	567
151	GlyIysSerTrpAspLeuAsnLysIleCysTyrIysSerGlyValProLeuIleGluAsn	170
568	AACAGCGAGTGGAAATTCGAACATTTGTGTGTACAAATCAGGAGAGCTTATCACAGAAACA	627
171	GlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrProLeuAsp	190
628	GGTTACATGGATCAGATAATAGATAATCTTTACCCCTGTTGTGATATTATACACCTTTGGAC	687
191	CysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyIleValProAsp	210
688	TGCTTCTGGGAAGGGCGAAATTACAGTCTGGGACAGCATACCTCCTAGGTAAACCTCCT	747
211	IleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluLeuGlyProPhe--Ala	229
748	TTGGCGTGGACAAACTTCGACCCCTTGGAAATTCCTTGGGAAGAGTTAAAGAAATAACATAT	807
230	SerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGly	249
808	CAAGTGGACAGCTGGGAGAAATGCTGAATAAGGCTGAGGTGGTTCATGGTTTACATGGAC	867

[illegible]

QY	349	SerThrValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaLeuPro	368
		::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::	
DB	1165	GCAGCCATCTCTGAGGCGCTGGCAGAGGACATATGTGGAGTGGTTCATCAGAGTGTGGCA	1224
		::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::	
QY	369	GluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHis	388
		::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::	
		1284

...-P₁-G₂-G₃...Val¹Val²Val³Val⁴Gly⁵Gly⁶Gly⁷Val⁸Met⁹Leu¹⁰Ala¹¹Tyr¹² 408

1285	TCCTTCTCAGCTCAGTGTCA	TCGCGTGGCCAGCGGTACTTACTCATGCTCGCCTAT	1344
	:::	:::	
409	AlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeuAla	428	
	:::	:::	
1345	GCCTGTCTAACCATGTGCGCTGGAGTGTCTCCAAAGTCCACAGGTCCGCTGGGGCTGGCT	1404	
	:::	:::	
429	GlyValLeuLeuValAlaAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGly	448	
	:::	:::	
1405	GGCGTCTGCTGGTGTGCACCTGTCAAGTGGCCAGGACTGGCGCTGTGCTCATTTGATCGGA	1464	
	:::	:::	
449	IleThrPheAsnAlaIleThrThrGlnValLeuProPheLeuAlaLeuGlyIleGlyVal	468	
	:::	:::	

[illegible]

D	b		2536	GACTGGCTTCAGGACATTCAGATGCATTGTGACAGTGA	CCTGGGAAACCGGAAAAATCATG	2595
Q	y		807	ArgHisSerThrArgAsnGlySerGluAspGlyAlaLeuAla	TyrlsLeuLeuIleGln	826
D	b		2596	CCAAACAATTACAGNATGGATCAGACGATGAGTCCIT	GGCTCAAAACTCCTGGTGCAA	2655
Q	y		827	ThrGlyAspAlaGlnclupProLeuAspPheSerGlnLeu	ThrThrArgLysLeuValAsp	846
D	b		2656	ACCGGAGCGCGATAAAGCCATCAGATCGACCAGTTGAT	AACACAGCGCTCGTGGAT	2715
Q	y		847	ArgGluGlyLeuIleProProGluLeuPheTyrlMetGly	LeuThrValTrpValserSer	866
D	b		2716	GCAGATGGCATTAATCCAGCGCTTTTACATCTACCT	ACGCGGTGGGTGAGTCA	2775
Q	y		867	AspProLeuGlyLeuAlaAlaserGlnAlaAsnPheTyrl	ProProProGluTrpLeu	886
D	b		2776	GACCCCGTCGGTAGTCTGCCCTCCAGGCCAACATCC	GGCCACACCGACAGAATGGTC	2835
Q	y		887	HisAspLysTyrlAspThrThrGlyclu---	AsnLeuArgIleProProAlaGlnProLeu	905
D	b		2836	CACGACAAAGCCGACTACATGCCTGAAACAGGCTG	AGAAATCCCGGCAGACAGCCCATC	2895
Q	y		906	GluPheAlaGlnPheProPheLeuLeuArgGlyLeuGln	LysThrAlaAspPheValGlu	925
D	b		2896	GAGTAGCCCAAGTTCCTCTTCTACTCAACGGCTT	GGGACACCTCAGACTTTGTGGAG	2955
Q	y		926	AlalIeGluGlyAlaArgAlaAlaCyAlaGlnAlaGly	GlnAlaGlyValHisAlaTyrl	945
D	b		2956	GCAATTGAAAAGTAAGGACCATCTGCAGCACTAT	ACAGACCTGGGGCTGTCCAGTTAC	3015
Q	y		946	ProSerGlySerProPheLeuPheTrpGluGlnTyrl	LeuGlyLeuArgArgCysPheLeu	965
D	b		3016	CCCCACGGCTACCCCTCTCTCTGGAGCAGTACAT	CGCCTCCGCCACTGGCTGCTG	3075
Q	y		966	LeuAlaValCysIleLeuLeuValCysThrpheLeuVal	CysAlaLeuLeuLeuLeuAsn	985
D	b		3076	CTGTTCACACGGTGGTGGCGCTGCACATCTCT	GTGGCTGTCTCTCTCTGAAAC	3135
Q	y		986	ProTrpThrAlaGlyLeuIleValLeuValLeuAla	MetMetThrValGluLeuPheGly	1005
D	b		3136	CCCTGGACGGCGGATCAATTGTGATGCTCTGG	CGCTGATGACGCTGAGCTGTTCGGC	3195
Q	y		1006	IleMetGlyPheLeuGlyIleLysLeuSerAlaIle	ProValValIleLeuValAlaser	1025
D	b		3196	ATGATGGCCCTCATCGGAATCAAGCTCAGTCC	CGTCCCGTGGTCACTCTGATCGCTTCT	3255
Q	y		1026	ValGlyIleGlyValGluPheThrValHisValAla	LeuGlyPheLeuThrThrGlnGly	1045
D	b		3256	GTGGCATAGAGTGGAGTTACCGTTACGTTGCT	TTTGGCCCTTCTGACGGCCCATCAGC	3315
Q	y		1046	SerArgAsnLeuArgAlaAlaHisAlaLeuGluH	isThrPheAlaProValThrAspGly	1065
D	b		3316	GACAAAGACCGCAGGCTGTGCTTGGCCCTGG	AGCACATGTTTGACCCGCTCTGGATGGC	3375
Q	y		1066	AlaIleSerThrLeuLeuGlyLeuLeuMetLeu	AlaGlySerHisPheAspPheIleVal	1085
D	b		3376	CGCGTGTCCA	CTCTGTGGAGTGTGATGCTGGCGGATCTGAGTTCGACTTCATTCATGTC	3435
Q	y		1086	ArgTyrlPhePheAlaAlaLeuthrValLeuThr	LeuLeuGlyLeuLeuHiGlyLeuVal	1105
D	b		3436	AGGTATTTCTTGCTGTGTGGACATCC	TACCATCTCGCGGTCTCAATGGGTGTT	3495
Q	y		1106	LeuLeuProValLeuLeuSerIleLeuGlyPro	ProProGluVal-	1120
D	b		3496	TTGCTTCCCGTGCTTTGTCTTTTGACCATAT	CTCTGAGGTGTCTCCAGCCACGGC	3555
Q	y		1120	-----	-----	1120
D	b		3556	TTGAACCGCTGCCACACCCCTCCCTTGAGCC	ACCCCCACCGCGTGGTTCGCTTCGCCATG	3615
Q	y		1120	-----	-----	1120
D	b		3616	CCGCCCGGCCACAGCACAGCGGTCTGATTC	TCTCCGACTCGAGTAGTATTCACGACG	3675

Db 1225 CAGAACTCCACTCAAAAGGTGTTCTTCCTCACCACCAGCAGCCTGGACGACATCCTGAAA 1284
 QY 389 AlapheSerGluValSerAlaAlaargValValGlyGlyrleuLeuMetLeuAlaTyr 408
 Db 1285 TCCTTCTCTGAGCTCAGTGTCTATCGCGTGGCCAGCGGTACTTACTCAATGCTCGCCTAT 1344
 QY 409 AlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGlyLeuAla 428
 Db 1345 GCCTGTCTAAACCATCTCGCTGGGACTGCTCCAAGTCCAGGGTGGCGTGGGGTGGCT 1404
 QY 429 GlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGly 448
 Db 1405 GCGTCTCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1464
 QY 449 IleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIleGlyVal 468
 Db 1465 ATTTCTTTAACGCTGCAACAACTCAGGTTTGGCTTTCTGCTTCTGGTGGTGGTGGT 1524
 QY 469 AspAspValPheLeuLeuAlaAlaPheThrGluAlaLeuProGly-----ThrPro 486
 Db 1525 GATGATGTTTCTTCTGCGCCAGCCTTCAGTGAACACAGGACAGAAATAAAGATCCCT 1584
 QY 487 LeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyThrSerValLeuLeuThrSer 506
 Db 1585 TTTGAGGACAGGACCGGGAGTGGCTGAAGCGCAACAGGACGAGCGTGGCCTCACGTC 1644
 QY 507 IleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeuArgAla 526
 Db 1645 ATCAGCAATGTCACAGCTTCTTCAATGGCCGCTTAATCCCAATTCGCGCTCTCGGGCG 1704
 QY 527 PheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeuValPhe 546
 Db 1705 TTCTCCCTCAGGACGCGGTAGTAGTGTGTTCAATTTTGCCATGGTTCCTCATTTT 1764
 QY 547 ProAlaIleLeuSerLeuArgArgArgHisCysGlnArgLeuAspValLeuCys 566
 Db 1765 CTGTCAATTCAGCTGAGTATATATCGAGCGGACGAGGACTGGATATTTCTGC 1824
 QY 567 CysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeuGlyAsp 586
 Db 1825 TGTTTTACAAGCCCTGGCTCAGCAGAGTATTCAGGTTGAACCTCAGGCTCACCGAC 1884
 QY 587 -----GlyThrValProValGlyIleAlaHis----- 595
 Db 1885 ACACAGCAATACCGCTACAGCCGCCACCTCCCTACAGCAGCCACAGCTTGGCCAT 1944
 QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAlaSerSer 610
 Db 1945 GAAACCGCAGATTACCATGAGTCCATGTCCAGCTCCGACGAGGTACGACCCCCACAG 2004
 QY 611 GlnHisValThrIleLeuProProGlnAlaHisLeuValProPro----- 627
 Db 2005 CAGGTGTACTACACCCGCTGAGCGCGCTCGAGATCTCTGTGAGCCCGTCACCGTG 2064
 QY 628 ---SerAspProLeuGlySerGluLeuPheSerProGlySerThrArgAspLeuLeu 646
 Db 2065 ACACAGGACACCCCTCAGCTGCGCAGACCCAGAGCAGCAGCTCCACAGGACCTGCTC 2124
 QY 647 GlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAlaArgTrp 666
 Db 2125 TCCAGTCTCCGACTCC-----AGCTCCACTGCTCGAGCCCGCTGTACGAAGTGG 2178
 QY 667 AsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHisAlaLys 686
 Db 2179 ACACCTCATCTTTGCTGAGAGCACTATGCTCTCTTCTTGAACCAAAAGCCCAAG 2238
 QY 687 AlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAlaThrLeu 706
 Db 2239 GTAGTGGTGTCTTCTTCTGCGCTTGTGGGGTCAAGCTTTATGGCACACCCGA 2298
 QY 707 ValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHisAlaPhe 726
 Db 2299 GTGAGAGAGCGGCTGGACCTTACCGACATTTGACCTCGGGAACACAGAGATATGACTTT 2358

QY 727 LeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGlnGlyGly 746
 Db 2359 AATTGCTGCACAATTCAAATACTTTTCTTACACATGATATAGTACCCAGAAAGCA 2418
 QY 747 PheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSerSerLeu 766
 Db 2419 ---GACTACCCGAATATACGACCTTACTTTACGACCTACACAGGAGTTTCAGTACG 2475
 QY 767 LysAlaValLeuProProAlaThrGlnAlaProArgThrThrPleuHisTyrTyrArg 786
 Db 2476 AAGTATGTCATGTGGAGAAACAAACAGCTTCCAAATGTGGCTGCCTACTTCTCAGA 2535
 QY 787 AsnTrpLeuGlnGlyIleGlnAlaPheAspGlnAspTrpAlaSerGlyArgIleThr 806
 Db 2536 GACTGGCTTCAGGACTTCAGATGCATTTGACAGTGACTGGGAAACCGGAAATCATG 2595
 QY 807 ArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGln 826
 Db 2596 CCAACAACATTAACAAGATGGATCAGATCGATGGATGCTTGCCTACAACTCCTGTGTCAA 2655
 QY 827 ThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeuValAsp 846
 Db 2656 ACCGCGACCCGATAGCCCATCGACATCAGCAGTGTGCTAAACAGCGTCTGTGTGAT 2715
 QY 847 ArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTyrValSerSer 866
 Db 2716 GCAGATGGCATTAATCCAGCGCTTCTACATCTACCTGACGGTGGGTGAGCAAC 2775
 QY 867 AspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProProGluTrpLeu 886
 Db 2776 GACCCGCTCGCGTATGCTGCTTCCAGGCCAACATCCGCGCACACCCAGAGATGGTGC 2835
 QY 887 HisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGlnProLeu 905
 Db 2836 CACGACAAAGCCGACTACATGCTGCTGAAACAAAGCTGAGAAATCCCGGACAGACCCATC 2895
 QY 906 GluPheAlaGlnPheProPheLeuArgGlyLeuGlnLysThrAlaAspPheValGlu 925
 Db 2896 GAGTATGCCAGTCTCCCTTCTACCTCAAGCGCTTGGGGACACCTCAGACTTTGTGGAG 2955
 QY 926 AlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyr 945
 Db 2956 GCAATTTGAAAAAGTAAGGACCATCTGCAGCACTATACGAGCGCTGGGCTGTCCAGTTAC 3015
 QY 946 ProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeu 965
 Db 3016 CCCAAGCGTACCCCTTCTCTTCTGGGAGCAGTACATCGGCTCCGCCATCGGCTGTCT 3075
 QY 966 LeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsn 985
 Db 3076 CTGTTCATCAGCGTGGTGTGGCTGCATTTCTCGTGTGGCTGTCTCTTCTTGAAC 3135
 QY 986 ProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeuPheGly 1005
 Db 3136 CCCTGGAGCGCGGATCATTTGTATGTGTCTGGCGCTGATCAGGTCTCGAGCTTTCGCG 3195
 QY 1006 IleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaSer 1025
 Db 3196 ATGATGGCGCTCATCGGAATCAGCTCAGTGGCGGCGGTGCTGCTGATCGCTCTCT 3255
 QY 1026 ValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThrGlnGly 1045
 Db 3256 GTTGTCATAGGAGTGGAGTTCCCGTTCAGCTTGTGCTTGGCTTCTGACGCCCATCAGC 3315
 QY 1046 SerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGly 1065
 Db 3316 GACAAGAACCCGAGGGCTGTGCTTGGCCCTGGAGCACATGTTTGACCCCGTCTGTGATGCG 3375
 QY 1066 AlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal 1085
 Db 3376 CCGGTGCTCCTGCTGGGAGTGTGATGTGCGGGATCTGACTTTCGACTTCTGCTTCTGCTC 3435

Sun Nov 28 09:38:32 2004

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QY 1086 ArgTyrPheAlaLeuThrValLeuThrLeuGlyLeuHisGlyLeuVal 1105
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3436 AGGTATTTCTTGCTGTGTCATCTCACCATCTCGGCTTCTCAATGGCTGGTT 3495
QY 1106 LeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3496 TTGCTTCCCGTCTTGCTTCTTCTTGACCATATCTGAGGTGTCTCCAGCCACGGC 3555
QY 1120 ----- 1120
Db TTGAACGGCTGCCACACCTCCCTGAGCCACCCGAGCTGGTTCGCTTCGCCATG 3615
QY 1120 ----- 1120
Db CGCCCGGCCACACGACGACGGGTCTGATTCTCGACTCGGAGTATAGTTCCAGAGC 3675
QY 1121 ----- IleGlnMetTyr ----- 1124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3676 ACAGTGTACGGCTCAGCAGGAGCTTCGGCACTACGAGGCCCGAGCGCGGGAGGC 3735
QY 1124 ----- 1124
Db CCTGCCCAACCAAGTATGCTGGAAGCCACAGAAAACCCCTCTTCGCCCACTCCACTGTG 3795
QY 1125 ----- LysGluSerProGluIleLeu 1131
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3796 GTCCATCCGAAATCCAGGCATCACCCACCTCGAACCAGAAACAGAGCCGCCCTGGAC 3855
QY 1132 Ser-----ProAlaProGlnGly-----Gly 1139
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3856 TCAGGGTCCCTGCTTCCGGACGCGAGGCCAGCAGCCCGCAGGGACCCCGCAGAAA 3915
QY 1140 GlyLeu----- 1141
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3916 GGCTTGTGGCACCCCTCTACAGACCGCGCAGAGAGCTTTTGAAATTTCTACTGAAGG 3975
QY 1142 ----- ArgTyrGly----- 1144
Db CATTCGTGCCCTAGCAATAGGCGCCGCTGGGGCCCTCGCGGGCCGTTCTCAACCCCT 4035
QY 1145 ----- AlaSerSerLeuProGlnSerPheAlaArgValThr 1157
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4036 CGGAACCAACGTCCTACTGCCATGGCGAGCTCCGTCGCCGCTACTGCCAGCCCATCACC 4095
QY 1158 Thr-----SerMetThrValAlaIleHisProProLeuProGlyAla 1172
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4096 ACTGTGACGGCTTCGCTCGCTGACTGTCGCGGTGACCGCGCGCTGTCCCTGGGCT 4155
QY 1173 TyrIleHisPro 1176
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4156 GGGCGGAACCCC 4167

```

Search completed: November 22, 2004, 14:19:04
Job time : 1122 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:15 ; Search time 842 Seconds
(without alignments)

7500.064 Million cell updates/sec

Title:

Perfect score: 6272

Sequence: 1 MTRSPPLRELPSPYTPPART.....SPAATSSGNLSRRGPGPATG 1203

Scoring table:

BLOSUM62
Gapop 10.0 , Xgapext 0.5
Gapop 10.0 , Xgapext 0.5
Gapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO spool/US0990046/runat_21112004.130919.18522/app_query.fasta_1.1351
-DB=N_Geneseq 23Sep04 -QFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-USER=US0990046 @CGN 1.1.478 @runat_21112004.130919.18522 -NCFU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6272	100.0	4030	2	AAZ31717	Aaz31717 Human pat
2	6272	100.0	4030	6	AAZ31576	Aaz31576 Human pat
3	6272	100.0	4030	8	ABX15919	Abx15919 Human pat
4	6248	99.6	4391	2	AAZ89478	Aaz89478 Human pat
5	5911	94.2	3453	3	AAA09081	Aaa09081 Human pat
6	4682.5	74.7	12886	3	AAA09084	Aaa09084 Human pat

7	3955	63.1	4004	2	AAZ31728	Aaz31728 Human pat
8	3955	63.1	4004	6	AAZ31580	Aaz31580 Human pat
9	3955	63.1	4004	8	ABX15923	Abx15923 Human pat
10	3987	54.0	2082	2	AAZ31729	Aaz31729 Human pat
11	3987	54.0	2082	6	AAZ31581	Aaz31581 Human pat
12	3987	54.0	2082	8	ABX15924	Abx15924 Human pat
13	3949	53.4	5288	2	AAZ14220	Aat14220 Human pat
14	3949	53.4	5288	2	AAV64093	Aav64093 Human pat
15	3949	53.4	5288	5	AAF32185	Aaf32185 Human pat
16	3949	53.4	5288	9	ACA62839	Ac62839 Human pat
17	3949	53.4	5288	10	ADE94223	Ade94223 Human pat
18	3949	53.4	5288	10	ADH62730	Adh62730 Human pat
19	3949	53.4	5288	12	ADA48988	Ade48988 Human pat
20	3949	53.4	5288	6	ABA00374	Aba00374 Human pat
21	3937	53.2	5187	2	AAV21587	Aav21587 Mouse pat
22	3937	53.2	5187	2	AAV21589	Aav21589 Mouse pat
23	3937	53.2	5187	2	AAV64099	Aav64099 Mouse pat
24	3937	53.2	5187	2	AAV64092	Aav64092 Mouse pat
25	3937	53.2	5187	5	AAF32177	Aaf32177 Butterfly
26	3937	53.2	5187	5	AAF32180	Aaf32180 Murine pa
27	3937	53.2	5187	9	ACA62831	Ac62831 Full leng
28	3937	53.2	5187	9	ACA62834	Ac62834 Mouse pat
29	3937	53.2	5187	10	ADE94208	Ade94208 Peacock b
30	3937	53.2	5187	10	ADE94214	Ade94214 Murine pt
31	3937	53.2	5187	10	ADH62715	Adh62715 Butterfly
32	3937	53.2	5187	10	ADH62721	Adh62721 Mouse pat
33	3937	53.2	5187	12	ADH48979	Ade48979 Mouse pat
34	3937	53.2	5187	12	ADH48973	Ade48973 Butterfly
35	3937	53.2	5288	2	AAV21590	Aav21590 Human pat
36	3936	53.2	5288	2	AAV15949	Aav15949 Nevoid ba
37	3935	53.2	5187	2	AAV15948	Aat15948 Mouse pat
38	3931	53.1	5187	6	ABA00375	Aba00375 Mouse pat
39	3930	53.1	5187	6	ABA00376	Aba00376 Butterfly
40	3929	53.1	5187	6	ABX67232	Abx67232 Thyroid c
41	3929	53.1	5187	6	ABR84327	Abk84327 Human cDN
42	3173	50.6	7753	10	ADF81708	Adf81708 Leukaemia
43	3173	50.6	7753	10	ADF81706	Adf81706 Leukaemia
44	2797.5	44.6	2032	2	AAV69382	Aav69382 Human Pat
45	2003	31.9	3861	4	ABL04551	Ab104551 Drosophil

ALIGNMENTS

RESULT 1	AAZ31717	standard; DNA; 4030 BP.
ID	AAZ31717	
XX	AAZ31717	
AC	AAZ31717	
XX	AAZ31717	
DT	19-JAN-2000	(first entry)
XX	Human patched-2	coding sequence.
DE	Human patched-2	coding sequence.
XX	Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke; cell proliferation; cell differentiation; testicular cancer; gut disease; degenerative disorder; nervous system disorder; Parkinson's disease; memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia; Huntington's disease; drug addiction; bone disease; skin disease; ulcer; infertility; lung disease; pancreatic disorder; diabetes; osteoporosis; therapy; ss.	
OS	Homo sapiens.	
XX	WO9953058-A1.	
PN	WO9953058-A1.	
XX	21-OCT-1999.	
PD	21-OCT-1999.	
XX	02-APR-1999;	99WO-US007417.
PF	02-APR-1999;	99WO-US007417.
XX	15-APR-1998;	98US-00060939.
PR	15-APR-1998;	98US-00060939.
XX	(GETH) GENENTECH INC.	
PA	(GETH) GENENTECH INC.	
XX		

PI De Sauvage FU, Carpenter DA;
 XX WPI; 1999-620428/53.
 DR P-PSDB; AAY43261.
 XX
 XX New isolated human patched-2 gene, used to develop products for treating,
 PT e.g. cancer and Alzheimer's disease.
 XX
 XX Claim 1; Fig 1; 124pp; English.
 XX
 CC This sequence encodes the human patched-2 (ptch-2) protein of the
 CC invention. The patched-2 polypeptides are signalling molecules,
 CC specifically for signalling and mediator molecules in the hedgehog (hh)
 CC cascade which are involved in cell proliferation and differentiation.
 CC They can be used for the treatment of disorders which are mediated at
 CC least in part by hh, especially Dhh, e.g. testicular cancer. They can
 CC also be used for treating degenerative disorders of the nervous system,
 CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou
 CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
 CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
 CC diseases, skin diseases, diseases of the testis (including infertility),
 CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
 CC osteoporosis. Antagonists or agonists of patched-2 may be used for
 CC treating disorders or creating a desirable physiological condition
 CC effected by blocking hh signalling, especially Dhh signalling, e.g.
 CC contraception or infertility treatment. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic animals
 XX
 XX Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 0 Length: 4030
 Score: 6272.00 Matches: 1203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-990-046-2 (1-1203) x AAZ31717 (1-4030)

QY 1 MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
 Db 233 ATGACTGTGTCGGCGCCCTCAGAGAGCTGCCCGGAGTTACACCCCGAGCTCGAACC 292
 QY 21 AlaAlaProGlnLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 Db 293 GCACACCCAGATCCTAGCTGGGAGCTCGAAGGCTCCACTCTGGCTTCGTCTACTTC 352
 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 Db 353 CAGGGCTGCTCTCTCTGGATGGGATCCAGAGACATTGTGGCAAGTGTCTTT 412
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
 Db 413 CTGGGACTGTGGCTTGGGGCCCTGGCATAGTCTCCGATGGCCATTATTAGACA 472
 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 473 AACTTGGACAGCTCTGGTAGAAGTGGGAGCGGTGAGCGAGCTGCATTACACC 532
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 533 AAGGAGAAGCTGGGGAGAGGCTGCATACACCTCTCAGATGCTGATACAGCCGACGC 592
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
 Db 593 CAGGAGGAGAGAACATCTCTACACCCGAGACATTGGCTCCACCTCCAGGAGCCCTC 652
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 653 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAGTCTCTGGGATTTGAACAAATCTGC 712
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180

713 TACAAGTCAGGAGTTCCTCCCTTATTGAATAATGAATGATTGAGTGGATGATTGAGAGCTG 772
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyValAlaLysLeuGlnGly 200
 Db 773 TTTCCGTGCGGTGATTCCTTACCCCTTCTGAGGCTTCCGGAGGAGCAAACTCCAAAGG 832
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 Db 833 GGCTCCGCTTACCTGCGCGCGCGCGGATATTCAGTGGACCAACTGGATCCAGAGCAG 892
 QY 221 LeuLeuGluLeuGlyProPheAlaSerLeuGlyPheArgGluLeuLeuAspLys 240
 Db 893 CTGCTGGAGGAGCTGGGTCCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 952
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 Db 953 GCACAGGTGGGCGAGGCTTACGTGGGGGGGCTCTCTGTGCACCTGATGACCTCCACTGC 1012
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 Db 1013 CCACCTAGTGGCCCCCAACCATCACAGCAGGAGGCTCCCAATGTGGCTCACGAGTGA 1072
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGlnGluLeuLeuGly 300
 Db 1073 GGCGGCTGCATGGCTTCTCCCAAAATTCATGCACCTGGCAGAGGAATTCGTCTGGGA 1132
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
 Db 1133 GGATGGCCAGAGACCCCAAGAGAGCTGCTGAGGCGAGAGCCCTGCAGAGCACTTC 1192
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 Db 1193 TTGCTGATGATGCTCCCGCGAGCTGTACAGCAATTCGGGGGTGACTATCAGACATGAC 1252
 QY 341 IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
 Db 1253 ATTGCTGGAGTGAGGAGGAGCCACAGCTCTCAAGCTCAGTGTGCTGCTGCTGCTGCT 1312
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 Db 1313 CAGCTGGCCCGAGGAGGCTGCTGAGAGCTTCCAGCAGATCCATGCTCTCTCTCTCT 1372
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 Db 1373 ACCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
 QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
 Db 1433 GGCTATCTGCTCATGCTGGCTTATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1492
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 Db 1493 TCCGAGGGTTCCTGGGGGCTTCCCGGGGTACTGTGTGTGGCTTGGCGGTGGCTCAGGC 1552
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 Db 1553 CTGGGCTCTGTGGCTTCTGGCTTCTGGCTTCTGGCTTCTGGCTTCTGGCTTCTGGCT 1612
 QY 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 Db 1613 TTTCTGGCTCTGGGAATCGGGCTGGATGACGATTTCTTCTTCTGGCGCATGCCTTTCACAG 1672
 QY 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 Db 1673 GCTCTGCTGGCACTTCCAGGAGGCTGCGGAGTGTCTGTCAGCGCAGCGCGCACC 1732
 QY 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaValPro 520
 Db 1733 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1792
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540

Db	1793	ATCCCTGGCGTGGAGCCCTCTCCCTACAGCGCGCATAGTGGTGGCTGCACCTTTGTA	1851
Qy	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
Db	1853	GCCTGATGCTTGTCTTCCAGCCATCTTCAGCTGGACCTTACCGCGCGCCACTGCGCAG	1912
Qy	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db	1913	CGCCTTGATGTCTCTGTGCTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTG	1972
Qy	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
Db	1973	CCCCAGAGAGCTGGGGAGCGGACAGTACAGTGGGCATTGCCACCTCACTGCACAGTT	2032
Qy	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	2033	CAAGCCTTTACCCACTGTGAAGCAGCAGCAGCATGTGGTCAACATCTGCCTCCCAA	2092
Qy	621	AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db	2093	GCCCACTTGGTGCCCCCACTTTCGACCCACTGGGCTCTGAGCTCTTACGCTTGAGGG	2152
Qy	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnIleAlaCysIleSer	660
Db	2153	TCCACACGGGACCTTTAGGCCAGAGGAGAGAGCAAGGCAGAGAGCAGCTGCAAGTCC	2212
Qy	661	LeuProCysAlaArgTyrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
Db	2213	CTGGCCTGTGCCGCTGGAACTCTTGCCCATTTGCCCGCTATCAGTTTGCCTCGTGTGTG	2272
Qy	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
Db	2273	CTCCAGTCAATGCACAAAGGCATCTGCTGGTGTCTTTGGTGTCTTCTTGGGCTTGAGC	2332
Qy	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIleLeuThrAspValValProArgGly	720
Db	2333	CTCTACGGAGCCACTTGGTGGAGAGCGGCTGGCCCTCAGCGATGTGGTGTGCTCGGGGC	2392
Qy	721	ThrIysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
Db	2393	ACCAAGAGCATGCCTTCTGAGCGCCAGCTCAGTACTTCTCTCTGTACGAGGTGGCC	2452
Qy	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760
Db	2453	CTGGTGACCCAGGGTGGCTTTGACTACGGCCATTCACACGGCGCTCTTTGATCTGCAC	2512
Qy	761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780
Db	2513	CAGCGCTTCAGTTCCTCAAGCGGTGTCTGCCCCACCGGCCACCGACGCCCGGACC	2572
Qy	781	TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp	800
Db	2573	TGGCTGCATATTACCGCACTGGCTACAGGAAATCCAGGTGCTTTTGACACGAGATGG	2632
Qy	801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820
Db	2633	GCTTCTGGGGGATACCCCGCCACTCGTACCGCAATGGCTCTGAGAGTGGGGCCCTGGCC	2692
Qy	821	TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr	840
Db	2693	TACAAGCTCTCATCCAGACTGGAGACGCCCGCAGGAGCCTCTGGATTTTCAGCCAGCTGACC	2752
Qy	841	ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu	860
Db	2753	ACAAGGAAGCTGGTGACAGAGAGGAGCTGATTCCACCCGAGCTCTTCTACNTGGGGCTG	2812
Qy	861	ThrValTrpValSerSerAspProLeuGlyIleAlaAlaSerGlnAlaAsnPheTyrPro	880
Db	2813	ACCGTGTGGGTGAGCAGTGAACCCCTGGGCTCTGGCAGCCTCACAGGCGCACTTCTACCCC	2872
Qy	881	ProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro	900
Db	2873	CCACCTCTCTGAATGCTGCACGACAAATACAGACACACGGGGGAGAACCTTCGCATCCCG	2932

QY	901	ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr	920
Db	2933	CCAGCTCAGCCCTTGGAGTTTGGCCAGTTCCTCTTCTGCTGGCTGGCCTCCAGAAAGACT	2992
QY	921	AlaAspPheValGluAlaIleGluAlaArgAlaAlaCysAlaGluAlaGlyGlnAla	940
Db	2993	GCAGACTTTGTGGAGGCCCATCGAGGGGCCCCGGCAGCATGCGCAGAGCGCGCCAGGCT	3052
QY	941	GlyValHisAlaTyrProSerGlySerProPheLeuPheThrGluGlnTyrLeuGlyLeu	960
Db	3053	GGGGTGACCGCTACCCAGCGGCTCCCCCTTCTCTCTGGAAACAGTATCTGGGCGCTG	3112
QY	961	ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla	980
Db	3113	CGGCGCTGCTCTCTGCTGGCGGTCTGCATCTGTGTGGTGTGCATTTCTCGTCTGTGCT	3172
QY	981	LeuLeuLeuLeuAenProTyrThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr	1000
Db	3173	CTGCTGCTCTCTAACCCCTTGACGGCTGGCCCTCATAGTGTGGTCTGCGCATGTATGACA	3232
QY	1001	ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal	1020
Db	3233	GTGGAACTCTTTGGTATCATGGGTTTCTCGGCATCAAGCTAGTGGCCATCCCCGTGTGTG	3292
QY	1021	IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe	1040
Db	3293	ATCCTTTGTGGCCTCTGTAGGCATTTGGCGTTGAGTTTCACAGTCCAGTGGCTCTGGGCTTC	3352
QY	1041	LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla	1060
Db	3353	CTGACCACCCAGGGCAGCGGAACCTTCGGGCGGCCCATGCGCTTGAGCACACATTTGCC	3412
QY	1061	ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis	1080
Db	3413	CCCGTGACCGATGGGGCCATCTCCACATTTGCTGGGCTGTCTATGCTTGTGGTTCGCCAC	3472
QY	1081	PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu	1100
Db	3473	TTTGACTTCATTTGAAGTACTCTTTGGGGCGCTGACAGTGTCTCACGCTCCTGGGCTTC	3532
QY	1101	LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal	1120
Db	3533	CTCCATGGACTCGTGTCTGCTGTGCTGTGTCTCCATCTCTGGGCGCGCCAGAGGTG	3592
QY	1121	IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGlyGly	1140
Db	3593	ATACAGATGTACAAGAAAGCCAGAGATCTCTGAGTCCACGACTCCACAGGAGGGCGGG	3652
QY	1141	LeuArgTyrTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet	1160
Db	3653	CTTAGTGGGGGGCATCTCTCTCCCTGGCCCCAGAGCTTTGCCAGAGTGAACCTCCATG	3712
QY	1161	ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu	1180
Db	3713	ACCGTGGCCATCCACCCACCCCTCGCTGTGTGCTACATCATCCAGCCCTGTATGAG	3772
QY	1181	ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro	1200
Db	3773	CCCCCTGGTCCCTGCTGGCCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCGAGTCCA	3832
QY	1201	AlaThrGly	1203
Db	3833	GCCACTGGG	3841
RESULT 2			
AAD31576			
ID	AAD31576	standard; cDNA; 4030 BP.	
XX			
AC	AAD31576;		
XX			
DT	18-JUN-2002	(first entry)	
XX			

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us-09-990-046-2.rng

DE Human patched-2 (Ptc-2) cDNA.
 XX Human; patched-2; Ptc-2; cell proliferation; differentiation; therapy;
 KW cytostatic; testicular cancer; hedgehog protein signalling; ss.
 XX Homo sapiens.
 OS
 XX Location/Qualifiers
 FH Key 233..3844
 FT CDS
 FT /tag= a
 FT /product= "Human Ptc-2 protein"
 XX US6348575-B1.
 XX 19-FEB-2002.
 XX
 PF 15-APR-1999; 99US-00293505.
 XX
 PR 15-APR-1998; 98US-0081884P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX De Sauvage F, Carpenter DA;
 PI WPI; 2002-215260/27.
 DR P-PSDB; AAE19829.
 XX
 XX Native human patched-2 polypeptide for treating disorders caused by
 PT Hedgehog protein signaling such as testicular cancer, and for screening
 PT cDNA libraries.
 XX
 XX Example 1; Fig 1; 82pp; English.
 XX
 CC The invention relates to an isolated sequence comprising a native human
 CC patched-2 (Ptc-2) polypeptide. The invention also relates to signalling
 CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
 CC cell proliferation and differentiation. The isolated sequence is useful
 CC for the treatment of disorders which are linked to Hedgehog, especially
 CC Desert hedgehog expression, such as testicular cancer. It may also be
 CC used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its
 CC homologues, and to diagnose whether a disorder is driven by Ptc-2 or
 CC Hedgehog protein signalling. The present sequence is human patched-2
 CC (Ptc-2) cDNA
 XX
 XX Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 4030
 Score: 6272.00 Matches: 1203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-990-046-2 (1-1203) x AAD31576 (1-4030)
 QY 1 MetThrArgSerProLeuArgGluLeuProSerTyrThrProProAlaArgThr 20
 DB 233 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCCGAGCTCGAACC 292
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuAlaProLeuTrpLeuArgAlaTyrPhe 40
 DB 293 GCAGACCCCGAGATCCTAGCTGGAGCTGGAAGCTCCACTTGGCTTCGCTTACTTTC 352
 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 DB 353 CAGGGCTCTGCTCTCTCTGGAGCGGGATCCAGACATTTGTGGCAAGTGTCTTT 412
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGlnThr 80
 DB 413 CTGGGACTTGTGGCTTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT 472
 QY 81 AsnLeuGlnLeuTrpValGluValGlySerArgValSerGlnLeuLeuHisTyrThr 100

473 AACTTGGAACAGCTCTGGGTAGAGTGGCGAGCCGGGTGAGCCAGGAGCTGCATTACACC 532
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 DB 533 AAGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATCTGTATACAGACCCGACGC 592
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 DB 593 CAGGAGGAGAGACATCTCTACACCCGAGACCTTGGCTCCACCTCCAGGAGCCCTC 652
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTyrAspLeuAsnLysIleCys 160
 DB 653 ACTGCCAGTAAAGTCCAAAGTATCACTATATGGGAAGTCTCTGGGATTTGAACAAAATCTGC 712
 QY 161 TyrLysSerGlyValProLeuIleGluAenGlyMetIleGluTyrMetIleGluLysLeu 180
 DB 713 TACAAGTCAGGAGTTCCTCTTATGAAATGGAATGATTTAGTGGATGATTGAGAAGCTG 772
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTyrGluGlyAlaLysLeuGlnGly 200
 DB 773 TTTCCGTGCTGATCTCTACCCCTCGACTGCTTCTGGGAGGAGCCAACTCCCAAGGG 832
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTyrThrAsnLeuAspProGluGln 220
 DB 833 GGCTCCGCTTACCTGCGCCCGCGCCGATATCCAGTGGACCACTGGATCCAGAGCAG 892
 QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 DB 893 CTGCTGGAGAGCTGGGTCTCTTGGCTCCCTTGGAGGCTTCCGGGAGCTGTAGACAAG 952
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
 DB 953 GCACAGTGGCCAGGCTAGCTGGGCGCCCTGTCTGCACCTGATGACCTCCACCTGC 1012
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 DB 1013 CCACCTAGTGGCCCAACCATCAACAGCAGCAGGCTCCCAATGTGGCTCAGAGCTAGT 1072
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTyrGlnGluGluLeuLeuGly 300
 DB 1073 GGGGCTGGCTGGCTTCTCCCAAAATTCATGACCTGGCAGGAGGAATTTGCTGTGG 1132
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeuGlnSerThrPhe 320
 DB 1133 GGCTATGCCAGAGACCCCAAGGAGAGCTGTGAGGGCAGAGGCTTCGACAGACCTTC 1192
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 DB 1193 TTGCTGATGATCCCGCCAGCTGTACAGACATTTCCGGGGGTGACTATCAGACACATGAC 1252
 QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTyrGlnArgPheVal 360
 DB 1253 ATTGGCTGGAGTGGAGGAGCGCCAGCAGTGTCTACAGCTGGCAGCGCGCTTGTG 1312
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 DB 1313 CAGCTGGCCAGAGGCTCTGCTGAGAACCTTCCAGCAGATCCATGCTCTCTCTCC 1372
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValGly 400
 DB 1373 ACCACCTGGATGATCCTGCTGCTTCTTGAAGTCAGTGTGCCCGTGGTGGGA 1432
 QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTyrAspCysAlaGln 420
 DB 1433 GCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGCTGCTGGTGGAGCTGCGCCAG 1492
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAspGly 440
 DB 1493 TCCAGGCTTCCGTGGGCTTGGCGGGTACTGTGTGGTGGCTGGCTGGCTGGCTGGCT 1552
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460

Db 1553 CTTGGGCTCTGTGGCCCTGTGGCATACCTTCAATGTGTGCGCATACCCAGGTGTGCGCT 1612
Qy 461 PheLeuAlaLeuGlyVileGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTTCTGGCTCTGGGAATCGGCTGATGACGATATTCCTGTGGCGCATGCTTTCACAGAG 1672
Qy 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCTGCACCCCTCTCCAGAGCGCATGGCGAGTGTCTGCAGCGCACGGGCACC 1732
Qy 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
Db 1733 AGTGTGTACTCATCATCATCAACAACATGCGCGCTTCTCTCATGGCTGCGCTCGTTCCC 1792
Qy 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGCGTGCAGGCTTCTCCCTACAGCGGCATAGGTGTGGCTGCACCTTTGTA 1852
Qy 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db 1853 GCCGTGATGTGTCTTCCCGCATCTCTCAGCGCTGGACCTACGGCGCGCCACTGCGAG 1912
Qy 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCTTGTATGTCTGTCTCTCCAGTCCCTGCTCTCTCAGGTGATTCAATCCTG 1972
Qy 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCAGAGCTGGGGACGGGACAGTACAGTGGGCATTGCCACCTCACTGGCCACAGTT 2032
Qy 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGTGTACCATCTCGCTCCCAA 2092
Qy 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCACTGTGTGCCCCACCTCTGACCCACTGGGCTCTGAGCTTTCAGCCCTGGAGG 2152
Qy 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnIlyAlaAlaCysIlySer 660
Db 2153 TCCACAGGGACCTTCTAGCCAGGAGGAGGAGACAGGACAGGACGCTGCAAGTCC 2212
Qy 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCGCGCTGGAATCTTGCCATTTCGCCCGCTATCAGTTTGCCCGGTGCTG 2272
Qy 681 LeuGlnSerHisAlaIlyAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCAGTCACATGCCAAGGCCATCGTGTGTGTCTTTTGTGTCTCTTCTGGGCTGAGC 2332
Qy 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCACGGAGCCACTTGTGTGCAAGCGCCCTGGGCCCTGACGGATGTGTGTCTCGGGC 2392
Qy 721 ThrIlyGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGAGCATGCTTCTGAGCGCCCGAGCTCAGGTACTTCTCCCTGTACAGGTGGCC 2452
Qy 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTGACCCAGGGTGGTCTTGACTACGCCCATTCCTCCCAACGGCGCTCTTTGATCTGAC 2512
Qy 761 GlnArgPheSerSerLeuIlyAlaValLeuProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTTCCTCAAGCGGTGTGTGCCCCCAGCCCGGCACCCCGCACC 2572
Qy 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2573 TGGCTGCACTATTACCGCACTGGCTACAGGGAATCCAGGCTGCTTTGACACAGACTGG 2632
Qy 801 AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GCCTTCTGGGCGCATCACCGGCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692

Qy 821 TyrIlyLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAAGCTGTCTCATCCAGACTGGAGACCCAGAGGCTCTTGATTTTCAGCCAGCTGACC 2752
Qy 841 ThrArgIlyLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGGAAGCTGGTGGACAGAGAGGACTGATTCCACCCGAGCTCTTCTACATGGGGCTG 2812
Qy 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
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Qy 881 ProProGluTrpLeuHisAspIlyTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCTGAATGGCTGCACGCAAAATACGACACACAGGGGGAGAACCTTTCGCATCCCG 2932
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Qy 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
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Qy 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
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Qy 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3113 CGCGCTGTCTCTGTGTGGCGCTGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3172
Qy 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
Db 3173 CTGCTGCTCTCAACCCCTGGAGCGGCTGGCCTCATAGTCTGCTGCTGCGATGATGACA 3232
Qy 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3233 GTGGAACCTTTTGGTATCATGGGTTCTTGGGATCAAGCTGAGTGCCATCCCGTGGGTG 3292
Qy 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3293 ATCCTTGTGGCTCTGTAGGCAATTGGCGTTGAGTTACAGTCCACGTGCTGCTGGCTTC 3352
Qy 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3353 CTGACACCCAGGGCAGCGGAACTGCGGGCGGCCCATGCGCTTTCAGCACACATTTGCC 3412
Qy 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis 1080
Db 3413 CCCGTGACCGATGGGGCCATCTCCACATTTGTGGGTCTGTCTCATGCTTGTGGTTCCTCCAC 3472
Qy 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3473 TTTGACTTCAITGTAAAGTACTTCTTTGCGCGCTGACAGTGTCTACGCTCTGGGCTC 3532
Qy 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db 3533 CTCCATGAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3592
Qy 1121 IleGlnMetTyrIlyGlySerProGluIleLeuSerProProAlaProGlnGlyGly 1140
Db 3593 ATACAGATGTACAAAGGAAGCCAGAGATCTGTAGTCCACAGCTCCACAGGAGGGGG 3652
Qy 1141 LeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3653 CTTAGTGGGGGGCATCTCTCTCCCTGCCCGAGAGCTTTGCCAGAGTACTACCTCCATG 3712
Qy 1161 ThrValAlaIleHisProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3713 ACCGTGGCCATCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3772

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QY 1151 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
    |||||
Db 3773 CCCTCTGGCTCCCTGCTGCCACTAGCTCTGGCAACCTCAGTTCAGGGGACAGGTCCA 3832

QY 1201 AlaThrGly 1203
    |||||
Db 3833 GCCACTGGG 3841

RESULT 3
ABX15919
ID ABX15919 standard; DNA; 4030 BP.
XX
AC ABX15919;
XX
DT 02-APR-2003 (first entry)
XX
DE Human cDNA for patched-2 with vector sequences.
XX
KW Human; patched-2; Dhh signalling; proliferation; differentiation; ds;
KW chromosome lp33-34; male contraceptive; infertility; spermatogenesis;
KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; SNP;
KW single nucleotide polymorphism; desert hedgehog.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..212
FT /tag= a
FT /note= "Vector sequence"
FT CDS 233..3844
FT /tag= b
FT /product= "Patched-2"
FT /replace(3925,T)
FT /tag= c
FT /standard name= "Single nucleotide polymorphism"
FT misc_feature 3997..4030
FT /tag= d
FT /note= "Vector sequence"
XX
XX US2002156245-A1.
XX
XX 24-OCT-2002.
XX
XX 20-NOV-2001; 2001US-00990046.
XX
XX 15-APR-1998; 98US-0081884P.
XX 15-APR-1999; 99US-00293505.
XX (GETH ) GENENTECH INC.
XX
XX De Sauvage FU, Carpenter DA;
XX WPI; 2003-182650/18.
XX P-PSDB; ABG74104.
XX
XX New nucleic acid, useful for manufacturing a medicament for diagnosing or
XX treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
XX e.g., testicular cancer.
XX
XX Example 1; Fig 1; 85pp; English.
XX
XX The invention relates to a new isolated nucleic acid encoding a
XX polypeptide having patched-2 biological activity, comprises DNA having at
XX least 95% sequence identity with a DNA molecule or its complement
XX encoding: (a) a human patched-2 polypeptide comprising the sequence
XX ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ARCC
XX Deposit No. 209778 designation). Also included are a vector comprising
XX the nucleic acid, a host cell transformed with the vector, a process for

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CC producing patched-2 polypeptides, an isolated native sequence of human
CC patched-2 polypeptide, a chimeric molecule comprising the vertebrae of
CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC patched-2 that stimulates or enhances the normal functioning of patched-2
CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC and diagnosing to determine whether a particular disorder is modulated
CC The nucleic acid is useful for manufacturing a medicament for diagnosing
CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC Patched-2 may also be used to develop male contraceptives. The gene for
CC Patched-2 is located on human chromosome lp33-34. The present sequence is
CC the human cDNA for patched-2 (along with some vector derived sequences)
XX
XX Sequence 4030 BP; 728 A; 1297 C; 1141 G; 864 T; 0 U; 0 Other;
SQ
Alignment Scores: Length: 4030
Pred. No.: 0 Matches: 1203
Score: 6272.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB:
US-09-990-046-2 (1-1203) x ABX15919 (1-4030)
QY 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
    |||||
Db 233 ATGACTCGATCGCGCCCTCAGAGAGTCCGCCCGAGTTACACACCCCGAGCTCGAACC 292
QY 21 AlaAlaProGlnLeuAlaGlySerLeuLeuAlaProLeuTrpLeuArgAlaTyrPhe 40
    |||||
Db 293 GCAGACCCAGATCCTAGTGGGAGCCTGAAGGCTCCACTCTGGCTTCTGGTCTGTTACTTC 352
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
    |||||
Db 353 CAGGGCTGCTCTTCTCTCTGGGATGCGGATCCAGAGACATTGTGCAAGTCTCTTT 412
QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
    |||||
Db 413 CTGGGACTGTGGCTTTGGGCGCTTGGCATTTAGTCTCGCATGGCCATTATTAGAGACA 472
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
    |||||
Db 473 AACTTGGAAACAGCTCTGGGTAGAGTGGCGAGCGGGTGAGCCAGGAGCTGCATTACACC 532
QY 101 LysGlyLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
    |||||
Db 533 AAGGAGAGCTGGGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGACCCGACGC 592
QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGluAlaLeu 140
    |||||
Db 593 CAGGAGGGAGAGAAACATCTCACACCCGAGCACTTGGCCCTCCACCTCAGGAGCCCTC 652
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
    |||||
Db 653 ACTGCAGTAAAGTCCAAAGTATCCTCTATGGGAGTCTTGGGATTTGAAACAAATCTGC 712
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
    |||||
Db 713 TACAAGTCCAGAGTTCCTCCCTATTGAAATGGAATGATTGATGGATGATTGAGAAGCTG 772
QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
    |||||
Db 773 TTTCCGTGCGTGATCTCTCACCCCTCGACTCTTCTGGGAGGAGGCCAAATCTCAAGGG 832
QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTyrThrAsnLeuAspProGluGln 220
    |||||

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Db 833 GGCTCCGCTACTCTCCCGCGCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 892
QY 221 LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 893 CTGCTGGAGGAGCTGGGTCCCTTTGGCTTCCCTTTGAGGGCTTCCGGGAGCTGCTAGACAAG 952
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
Db 953 GCACAGGTGGGCCAGGCTACGTGGGGGGCCCTGTCTGCACTCCCTGATGACCTCCACTGC 1012
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 1013 CCACCTAGTGGCCCAACCAATCACAGCAGGAGGCTCCCAATGTGGCTCAAGAGCTGAT 1072
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
Db 1073 GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACTGGCAGGAGGAATTCCTCTCGGA 1132
QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 1133 GGCAATGGCCAGACACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGAGCACCTTC 1192
QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 1193 TTGCTGATGAGTCCCGCCAGCTGTACAGCATTTCCGGGGTGACTATCAGACACATGAC 1252
QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
Db 1253 ATTGGCTGGAGTGAGAGCAGCCAGCACAGTGTCTCAAGCCCTGGCAGCGCGCTTTGTG 1312
QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
Db 1313 CAGCTGGCCAGGAGGCCCTGCTGAGAACGCTTCCAGCAGATCCATGCTTCTCTCC 1372
QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
Db 1373 ACCACCTGTGATCAGATCCCTGTCATGGGTCTCTGAAGTCACTGCTGCGCGTGTGGGA 1432
QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
Db 1433 GGCTATCTGCTCATGTGGCCCTATGCTGTGTGACCATGCTGGGTGGGACTGCGGCCAG 1492
QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
Db 1493 TCCCAAGGTTCGCTGGCCCTTCCCGGGTACTGCTGTGGCCCTGGCGTGGCTCAGGC 1552
QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
Db 1553 CTGGGCTCTGTGCCCTGCTCGGCATCACCTTCAATGCTGCCACTACCCAGGTGCTGCCT 1612
QY 461 PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu 480
Db 1613 TTCTTGGCTCTGGGAATCGGCTGGATGACGATTCCTGCTGGCGATGCCCTTCACAGAG 1672
QY 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
Db 1673 GCTCTGCTGGCACCCCTCTCCAGAGGCCATGGGGGAGTGTCTGAGCGCACGGGCACCC 1732
QY 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaLeuValPro 520
Db 1733 AGTGTGCTACTCACATCCATCAACAACATGGCGGCTTCTCATGGCTGCCCTGCTTCCC 1792
QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTGGCTGCGAGCCTTCTCCCTACAGGGCCCATAGTGTGGTGGCTGCACCTTTGTA 1852
QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db 1853 GCCGTGATGTCTTCTCCAGCCATCTCAGCCTGGACCTACGGCGGGCCACTGGCCAG 1912
QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 GGCCTTGATGTGCTGTGCTGTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCTGT 1972

QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCCAGAGAGCTGGGGAGCGGACAGTACAGTGGGCATGGCCACTCCTGCCRACAGTT 2032
QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln 620
Db 2033 CAAGCCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGGTCACCATCTGCTCCCCCAA 2092
QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
Db 2093 GCCCAGCTGTGGTGGCCCACTTCTGAGCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 2152
QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
Db 2153 TCCACACGGGACCTTCTAGCCAGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGTCC 2212
QY 661 LeuProCysAlaAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCGCTGTGCGCGCTGGAATCTTGCCCAATTCGCCCGCTATCAGTTTGGCCCGTGTCTG 2272
QY 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
Db 2273 CTCCAGTCACTGCCAAGGCCATCGTGTGGTCTCTTTGGTGTCTTCTTGGGCTCAGC 2332
QY 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCTACGGAGCCACCTTGGTGCAGAGCGCTGGCCCTGACGATGTGGTGGCTTCGGGGC 2392
QY 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
Db 2393 ACCAAGGAGCATGCCCTTCTGAGCGCCAGCTCAGGTACTTCTTCTCCCTGTACGAGGTGCC 2452
QY 741 LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
Db 2453 CTGGTGACCCAGGTGGCTTGTACTACGCCCAATTCCTCAACGCGCCCTCTTGTATCTGCAC 2512
QY 761 GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
Db 2513 CAGCGCTTCAGTTCCCTCAAGCGGTGTGTCGCCCAACCGGCCACCCAGGACCCCGGCACC 2572
QY 781 TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrp 800
Db 2573 TGGCTGCATATTACCGCAACTGGGTACAGGGAATCCAGGCTGCCCTTTCACCGAGACTGG 2632
QY 801 AlaSerGlyArgGlnThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla 820
Db 2633 GTTCTGGGGCGCATCACCCGCCACTCGTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC 2692
QY 821 TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr 840
Db 2693 TACAAGCTGCTCATCCAGACTGGAGCGCCAGGAGCCCTCTGGATTTACGCCAGCTGACC 2752
QY 841 ThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeu 860
Db 2753 ACAAGAAAGCTGGTGGACAGAGGAGCTGATTCACCCGAGCTCTTCTACATGGGGCTG 2812
QY 861 ThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro 880
Db 2813 ACCGTGGGTGGAGCAGTGACCCCTGGGTCTGGCAGCTTCACAGGCCAACTTCTTACCCC 2872
QY 881 ProProGluTyrTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro 900
Db 2873 CCACCTCTGATGGCTGCACAGCAATATACACACACCGGGGAGAACCTTCGATCCCGC 2932
QY 901 ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr 920
Db 2933 CCAGCTCAGCCCTTGGAGTTGGCCAGTTTCCCTTCTGCTGCTGGCTCCAGAGACT 2992
QY 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 2993 GCAGCTTTGTGGAGGCCATCGAGGGGGCCCGGGCAGCATGCGCAGAGCGCGGCAGGCT 3052

QY 941 GlyValHisAlaTyrProSerClySerProPheLeuPheTrpGluGlnTyrLeuGlyLeu 960
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 Db 3053 GGGGTGCACGCCATACCCAGCGGCTCCCTTCCTCTTCTGGGAACAGTAATCTGGGCTG 3112
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 QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
 |||||
 Db 3113 CGCGCTGCTTCTCTGCTGCCCTGTGCATCTGCTGCTGGTGACATTCCTGCTGTGCT 3172
 |||||
 QY 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuLeuValLeuValLeuAlaMetMetThr 1000
 |||||
 Db 3173 CTGCTGCTCTCAACCCCTGGACGGCTGGCTCATAGTCTGCTGCTGGCATGATGACA 3232
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 QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLeuLeuSerAlaIleProValVal 1020
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 Db 3233 GTGGAACTCTTTGGTATCATGGTTCTCGGGCATCAAGCTGAGTGCCATCCCTGGTG 3292
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 QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
 |||||
 Db 3293 ATCTCTGTGGCTCTGTAGGCATTGGCTGTGAGTTCACAGTCCACGTGGCTCTGGGCTTC 3352
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 QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
 |||||
 Db 3353 CTGACCACCCAGGCGACCGGAACCTCGCGGCGCCCATGCTTGGAGCACATTTGCC 3412
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 QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuMetLeuAlaGlySerHis 1080
 |||||
 Db 3413 CCGCTGACCGATGGGCGCATCTCCACATTGCTGGGTCTGCTCATGTGCTGTTCCAC 3472
 |||||
 QY 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
 |||||
 Db 3473 TTTGACTTCTATTGTAGGTACTTCTTTGGCGCTGACAGTGTCTCGCTCTCTGGGCTC 3532
 |||||
 QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
 |||||
 Db 3533 CTCATGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3592
 |||||
 QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
 |||||
 Db 3593 ATACAGATGTACAGGAAGAACCCAGAGATCTGAGTCCACAGCTCCACAGGAGGCGG 3652
 |||||
 QY 1141 LeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrSerMet 1160
 |||||
 Db 3653 CTTAGTGGGGGCGCATCTCTCTCCCTGCCAGAGCTTGGCAGAGTACTACCTCCATG 3712
 |||||
 QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 |||||
 Db 3713 ACCGTGGCCATCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3772
 |||||
 QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 |||||
 Db 3773 CCCCCTGGTCCCTGCTGCCATAGCTCTGGCAACCTCAGTTCAGGGGACCAAGTCCA 3832
 |||||
 QY 1201 AlaThrGly 1203
 |||||
 Db 3833 GCCACTGGG 3841
 |||||
 RESULT 4
 AAX89478
 ID AAX89478 standard; cDNA; 4391 BP.
 AC AAX89478;
 XX AAX89478;
 DT 03-DEC-1999 (first entry)
 XX Human ptc-2 cDNA.
 DE
 XX Patched-2; ptc-2; human; hedgehog receptor; neurotropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW val injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
 KW

KW Parkinson's disease; Huntingdon's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 KW lesion-induced death; neuron regeneration; damage repair; skeletal;
 KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 KW prosthetic cartilage device; spermatogenesis; fertility enhancer; ds.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 297..3908
 FT /*tag= a
 FT /product= "ptc-2"

XX WO929854-A1.

XX 17-JUN-1999.

XX 08-DEC-1998; 98WO-US026009.

XX 08-DEC-1997; 97US-0067940P.

XX (ONTO-) ONTOGENY INC.

XX Bumcrot DA;

XX WPI: 1999-561298/47.

XX P-PSDB; AAY28444.

XX New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 XX prevention and/or reduction of the severity of neurological conditions.

XX Claim 2; Page 66-72; 80pp; English.

CC This invention describes a novel recombinantly produced human patched-2
 CC (ptc-2) polypeptide which has neurotropic, neuroprotective, cardiant,
 CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
 CC protein is a hedgehog receptor and is therefore capable of modulating
 CC hedgehog signalling, and so affect a number of hedgehog-mediated
 CC biological activities. The human patched-2 (ptc-2) protein can be used to
 CC screen for modulators, antagonists and agonists, which are likely to play
 CC an important role in the modulation of cellular proliferation and
 CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
 CC tissues during disease states. Modulators of ptc-2 protein can be used
 CC for in vivo reformation of tissue; to improve grafting and morphology of
 CC transplanted tissue; for the treatment, prevention and/or reduction of
 CC the severity of neurological conditions deriving from: injury to the
 CC nervous system including traumatic injury, chemical injury, vascular injury
 CC and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
 CC system including Alzheimer's disease; chronic neurodegenerative diseases
 CC of the nervous system including Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis, as well as spinocerebellar degenerations;
 CC and chronic immunological diseases of the nervous system including
 CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
 CC of autonomic disorders of the peripheral nervous system, and endocrine
 CC disorders affecting the innervation of smooth muscle and cardiac
 CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
 CC Antagonists of ptc-2 protein can be used to prevent differentiation of
 CC cells in culture, as well as for treatment of chronic pain syndromes.
 CC Agonists may be used to rescue neurons from lesion-induced death as well
 CC as neuron regeneration, in diseases such as CNS trauma infarction, (viral)
 CC infection, metabolic disease, nutritional deficiency, toxic agents, and
 CC so on. ptc-2 therapeutics may also be used for the repair of central and
 CC peripheral nerve damage, for repair and regeneration of non-neuronal
 CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
 CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
 CC for generation of prosthetic cartilage devices, and to induce
 CC spermatogenesis and as fertility enhancers. This sequence encodes the
 CC human ptc-2 protein described in the invention

XX Sequence 4391 BP; 769 A; 1475 C; 1224 G; 923 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 0 Length: 4391
 Score: 6248.00 Matches: 1200
 Percent Similarity: 99.75% Conservative: 0
 Best Local Similarity: 99.75% Mismatches: 3
 Query Match: 99.62% Indels: 0
 DB: 2 Gaps: 0

US-09-990-046-2 (1-1203) x AAX89478 (1-4391)

QY 1 MetThrArgSerProLeuArgGluLeuProProSerTyrThrProProAlaArgThr 20
 DB 297 ATGACTCGATCCGCCCTCAGAGAGCTGCCCGGAGTTACACACCCCGAGTCAACC 356
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 DB 357 GCAGCACCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTCGTCTTACTTC 416
 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 DB 417 CAGGCGCTGCTCTCTCTCGGATGCGGATCCAGAGACATTTGGCAAGTGTCTTT 476
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 DB 477 CTGGGACTGTTGGCTTTGGGCGCCTGGCATATTAGGTCTCCGATGGCCATTATTGAGACA 536
 QY 81 AsnLeuGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 DB 537 AACTTGAACAGCTCTGGTAGAAGTGGGAGCGGAGTGGGAGCCAGGAGCTGCATTACACC 596
 QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 DB 597 AAGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGCCGACGC 656
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeu 140
 DB 657 CAGAGGAGAGAGAACATCTTCACACCGCAAGCACTTGGCCTCCACCTCCAGGACGCCCTC 716
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 DB 717 ACTGCAGTAAGTCCCAAGTATCACTCTATGGGAAGTCTGGGATTTGAACAAATCTGC 776
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 DB 777 TACAAGTCAGGAGTTCCTCTATTGAAATGGAATGATTCAGCGGATGATTGAGAGCTG 836
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 DB 837 TTTCCGTGGTGTATCTCACCCCTCTGACTGCTTCTGGAGGAGGCCAACTCCAAAGG 896
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 DB 897 GGCCTCGCTACTGCTCGCGCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 956
 QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 DB 957 CTGCTGGAGGAGCTGGGTCCCTTTGCTCCCTTGGGGCTTCGGGAGCTGTAGACAG 1016
 QY 241 AlaGlnValGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 DB 1017 GCACAGTGGGCGAGGCTACGTGGGGCGGCCCTGTCTGACCTCATGACCTCCACTGTC 1076
 QY 261 ProProSerAlaProAsnHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 DB 1077 CCACCTAGTGGCCCCCAACCATCACAGCAGCAGGCTCCCAATGTGGCTCACAGCTGAGT 1136
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
 DB 1137 GGGGCTGCCATGGCTTCTCCACAAATTCATGCATCTGGCAGGAGGAATTCGTCTGGGA 1196
 QY 301 GlyMetAlaArgAspProGlnGlyIleLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320

DB 1197 GGCATGGCCAGAGACCCCAAGAGAGAGCTGCTGAGGGCAGAGGCCCTGCAGACACCTTC 1256
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 DB 1257 TTGCTGATGAGTCCCGCCCGCAGCTGACAGACATTTCCGGGGTGACTATCAGACACATGAC 1316
 QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTyrGlnArgArgPheVal 360
 DB 1317 ATTGGCTGGAGTGGAGAGCAGGCCAGCACAGTGTCTAAGCCTGGCAGCGGGCTTTGTG 1376
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 DB 1377 CAGCTGGCCCGCAGAGGCCCTGCTCGAGAACGCTTCCAGCAGATCCATGCTCTCTCTCC 1436
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 DB 1437 ACCACCTGGATGACATCTCGATCGCTTCTTGAAGTCAGTGTGCCCGTGTGTGGGA 1496
 QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTyrAspCysAlaGln 420
 DB 1497 GGCTATCTGCTCATGCTGGCTATGCTGTGTGACCATGCTGGGTGGGACTGCGCCAG 1556
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 DB 1557 TCCAGGGTTCCGTGGGCTTGGCGGGTACTGCTGTGGTGGCCTGGCGGTGGCTCAGGC 1616
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 DB 1617 CTTGGGCTCTGTGCCCTGTGCGCATCACCTTCAATGCTGCACATACACAGGTGTGCC 1676
 QY 461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 DB 1677 TTCTTGGCTCTGGGAATCGCGTGGATGACGTATTCCTGTGGCGCATGCTTCACAGAG 1736
 QY 481 AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 DB 1737 GCTCTGCTGGCAGCCCTCTCCAGGAGCGATGGCGAGTGTCTGACGCGCACGGCACC 1796
 QY 501 SerValValLeuThrSerIleAsnAspMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
 DB 1797 AGTGTGCTACTACATCCATCAACATGGCCGCTTCTCATGGCTGCTGCTGCTTCCC 1856
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 DB 1857 ATCCCTGCGTGGAGCTTCTCCCTACAGCGGCCATAGTGTGGTGGCTGACCTTTGTA 1916
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 DB 1917 GCGGTGATGCTTGTCTTCCAGCCATCTTTCAGCTTGGACTTACGGCGGCCACTGCCAG 1976
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 DB 1977 CGCCTTGATGCTCTGCTGCTTCTCCAGTCCCTGCTGTGCTCAGGTGATTGAGATCTCTG 2036
 QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 DB 2037 CCCCAGGAGCTGGGGAGCGGAGACAGTACAGTGGGCATTGCCCATCTCACTGCCACAGTT 2096
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
 DB 2097 CAAAGCTTTTACCCATGTGGAGCCAGCAGCATGTGTGTGTCCTGCTCAGGTGATTGAGATCT 2156
 QY 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 DB 2157 GCCCAGCTGTGGCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGG 2216
 QY 641 SerThrArgAspLeuLeuGlyGlnGluGluGluThrArgGlnLysAlaAlaCysLysSer 660
 DB 2217 TCCACAGGGACCTTCTAGGCCAGGAGGAGACAGGACAGGACAGGACCTGCAAGTCC 2276
 QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
 DB 2277 CTGCCCTGTGCCGCTGGAATCTTGGCCCATTTTCCCGCTATCAGTTTGGCCCTGTGCTG 2336

XX Isolated human protein capable of participating in human patched
 PT gene/Sonic hedgehog pathway during embryonic development is used in
 PT medicament for treatment of condition involving tumors such as basal cell
 PT carcinoma.

PS Claim 4; Page 45; 55pp; English.

XX This cDNA is derived from the novel human patched 2 gene (PTCH2), which
 CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
 CC D1S211 and W11404 as closest flanking markers and with an estimated
 CC localisation 5.5 cR from D1S443. This region is often lost by LOH in
 CC various different tumour types, such as neuroblastoma, melanoma and
 CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
 CC gene in this region. It is also a candidate gene for involvement in
 CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
 CC hMOM1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
 CC exist (see AAA09082-84). PTCH2 is capable of participating in the PTCH2 gene
 CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent

XX Sequence 3453 BP; 600 A; 1135 C; 989 G; 729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3453
 Score: 5911.00 Matches: 1139
 Percent Similarity: 99.74% Conservative: 0
 Best Local Similarity: 99.74% Mismatches: 3
 Query Match: 94.24% Indels: 0
 DB: 3 Gaps: 0

US-09-990-046-2 (1-1203) x AAA09081 (1-3453)

QY 1 MetThrArgSerProLeuArgGluLeuProSerTyrThrProAlaArgThr 20
 DB 13 ATGACTCGATCGCGCGCCCTCAGAGAGTGGCCCGGAGTTACACACCCCGAGCTCGAACC 72
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
 DB 73 GCAGCACCCAGATCTCTAGCTGGGAGCCTGGAAGGCTCCACTCTGGCTTCTGCTTACTTC 132
 QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 DB 133 CAGGCGCTCTCTCTCTCGGATCGGGATCCGAGATCCAGAGACATGTGGCAAGTGTCTTT 192
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 DB 193 CTGGGACTGTGGCTTTGGGGCCCTGGCATTAGGTCTCCGATGACCATTTATGAGACA 252
 QY 81 AsnLeuGlnLeuTrpValGluValGlySerArgValSerGlnIleuHisTyrThr 100
 DB 253 AACTTGGAAAGCTCTGGGTAGAGTGGGAGCGCGGTGAGCAGGAGTGCATTACACC 312
 QY 101 LysGluLysLeuGlyCyluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 DB 313 AAGGAGAAGCTGGGGAGGAGGAGCTGCATACACTCTCAGATGCTGATACAGACCGGACGC 372
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 DB 373 CAGGAGGAGAGAAACATCTCACCCGAGACACTTGGCTCCACCTCCAGCAGCCCTC 432
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 DB 433 ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGGAAGTCTCTGGGATTTGAACAAAATCTGC 492
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 DB 493 TACAAGTCAGGAGTCTCCCTTATTGAAATGAATGATGATGAGCGGATGATTGAGAAGCTG 552
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200

DB 553 TTTCCGTGCGTGAATCCTCACCCCTCAGCTGCTTCTGGAGGGAGGCAAACTCCAAAGG 612
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 DB 613 GGCTCCGCTACCTTGGCCGCGCCGCGATATCCAGTGGACCAACCTGGATCCAGAGCAG 672
 QY 221 LeuLeuGluLeuLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 DB 673 CTGCTGGAGGAGCTGGGTCCCTTTGCCCTTCAGGSGCTTCGGGAGCTCTAGACAAAG 732
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 DB 733 GCACAGTGGGCCAGGCTACGTGGGCGGCCCTGTCTGCACCTGATGACCTCCACTGC 792
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 DB 793 CCACCTAGTCCCCCAACCATCACAGGAGGAGCTCCCAATGTGGCTCAGAGCTGAGT 852
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly 300
 DB 853 GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCACCTGGCAGGAGGAATTGCTGCTGGA 912
 QY 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
 DB 913 GGCATGGCCAGAGACCCCAAGGAGAGCTCTGAGGCGCAGAGCCCTGCAGAGCACCTTC 972
 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 DB 973 TTGCTGATGAGTCCCGCCAGCTGTAGGACANTTCCGGGGTGACTATCAGACACATGAC 1032
 QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
 DB 1033 ATTGGCTGGAGTGAGGAGCAGGCGCAGACAGCTCTACAGCTGGCAGCGCGCTTTGTG 1092
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
 DB 1093 CAGCTGGCCAGGAGGCGCTGCTGAGAACGCTTCCAGCAGATCCATGCTTCTCTCTCC 1152
 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 DB 1153 ACCACCTCGATGACATCTCGATGCTTCTCTGAAAGTCAGTGCTGCCGCTGGTGGGA 1212
 QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
 DB 1213 GGCTATCTCTCATGTGCTGCTATGCTGTGACCATCTGCGTGGGAGCTCGGCCAG 1272
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 DB 1273 TCCAGGGGTTCGTTGGGCTTCCGCGGTACTGCTGTGGCGCTGGCGCTCAGGC 1332
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 DB 1333 CTGCGCTCTGCGCTCTGCTCGGATCACCTTCAATGCTGCCACTACCCAGGTGCTGCC 1392
 QY 461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 DB 1393 TTCTTGGCTCTGGGAATCGGCGTGGATGACGTATTCTCTGCGCGCATGCTTCCAGAG 1452
 QY 481 AlaLeuProGlyThrProLeuGlnArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 DB 1453 GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTCAGCGCAGCGGCACC 1512
 QY 501 SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaLeuValPro 520
 DB 1513 AGTGTCTGACTCAGATCATCATCAACATGGCCGCTTCTCCTCATGGCTGCTGCTGCC 1572
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
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 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560

Db	1633	GCCGTGATGCTTGTCTTCCAGCCATCTCAGCCTGCGATACGGGGCCCACTGCCAG	1692	QY	921	AlaAspPheValGluAlaIleGluGlyAlaAraGalaAlaCysAlaGluAlaGlyGlnAla	940
QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580	Db	2773	CGAGACTTTTGTGAGGCCATCGAGGGGCCCGGAGCATGCGCAGAGCGCCGAGGCT	2832
Db	1693	CGCCTTGATGTCTCTGCTGCTTCTCAGTCCCTGCTGCTCAGGTGATTCAGATCCTG	1752	QY	941	GlyValHisAlaTyrProSerGlySerPropheLeuPheTyrGluGlnTyrLeuGlyLeu	960
QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600	Db	2833	GGGFTGCAGCCTACCCAGCGCTCCCTTCTCTTCTGGGAAACAGTATCTGGGCGCTG	2892
Db	1753	CCCCAGAGCTGGGGACGGGACAGTACAGTGGGCAITGGCCACCTCAGTCCACAGTT	1812	QY	961	ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla	980
QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620	Db	2893	CGGCGTGTCTCTGCTGGCCCTGCACTCCTGCTGCTGTCACATTTCTCTGCTCTGCT	2952
Db	1813	CAAGCCTTTACCCACTGTGAGCCAGCAGCAGCATGTGTCACCATCTCTGCTCCCAA	1872	QY	981	LeuLeuLeuLeuAsnProTyrThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr	1000
QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640	Db	2953	CTGTGCTCTCTCAACCCCTGGAGCGCTGCCTCATAGTCTGGTCTCTGGCATGATGACA	3012
Db	1873	GGCCACCTGGTCCGCCACCTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGG	1932	QY	1001	ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLeuLeuSerAlaIleProValVal	1020
QY	641	SerThrArgAspLeuLeuGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660	Db	3013	GTGGAACTCTTTGGTATCATGGGTTTCTCTGGGCATCAAGCTGAGTGCCTCCCGTGGTG	3072
Db	1933	TCACACGGGACCTCTAGGCCAGGAGGAGACCAAGGAGAGGAGGAGCTCCAACTCC	1992	QY	1021	IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe	1040
QY	661	LeuProCysAlaArgTyrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680	Db	3073	ATCCTTTGTGGCCTCTGTAGGCATTTGGCGTTGAGTTTCCAGTCCACGTGGCTCTGGGCTTC	3132
Db	1993	CTGCCCTGTCCCGCTGGAACTCTTGCCCATTTCCCGGCTATCAGTTTGGCCCGTTGCTG	2052	QY	1041	LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla	1060
QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700	Db	3133	CTGACCCAGGAGGAGCGGAACCTGCGGGCCGCCATGCCCTTGAGCACACATTTGCC	3192
Db	2053	CTCCAGTCACTGCTAAGGCATCGTCTGCTGCTCTTTGGTGTCTCTCTCTGGGCCCTGAGC	2112	QY	1061	ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHis	1080
QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly	720	Db	3193	CCCGTGACCGATGGGGCCATCTCCACATTTGCTGGTCTGTCTCATGCTGTGCTGTCCAC	3252
Db	2113	CTCTAGCGAGCCACCTTGGTGCAGAGCGGCTGCGCCTGACGGATGGTGGCTCGGGCC	2172	QY	1081	PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu	1100
QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740	Db	3253	TTTGACTTCATTGTAAGTACTCTTTTGGCGGCGCTGACAGTCTCAGCTCTCTGGGCTC	3312
Db	2173	ACCAGAGAGATGCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCC	2232	QY	1101	LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal	1120
QY	741	LeuValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760	Db	3313	CTCATGGAGCTGTGTGTGCTGTGCTGTCTGTCCATCTCTGGGCGCCGCCAGAGGTG	3372
Db	2233	CTGGTACCCAGGGTGGCTTTGACTAGCGCCACTCCCAAGCGGCCCTCTTTGATCTGCAC	2292	QY	1121	IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly	1140
QY	761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780	Db	3373	ATACAGATGTACAAGAAAGCCAGAGATCTCTGAGTCCACAGTCCACAGGAGGCGGG	3432
Db	2293	CAGCGCTTCAGTTCCCTCAAGGGGGTGTGCTGCCCCCAGCCAGGACCCCGGACCC	2352	QY	1141	LeuArg	1142
QY	781	TrpLeuHisTyrTyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTyr	800	Db	3433	CTTAGG	3438
Db	2353	TGGCTGCACTATTACCGCACTGGCTACAGGGATCCAGGCTGCTTTGACCACTGG	2412	Db	3433	CTTAGG	3438
QY	801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820	Db	3433	CTTAGG	3438
Db	2413	GCTTCTGGCGCATCACCGCCACTCGCTACCGCAATGGCTCTGAGGATGGGGCCCTGGCC	2472	Db	3433	CTTAGG	3438
QY	821	TyrLysLeuLeuIleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThr	840	Db	3433	CTTAGG	3438
Db	2473	TACAGCTGCTCATCCAGCTGGAGAGCCCGCAGAGAGCTTCGATTTTCAGCCAGCTGACC	2532	Db	3433	CTTAGG	3438
QY	841	ThrArgLysLeuValAspArgGluGlyLeuIleProGluLeuPheTyrMetGlyLeu	860	Db	3433	CTTAGG	3438
Db	2533	ACAAGGAAGCTGGTGGACAGAGAGGAGTGTATCCACCGAGCTCTTCTACATGGGGCTG	2592	Db	3433	CTTAGG	3438
QY	861	ThrValTrpValSerSerAspProLeuGlyLeuAlaSerGlnAlaAsnPheTyrPro	880	Db	3433	CTTAGG	3438
Db	2593	ACCGTGTGGTGGAGTGCATCCCTGGGCTGCGAGCCTCACAGGCCAATCTTACCCCC	2652	Db	3433	CTTAGG	3438
QY	881	ProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsnLeuArgIlePro	900	Db	3433	CTTAGG	3438
Db	2653	CCACCTCTGAATGCTGCACACACANATACACACACCGGGAGAACTTTCGATCCCG	2712	Db	3433	CTTAGG	3438
QY	901	ProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThr	920	Db	3433	CTTAGG	3438
Db	2713	CCAGCTCAGCCCTTGGAGTTTGGCCAGTTCCCTTCTGCTGCTGGGCTCCAGAGACT	2772	Db	3433	CTTAGG	3438

RESULT 6

AAA09084
ID AAA09084 standard; DNA; 12886 BP.

XX
AC AAA09084;

XX
10-AUG-2000 (first entry)

XX
Human patched-like gene (PTCH2) genomic DNA.

XX
Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
familial adenomatous polyposis; hMomi; Michelin tire Baby Syndrome;
sonic hedgehog; SHH; development; carcinogenesis; cytosstatic;
basal cell carcinoma; gene therapy; chromosome 1p32-35; ds.

OS
Homo sapiens.

XX
Key Location/Qualifiers
FH 1. .290
FT exon
FT /*tag= c
FT /number= 1

FT CDS
219. .12033
FT /*tag= a
FT /product= "PTCH2"

FT	CDS	219..10206	FT	intron	6883..6966
FT		/*tag= b	FT		/*tag= af
FT		/product= "splice_variant"	FT	exon	6967..7147
FT	intron	291..1109	FT		/*tag= ag
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FT	exon	1110..1302	FT	intron	7148..7280
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FT	intron	/number= 2	FT	exon	7281..7561
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FT		2094..2162	FT	intron	7800..9235
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FT	intron	/number= 4	FT	exon	9236..9378
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FT	exon	/*tag= j	FT		/number= 19
FT		2340..2431	FT	intron	9379..9452
FT		/*tag= k	FT		/*tag= an
FT	intron	/number= 5	FT	exon	9453..9552
FT		2432..3093	FT		/*tag= ao
FT	exon	/*tag= l	FT		/number= 20
FT		3094..3289	FT	intron	9553..9951
FT		/*tag= m	FT		/*tag= ap
FT	intron	/number= 6	FT	exon	9952..10206
FT		3290..4108	FT		/*tag= ar
FT	exon	/*tag= n	FT		/number= 21a
FT		4109..4231	FT	exon	/note= "alternate splice variant"
FT		/*tag= o	FT		9952..10019
FT	intron	/number= 7	FT		/*tag= aq
FT		4232..4378	FT	intron	/number= 21
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FT		4379..4586	FT	exon	/*tag= as
FT		/*tag= q	FT		12018..12886
FT	intron	/number= 8	FT		/*tag= at
FT		4587..4605	FT		/number= 22
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FT		/*tag= s	XX		
FT	intron	/number= 9	PD		13-APR-2000.
FT		4739..4827	XX		
FT	exon	/*tag= t	PF		06-OCT-1999; 99WO-SE001784.
FT		4828..4983	XX		
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FT	intron	/number= 10	XX		(KARO-) KAROLINSKA INNOVATIONS AB.
FT		4984..5065	PA		(PHAA) PHARMACIA & UPJOHN CO.
FT	exon	/*tag= v	XX		
FT		5066..5158	PI		Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
FT		/*tag= w	PI		Hollingsworth RE;
FT	intron	/number= 11	XX		
FT		5159..5509	DR		WPI; 2000-303645/26.
FT	exon	/*tag= x	XX		P-PSDB; AAY92225, AAY92703.
FT		5510..5754	XX		
FT		/*tag= y	PT		Isolated human protein capable of participating in human patched
FT	intron	/number= 12	PT		gene/Sonic hedgehog pathway during embryonic development is used in
FT		5755..5858	PT		medicament for treatment of condition involving tumors such as basal cell
FT	exon	/*tag= z	PT		carcinoma.
FT		5859..6207	XX		
FT		/*tag= aa	XX		
FT	intron	/number= 13	PS		Claim 5; Page 46-49; 55pp; English.
FT		6208..6335	XX		
FT	exon	/*tag= ab	CC		This genomic DNA comprises the novel human patched 2 gene (PTCH2), which
FT		6336..6648	CC		has been localised by radiation hybrid mapping to chromosome lp32-35 with
FT		/*tag= ac	CC		DIS211 and WI1404 as closest flanking markers and with an estimated
FT	intron	/number= 14	CC		localisation 5.5 cM from D18443. A splice variant exists which is
FT		6649..6740	CC		generated by 2 forms of exon 21. This region is often lost by LOH in
FT		/*tag= ad	CC		various different tumour types, such as neuroblastoma, melanoma and
FT	exon	6741..6882	CC		breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
FT		/*tag= ae	CC		gene in this region. It is also a candidate gene for involvement in
FT		/number= 15	CC		familial melanoma CMM1, modifier locus for familial adenomatous polyposis

CC hMomi and Michelin Tire Baby Syndrome. Splice variants of the PTH2 gene
 CC exist (see AAA09082-84). PTH2 is capable of participating in the human
 CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent
 XX
 SQ Sequence 12886 BP; 2789 A; 3817 C; 3472 G; 2807 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 0 Length: 12886
 Score: 4692.50 Matches: 1166
 Percent Similarity: 38.40% Conservative: 1
 Best Local Similarity: 38.37% Mismatches: 13
 Query Match: 74.66% Indels: 1869
 DB: 3 Gaps: 20

US-09-990-046-2 (1-1203) x AAA09084 (1-12886)

QY	24	GlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPheGlnGlyLeu	43
DB	1107	CAGATCCTAGCTGGAGCCTGAAGCTCCACTCTGGCTTCGCTTACTTCCAGGGCTG	1166
QY	44	LeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeu	63
DB	1167	CTCTCTCTCTGGGATCGGGATCCAGAGACATTTGTGCAAGTGTCTTCTGGGACTG	1226
QY	64	LeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGlnThrAsnLeuGlu	83
DB	1227	TTGGCCCTTTGGGCCCCCTGGCATATTAGTCTCCGCATGGCCATTATTGAGACAACTTGAA	1286
QY	84	GlnLeuTrpValGlu	88
DB	1287	CAGCTCTGGGTAGAAGTAAAGTTGTGACACTGGCCATAGCTGCTCAGGTATGTGAGCC	1346
QY	88	-----	88
DB	1347	CAGACAAGAACGGGTGAGGAGTGGCTACTGAGCTCTAGCAGCCTGGCCCTGGGGCT	1406
QY	88	-----	88
DB	1407	GGAGGTCACCTGCTGGCCAGAGTCCACACTGGGCATCTAGGACACCGCTTCCCTCCC	1466
QY	88	-----	88
DB	1467	ACAACATAAATGGACATCTGCAGATGTTAGACCTTGTGAATTTGGGTGTATAGAATAFTT	1526
QY	88	-----	88
DB	1527	GTCTGTGATTTTGTCTTAAGCCCTAGACCACACAGAAATCCGAGAGCCACACACCAG	1586
QY	88	-----	88
DB	1587	GCTTCTCCACTTCCCTGGCAGAGTCCAGAGCCACAGAGCCTGGGAGTGGSCCTGGGCC	1646
QY	88	-----	88
DB	1647	ATGACAGGCCCTCAGGATTAAGGACGAGTCTCTCTCTGCGCACCTCTCCCACTTGTCT	1706
QY	88	-----	88
DB	1707	TGGGAGGCCCTCAGAGTTAGAGCCCTTCCCAAGTCTTGACCCGCTAGGCCCTTTCC	1766
QY	89	-----ValGlySerArgValSerGlnGlnLeuHisTyr	99
DB	1767	CCCCCAGCTTCTCTCTGCTCTGGCAGTGGGCGAGCGGGTGGAGCAGAGTGCATTA	1826
QY	99	rThrLysGlnLysLeuGlyGluGlnAlaAlaTyrThrSerGlnMetLeuIleGlnThrAl	119
DB	1827	CACCAAGAGAGAGCTGGGGGAGGAGGCTGCATACACCTCTCAGATGCTCATACAGCCGC	1896
QY	119	aArgGlnGluGlyGluAsnIleLeuThrProGlnAlaLeuGlyLeuHisLeuGlnAlaAl	139

DB	1887	ACGCCAGGAGGAGAGAACATCTCACACCCGAGCACTTGGCCTCCACCTCCAGCAGC	1946
QY	139	aleuThrAlaSerLysValGlnValSerLeuTyrGlyLysSer	153
DB	1947	CCTCACTGCCAGTAAAGTCCAAAGTATCACTCTATGGAAAGGT-GAGTCTGGTGAGCCCC	2005
QY	153	-----	153
DB	2006	TGAGCAGCTGGGGCGAGCGCTGCTGTGGGGGTCTTGAGTGGGAATCCCTCTTCTCTGC	2065
QY	154	-----TrpAspLeuAsnLysIleCysTyrLysSe	163
DB	2066	TGATCTCTATGCCCTGGCTATTGCACTCTGGGATTTGAACAAAATCTGTACAGTC	2125
QY	163	rGlyValProLeuIleGluAsnGlyMetIleGlu	174
DB	2126	AGGAGTTCCCTTATTGAAAATGGAATGATTGACGGGTAAAGTGTCTTGAGAGGAGTAG	2185
QY	174	-----	174
DB	2186	AGCAGAACTTTTCTGTAGCTGGGAGGACTCAGAGACCGAGCCCAAGCCCAACAGCCTGC	2245
QY	174	-----	174
DB	2246	AATCTGCCCTTTAAAACTAAGGAGGGGATTCAGAGGGCATCTCTACAAGGTGTGGG	2305
QY	175	-----Trp-----MetIleGlnLysLeuPheProCysVa	184
DB	2306	GCAGGACTGACGTGGCCCGGGGTATCCCTGGCAGATGATTGAGNAGCTGTTCCGTGGT	2365
QY	184	lIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTy	204
DB	2366	GATCTCACCCCTCGACTGCTTCTGGGAGGAGCCAAACTCCAGGGGGCTCCGCTA	2425
QY	204	rLeuProGly	207
DB	2426	CCTGCCGTG-AGTGCCACTCTGGGGCCCTGCTTCATCTCCGCTGGGACTCTCCGAGC	2484
QY	207	-----	207
DB	2485	AGAAAGAGGGGTCTGGGGAATGAGGATGATCAAAACCTTACCAGGTCTTAATTACCTC	2544
QY	207	-----	207
DB	2545	CCAGGCCAGGACAGAGAGCATGGCTTCCCAAGGCTCTCTCCACATCTCTCTTCTTCTT	2604
QY	207	-----	207
DB	2605	TCCCTCTCAGGAAGGAAGACCTGACTTATTTCACAAAACCTAAACACAAAAGATCTGTA	2664
QY	207	-----	207
DB	2665	GATCTGAGCAAGGAGAAAAAGATCCCAAGAGGCTTTGCTGGGGGAATTACCTAG	2724
QY	207	-----	207
DB	2725	GTGTTTGTAAAGCATTTGCCCGAGGCGAGAAAGAAACCTGCTACAGGCATGTGCTGTG	2784
QY	207	-----	207
DB	2785	GTGTATATTAGAACCAAGACACAGCTTGGTAAGGAACCTAGTGGGGCCCTTTCTGGGCC	2844
QY	207	-----	207
DB	2845	CTTCTATGATATTAGTAACCTTGCCTGATATTGCTCTCAGCCCTTGTACTCTTCTAC	2904
QY	207	-----	207
DB	2905	AGCTCACTGTAGCACCTTGGTGGGGCCATGCAGCCTGGCAGTCTTGAGAAAGTGGGCTT	2964
QY	207	-----	207

Db 2965 GCACACCCTCCATATGGAAGACAAATCGGCAGATAGAGGAGGTGGGTACAGCATGG 3024
 Qy 207 ----- 207
 Db 3025 CGCCCCCAGCAGAGTTTGGAGCCTGGGTTCGTCCTCGACCCCTCACCAACTATAGGCTT 3084
 Qy 208 -----ArgProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuG1 223
 Db 3085 TTCCCTCAGCGCGCGCCGGATATCCAGTGACCAACTGGATCCAGAGCAGCTGTGGA 3144
 Qy 223 uGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspIleAlaGlnVa 243
 Db 3145 GGAGCTGGTCCCTTTCCTCCCTTGGGGCTTCGGGAGCTGCTAGACAAAGGCACAGGT 3204
 Qy 243 lGlyGlnAlaTyrrValGlyArgProCysLeuHisProAspAspLeuHisCysProProSe 263
 Db 3205 GGGCCAGGCTTACGTGGGCGGCGCTGTCTGTCACCTGATGACCTCCACTGCCACCTAG 3264
 Qy 263 rAlaProAsnHisHisSerArg ----- 270
 Db 3265 TGCCCCCAACCATCACAGCAGCAGGTGGTTCACACCAGGTCTGCCAGGAAAGGCTGT 3324
 Qy 270 ----- 270
 Db 3325 TTTCCTTCCCTTCCCTTCCCTCATCTACTCTGTGTCTCTGGGAGCTGACTGCTCTGTGCC 3384
 Qy 270 ----- 270
 Db 3385 CTGACCCCCACTTCTCGGCCATTATTACCTGCTCTCCACAGTGCACAGGCCGCCCAATGTT 3444
 Qy 270 ----- 270
 Db 3445 CCATTCCCATTTAGTTATCCTAGGAGCCCTCAAGTGGTATATATGAAATCCCTTTTTCCT 3504
 Qy 270 ----- 270
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 Db 3565 ACCAGGCTGGAGTGAGTAGTTTCGATCTTGGTCTCACTGCACTCGGCTCAAGCAATTC 3624
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 Db 3625 TCCTGCCCTTAGCCTCTGAGTAGCTGGATTACAGGTGCCACCACCATGCCCGGCTAAT 3684
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 Db 3685 TTTTATTAGCCTCCCAAAGTGTGGGATTACAGCGGTGAGCCACTGCGCTGGCCAAAGC 3744
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 Db 3745 TGGACTTTTATCAAAATAGACTAATACAGGGAAACTAAGAACACACAGCAGGTAAGCATGA 3804
 Qy 270 ----- 270
 Db 3805 ATATCATACCTGGTTTCCACAGTTTCTTTGTGGCCCTGCAATGTGTACTTTTTTCAGA 3864
 Qy 270 ----- 270
 Db 3865 ATCCGCCAGTTACACCAGCTCTCCCAAGAGCCTACTTCCAGGCTCTGCTTCCCTCTGG 3924
 Qy 270 ----- 270
 Db 3925 GGCCTTCCTGTCTGGGGATACATAGTGTTCATCTCTCGCAGACAGTCAAGAGGCTCAGAA 3984
 Qy 270 ----- 270
 Db 3985 TAGTTACCTACACTCCAGCCCTACTGAGCTTCATGGCAGCGTGTTCCTGGAGGTGAAG 4044
 Qy 270 ----- 270
 Db 4045 CCCAGGGACACTCAGTTATCCAGGCCAGGGCTTTCAGCATTAACCCCTCTCTGTTCCCT 4104

Qy 271 -Gln-AlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSerHisLysP 290
 Db 4105 CCAGGGCTCCCAANGTGGCTCACGAGCTGAGTGGGGCTGCATGGCTTCTCCCAAAAT 4164
 Qy 290 heMetHisTrpGlnGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluL 310
 Db 4165 TCATGCACTGSCAGAGAAATTTGCTGTGGAGGATGGCCAGAGACCCCAAGGAGAGC 4224
 Qy 310 euLeu ----- 311
 Db 4225 TGCTGAGGTAGGTCTCTCTCTGGAGTTGGTGAGGGGACTCTGTTCATGAAACCCATAC 4284
 Qy 311 ----- 311
 Db 4285 TGTAAATGCCAGCAGCTCTGGCAAAAGGCCCTTCCATCCCTCACAGGTGTGTGGGCA 4344
 Qy 312 -----ArgAlaGluAlaLeuGlnSerThrPheL 321
 Db 4345 GCTCTGACCCCTGGTTCTCCACACACCCACCAGGGCAGAGGCCCTGCAGAGCACCTTCT 4404
 Qy 321 euLeuMetSerProArgGlnLeuTyrrClnHisPheArgGlyAspTyrrGlnThrHisaspI 341
 Db 4405 TGCTGATAGTCCCGCCAGCTGTAGAGCATTTCCGGGGTGACTATCAGACACATGACA 4464
 Qy 341 leGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArg ----- 358
 Db 4465 TTGGCTGGAGTGAGGAGCAGGCCAGACAGTGTCTACAGCTGGCAGCGCGCTTTGTGC 4524
 Qy 358 ----- 358
 Db 4525 AGCTCGGTATGGAAGAGCAAGGGGGTGCCTGAGGCCATTCCCTCTCTCTGCCCCCT 4584
 Qy 359 -----PheValGlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnG 374
 Db 4585 CCTATCCACCCCTGTTTCTC-CAGCTGGCCAGGAGGCCCTGCTGAGAGCTTCCAGC 4643
 Qy 374 lnIleHisAlaPheSerSerThrLeuAspAspileLeuHisAlaPheSerGluValS 394
 Db 4644 AGATCCATGCCCTTCTCTCCACACCCCTGGATGACATCTGTCATGATGGTCTCTGAAGTCA 4703
 Qy 394 erAlaAlaArgValValGlyGlyLeuLeuMetLeu ----- 406
 Db 4704 GTGCTGCCGTGTGGTGGAGGCTATCTGCTCATGTT-GGGTCTTGCACTGGCACCTTG 4762
 Qy 406 ----- 406
 Db 4763 CCCCCACCCCACTCCCAACCACTGCCACCCTGGGAGCCCTTGAGACTGCCCTTTCCCCC 4822
 Qy 407 -----AlaTyrrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlyS 424
 Db 4823 CACAGCTGGCCCTATGCCCTGTGTGACCATGCTCGGTGGGACTGCGGCCAGTCCAGGGTT 4882
 Qy 424 erValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValaSerGlyLeuGlyLeuC 444
 Db 4883 CCGTGGGCTTTCGCCGGGTACTGCTGTGGTGGCCCTGGCGGTGGCTCAGGCCCTTGGCTCT 4942
 Qy 444 ysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr ----- 456
 Db 4943 GTGCCCTCTCTGGCATCACCTTCAATGCTGCCACTTACCCAGGTACGCCAGGACTGCAAGG 5002
 Qy 456 ----- 456
 Db 5003 CAGACTCAGTGCAGTCCAGGCTTACGGGTCTCAGGGTCCCTCAGCTGCCGGCTCTCTGCCCCCTC 5062
 Qy 457 GlnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHis 476
 Db 5063 CAGGTGCTGCCCTTCTTGGCTCTGGAAATCGCGGTGGATGACGATTCTCTGCTGGCGAT 5122
 Qy 477 AlaPheThrGluAlaLeuProGlyThrProLeu ----- 487
 Db 5123 GCCTTTCAGAGGCTCTGCTGGCACCCCTCTCCAGGTGGGGCTTGTGTCCCCAGGGCTC 5182

QY	487	-----	487	6261	ACAGAGGGCTTAGTCCACTGCTGAGGGGCTGGGGGACGCCCTGGGGTCTCCAGCTTAGT	6320
Db	5183	ATCTGAGGAGCTCAGCTTACTGGTTAAGAGCCTCTGGTTCAAGTGACCTTGGGCTGC	5242	688	-----	701
QY	487	-----	487	6321	TGCTACATCCCGAGGCCATCGTGTGGTGGTCTCTTGGTGGTCTCTTGGGCTGAGCCTC	6380
Db	5243	TAATGAACCTCGGTGCTCTTGTGCCCATCTGTAAACAGGGGAATAATAGTGTCTGTGC	5302	702	TyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThr	721
QY	487	-----	487	6381	TACGGAGCCACCTTGGTGAAGACGGCCTGGCCCTGACGGATGTGTGCTCGGGGCACC	6440
Db	5303	CTAAGGGTTATTCTTTGGATCAGTGAGGTAACCTCAAGTTGAATGCTTAGAACAGCCCATC	5362	722	LysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGlnValAlaLeu	741
QY	487	-----	487	6441	MAGGACATGCTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTG	6500
Db	5363	ATACGTACATGTACCAATAAATAGTACCATGTGTGTATGACTGCGCCACCTCTGCAC	5422	742	ValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGln	761
QY	487	-----	487	6501	GTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAAGCGCCCTCTTTGATCTGTACAC	6560
Db	5423	CCCAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGA	5482	762	ArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrp	781
QY	488	-----	488	6561	CGCTTCAGTTCCTCAAGCGGTGCTGCCCAACCGCCACCCAGGACACCCCGCACCTGG	6620
Db	5483	GGGAGCTCCCACTCTGCTCGGACAGGCGCATGGCGAGTGTCTGCAGCGCACGGGC	5542	782	LeuHisTyrTyrArgAsnTrpLeuGlnGlyIle	792
QY	500	ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuVal	519	6621	CTGCACCTATTACCGCAACTGGCTACAGGGTGA-GAGGCGAGGAGACGGGAGGGGGT	6679
Db	5543	ACCAGTGTCTACTCATCATCAACATGCGCCCTTCTTCATGGCTGCCCTGTT	5602	792	-----	792
QY	520	ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe	539	6680	GCTGAGGAGAAACGCCCTGGGGCCACCAGCTAATAGAACCCCTATCTCGTCTCCCCCA	6739
Db	5603	CCCATCCCTCGCTGCGAGCTTCTCCCTACAGCGGCCCATAGTGTGGTGCACCTTT	5662	793	-----	810
QY	540	ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCys	559	6740	GGAATCCAGCTGCTTTGACAGGACTGGGCTTCTGGGGCATCACCCGCCACTCGAC-	6798
Db	5663	GTAGCGTGATGCTGTCTCCAGGCACTCTCAGCCTGACCTACGGCGCGCACTGC	5722	811	ArgAsnGlySerGluAspGlyAlaLeuAlaTyrIleLeuIleGlnThrGlyAspAla	830
QY	560	GlnArgLeuAspValLeuCysCysPheSer	569	6799	CGCAATGGCTCTGAGGATGGGGCCCTGGCTACAAGCTGCTCATCCAGACTGGAGACGCC	6858
Db	5723	CAGCGCCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGTGGTGGCGCCAGCCCTTCT	5781	831	GlnGluProLeuAspPheSer	837
QY	569	-----	569	6859	CAGGACTTCTGGATTTACGCCAGTTGGGAGGGGCTGGAGGGTCCACTAGTACAGG	6918
Db	5782	CCCGTACCCAGCGCAGCTGTCCCTCACCAGCATTTCAAGGCACAGACCTGTATCCA	5841	838	-----	842
QY	570	-----	570	6919	GCTGAGGCTCTCTGGGCCCGAGGCTTACGCCCTCTCTGCTCTGTGAGCTGACCAAGG	6978
Db	5842	CTCTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCCTGCCCGCAGAGCTG	5901	843	LysLeuValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrVal	862
QY	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604	6979	AAGCTGGTGGACAGAGAGGACTGATTCACCCGAGCTCTTTCTACATGGGGCTGACCGTG	7038
Db	5902	GGGACGGGACAGTACAGTGGGATTTGCCCACTCTCACTGCCACAGTTCAAGCCTTTACC	5961	863	TrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProPro	882
QY	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal	624	7039	TGGGTGAGCAGTACCCCTCGGGTCTGGAGCTCACAGGCCAATCTTACCCCCCACCCT	7098
Db	5962	CACGTGAGCCAGCAGCAGCATGTGTCAACATCTGCTCCCAAGCCACCTGGT	6021	883	ProGluTrpLeuHisAspLysTyrAspThrGlyGluAsnLeuArg	898
QY	625	ProProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644	7099	CCTGAATGGCTGCACGACAAATACGACACCGGGGAGAACTTTTCGAGTGTCTTGG	7158
Db	6022	CCCCACCTTCTGACCCACTGGGCTCTGAGTCTTTCAGCCCTGGAGGTTCCACAGGGAC	6081	898	-----	898
QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664	7159	GGGAGCTCGGCAAGAGCCTCAGCCTCGCCCCACAAAGCCCTGAGCCTGAGGCCCTGCC	7218
Db	6082	CTTCTAGGCCAGGAGGAGACAAAGGAGGAGGAGCTGCAAGTCTCCCTGCTGCTGCC	6141	898	-----	898
QY	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis	684	7219	ACTCTGCCCGTGTCTACCGCCCTGTCCCTCTCTCCCTCTTCTCCCTCCCTCCCTCCAC	7278
Db	6142	CGCTGAATCTTGCCCATTTGCGCCGCTATCAGTTTGGCCGCTTCTCTCTCTCTCTCT	6201	899	-IleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGln	918
QY	685	AlaLysAla	687	7279	AGTCCCGCAGCTCAGCCCTTGGAGTTTGGCCAGTTCCCTTCTCTCTCTCTCTCTCTCA	7338
Db	6202	GCTAAGGT-AAGACTGGGCGAGCAGGCGAGACTTAGCATCTCTGGGCCCGAAGGGC	6260	918	nLysThrAlaAspPheValGluAlaIleGluGlyAlaAlaArgAlaAlaCysAlaGluAlaGln	938
QY	687	-----	687			

QY 1119 ----- 1119
 Db 9557 CCACACCTCGGCACCATCTCTTCCAGCCCAAGGACGGGTAGGGAGGCAAG 9616
 QY 1119 ----- 1119
 Db 9617 GGAAGGACAGAGCCCTGTGGCCACAGACAGGTACCTCCCAACAGGTGCCACAGCTG 9676
 QY 1119 ----- 1119
 Db 9677 AAGGTGGCAGCCTCTCTTTCCAGACACCATGTTCTCTGCCCTCAGCCCTCTGGCT 9736
 QY 1119 ----- 1119
 Db 9737 TCTTCATGGGACCCACCTTAGACTTTTAGATCCAGAACAGGTGCAGGTTTGGCCCCAG 9796
 QY 1119 ----- 1119
 Db 9797 GCCTCAACATCTCTGTGCCTGCCAGCTCTCATATCTCTGTGGAGACCAACAGGGGCCCA 9856
 QY 1119 ----- 1119
 Db 9857 GCTTCCCAACAGTCATGTTAATCCACAGCGAGATGCTTAAGGGGACGGGACCCAGGG 9916
 QY 1120 -----
 Db 9917 CCGTGGGCTTACTGGGGCTGGTGTCTCCCAACAGGTGATACAGATGTACAGGAAGCC 9976
 QY 1128 roGluLeuSerProAlaProGlnGlyGlyLeuArgTrpGlyAlaSerSers 1148
 Db 9977 CAGAGATCTCTAGTCACACAGTCCACAGGAGCGGGCTTAGGTGGGGGCTATCTCTCT 10036
 QY 1148 erLeuProGlnSerPheAlaArgValThrThrSerMetThrValAlaHisProProp 1168
 Db 10037 CCCTGCCCAAGAGCTTTGCCAGAGTGACTACTCTCATGACCGTGGCCATCCACCCACC 10096
 QY 1168 roLeuProGlyAlaTyrIleHisProAlaProAspGluProProTrpSerProAlaAla 1188
 Db 10097 CCCTGGCTGGTGCTATCATCTCCATCCAGCCCTGATGAGCCCTTGGTCCCTGCTGCTCA 10156
 QY 1188 hrSerSerGlyAsnLeuSerSerArgGlyProGlyProAlaThrGly 1203
 Db 10157 CTAGCTCTGCACACTCAGTTCAGGGGACCAAGGTCCAGCAGCTGGG 10203

RESULT 7
 AAZ31728
 ID AAZ31728 standard; DNA; 4004 BP.

XX AC AAZ31728;
 XX AC

DT 19-JAN-2000 (first entry)

XX Human patched-2 coding sequence partial clone 3A.

DE Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
 KW cell proliferation; cell differentiation; testicular cancer; gut disease;
 KW degenerative disorder; nervous system disorder; Parkinson's disease;
 KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
 KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
 KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
 KW therapy; ss.

XX Homo sapiens.

XX WO9953058-A1.

XX 21-OCT-1999.

XX 02-APR-1999; 99WO-US007417.

XX 15-APR-1998; 98US-00060939.

XX (GETH) GENENTECH INC.

XX De Sauvage FU, Carpenter DA;
 PI MPI; 1999-620428/53.
 XX New isolated human patched-2 gene, used to develop products for treating,
 PT e.g. cancer and Alzheimer's disease.
 XX Example 1; Page 93-96; 124pp; English.

XX This sequence is a partial clone of DNA encoding the human patched-2
 CC (ptch-2) protein of the invention. The patched-2 polypeptides are
 CC signalling molecules, specifically for signalling and mediator molecules
 CC in the hedgehog (hh) cascade which are involved in cell proliferation and
 CC differentiation. They can be used for the treatment of disorders which
 CC are mediated at least in part by hh, especially Dhh, e.g. testicular
 CC cancer. They can also be used for treating degenerative disorders of the
 CC nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
 CC disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
 CC stroke and drug addiction. Patched-2 agonists can be used to treat gut
 CC diseases, bone diseases, skin diseases, diseases of the testis (including
 CC infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
 CC and osteoporosis. Antagonists or agonists of patched-2 may be used for
 CC treating disorders or creating a desirable physiological condition
 CC effected by blocking hh signalling, especially Dhh signalling, e.g.
 CC contraception or infertility treatment. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic animals

XX SQ Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2e-291 Length: 4004
 Score: 3955.00 Matches: 847
 Percent Similarity: 65.81% Conservative: 2
 Best Local Similarity: 65.66% Mismatches: 10
 Query Match: 63.06% Indels: 434
 DB: 2 Gaps: 10

US-09-990-046-2 (1-1203) x AAZ31728 (1-4004)

QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuLeuGlnThrAlaArg 120
 Db 11 CCGGAGAAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGTACAGACCGCACGC 70
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 71 CAGAGGGAGAGAACATCTCCACCCGGAAGACTTGGCCCTCCACCTCCAGGACGCCCTC 130
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 131 ACTGCCAGTAAAGTCCAAGTATCACTCTATGGGAAGTCTCTGGGATTTGAACMAATCTGC 190
 QY 161 TyrLysSerGlyValProLeuLeuGluAsnGlyMetIleGlnTrpMetIleGluLysLeu 180
 Db 191 TACAAGTCAGAGTCCCTTATTGAAATGGAATGATTCAGCGGATGATGTGAAGCTG 250
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db 251 TTTCCGTCGTGATCTCCACCCCTCGACTCTCTGGGAGGGAGGCCAACTCCAAAGG 310
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
 Db 311 GGCTCCGCTACCTCGCGCT----- 330
 QY 221 LeuLeuGluLeuLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 Db 330 ----- 330
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
 Db 330 ----- 330
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280

Db 331 -----|||-----CCCAATGTGGCTCAGAGCTGAGT 354
Qy 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGly 300
Db 355 GGGGGCTGCCATGCTCTTCCCAAAATTCATGCACTGGCAGGAGGAATTGCTGCTGGGA 414
Qy 301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
Db 415 GGCATGGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCGAGACACCTTC 474
Qy 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
Db 475 TTGCTGATGAGTCCCGCCAGCTGTACGAGCAATTCGGGGTGACTATCAGACACATGAC 534
Qy 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
Db 535 ATTGGCTGGAGTGAGGAGCAGCCAGCACAGTGTACAAGCCTGGCAGCGCGCTTTGTG 594
Qy 360 -----|||----- 360
Db 595 CAGTCTGGTATGGACAAGGACAGGGGGTGCCCTGAGGCCATTCCTCTCTGCCCCCT 654
Qy 361 -----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGly 374
Db 655 CCTATCCACCCCTGTTCTCCAGCTGGCCAGGAGGCCCTGCCTGAGACGCTTCCAGCA 714
Qy 374 nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSe 394
Db 715 GATCCATGCTCTCTCTCCACCACTGGATGACATCTGTCATGCGTCTCTGAAGTCAG 774
Qy 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet----- 405
Db 775 TGTGCCCGTGTGGGAGGCTATCTGCTCATGTTGGTGTCTTGACACCTGGCACTTGGCC 834
Qy 405 -----|||----- 405
Db 835 CCCACCCCACTCCAAACAGTGGCCACCTCTGGGAGGCCCTGAGACTGCCCTTTCCTCCC 894
Qy 406 -----LeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySe 424
Db 895 ACAGCTGGCCCTATGCTGTGTGACCATGCTGCGGTGGGACTGGGCCCAGTCCCAGGGTTC 954
Qy 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCTTTGCCGGGTACTGCTGGTGGCCCTGGCGGTGGCCCTCAGGCCCTTGGGCTCTG 1014
Qy 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr----- 456
Db 1015 TGCCCTGTCTGGCATCACCTTCAATGTGCTGCTACCCAGGTACGCCAGGACTGCAGGGC 1074
Qy 457 -----|||-----G 457
Db 1075 AGACTCAGTGTCCAGTCACAGGCTTTCACGGGTCTCAGCTGCCCGCTCCTCTGCCCCCTCC 1134
Qy 457 lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGTGCTGCCCTTCTTGACTCTGGGAATCGCGTGGATGACGATTCTCCTGCTGGCGCATG 1194
Qy 477 laPheThrGluAlaLeuProGlyThr----- 485
Db 1195 CCTTCACAGAGGCTCTGCTGTGGCACTCCCTCCAGGTGGGGCTTGTCCCCCAGGGCTCA 1254
Qy 485 -----|||----- 485
Db 1255 TCTGAGCGAGCTCAGCTTACTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA 1314
Qy 485 -----|||----- 485
Db 1315 ATGAACCTCGGTCTCTTGTCCCCATGTGTAAACAGGGGAAATAATAGTGTGTCTCT 1374
Qy 485 -----|||----- 485

Db 1375 AAGGTTATTGTTGGATCAGTGAAGTAACCTCAAGTTGAATGCTTAGAACAGCCCATCAT 1434
Qy 485 -----|||----- 485
Db 1435 ACGTACATGTTACCCAAATAAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCACCC 1494
Qy 485 -----|||----- 485
Db 1495 CAAATTCTTGAGCTCCCTTCACTCCACTTTGACAGCGGCCCTCCCTTGTGACTGAGG 1554
Qy 486 -----ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT 500
Db 1555 GCAGGTCCCACTCTGCTCTGG-CAGGAGGCGATGGCGGAGTGTCTGAGCGCAGGGCA 1613
Qy 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
Db 1614 CCAGTGTGTACTCACATCATCAACAACATGGCGGCTTCTTCATGCTGCTCGTCTC 1673
Qy 520 roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCCTTCTTC----- 1699
Qy 540 alaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTACAGCCTGGACCTTACGGCGCGCCACTGC 1730
Qy 560 GlnArgLeuAspValLeuCysCysPheSer----- 569
Db 1731 CAGCGCTTGTATGCTGCTCTGCTTCTC-CAGTACTGCTGCGCCCGCCCTTCTCCT 1789
Qy 569 -----|||----- 569
Db 1790 CCCGTGACCCACGCCAGCTGTCCCTCCACAGCAITTCAGGCACAGACTGTGATCCA 1849
Qy 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTTCTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCTGCCCCAGAGCTG 1909
Qy 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGGACGGGACAGTACACAGTGGGCATTGCCACCTCACTGCCACAGTTCAAGCCTTTACC 1969
Qy 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCAGCATGTGTGTCACCATCTGCTCCCAAGCCACCTGGTG 2029
Qy 625 ProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAAGCCTGGAGGCTCCACAGGGAC 2089
Qy 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGGCCAGGAGGAGAGCAAGGCAGAGCCCTGCAAGTCCCTGCCCTGTGCTGCC 2149
Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuGlnSerHis 684
Db 2150 CGCTGAAATCTTGCCCAATTCGCCCGCTATCAGTTTGCCTGCTGCTGCCAGTCACAT 2209
Qy 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2210 GCCAAGGCCATCTGCTGCTGCTGCTTCTTGTGCTCTTCTGGGCTGAGCCTTACGAGGC 2269
Qy 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGGTCAAGACGGCTGCGCTGACGGATGTGCTGCTCGGGCCACCAAGAGCAT 2329
Qy 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCTTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGTGGCCCTGTGTGACCCAG 2389
Qy 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTTGACTACGCCCACTCCCAACGCCGCCCTCTTTGATCTGCAGCGCTTCAGT 2449

QY 765 SerLeuIysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
 Db 2450 TCCCTCAGGGGCTGCTGCCCCACCCAGCCACCCGACCTGGCTGCATAT 2509
 QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
 Db 2510 TACCGCACTGGCTACAGGAATCCAGCTGCCTTTGACCAGGACTGGGCTTCTGGGCGC 2569
 QY 805 IleThrArgHisSerTyrArgAenGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
 Db 2570 ATCACCAGCCTGCTACCGCAATGGCTCTGAGATGGGGCCCTGGCTACAGCTGCTC 2629
 QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer----- 837
 Db 2630 ATCCAGACTGGAGACGCCAGGAGCCCTCTGGATTTACGCCAGGTTGGGAGGGCTGGAG 2689
 QY 837 ----- 837
 Db 2690 GGGTCCACTAGTACAGGGGCTGAGGCTCTCTGGGCCAGGCTTCAGCCCTCTCTGCT 2749
 QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
 Db 2750 CTGCAGCTGACCAAGAAAGCTGGTGACAGAGAGGAGCTGATTCACCCGAGCTCTTC 2809
 QY 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
 Db 2810 TACATGGGGTGTACCGTGGTGAGAGTGAGACCCCTGGGTGGGAGGCTTCACAGGCC 2869
 QY 877 AspPheTyrProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
 Db 2870 AACTTCTACCCCCACCTCTCTGAATGCTGCACGACAAATACGACACCCAGGGGAGAAC 2929
 QY 897 LeuArg----- 898
 Db 2930 CTTGGCAGTGAAGTTTGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCAACAGCCCT 2989
 QY 898 ----- 898
 Db 2990 GAGCTGAGGCCCTGCCACCTCTGCCCGGTGCTACGCGCTGTCTCTCCCTCTCTCTC 3049
 QY 899 -----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
 Db 3050 CCTTCCCTCCCTCCACAGTCCCGCCAGCTCAGCCCTTGAGTTTGCCAGTTCCCTT 3109
 QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
 Db 3110 CCTGCTCGTGGCTCCAGAGACTGACAGACTTTGTGGAGGCCATCGAGGGGCGCCGGC 3169
 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
 Db 3170 AGCATGCCAGAGGCCGCCAGGCTGGGTGTCACGCCCTACCCAGCGGCTCCCTCTCT 3229
 QY 952 upheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
 Db 3230 CTTCTGGGAACAGTATCTGGGCTCGCGCGTGTCTCTGCTGGCCCTGTGATCTGCT 3289
 QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProThrAlaGlyLeuIle 992
 Db 3290 GGTGTGACATTCCTCTGCTGTCTGCTCTCTCAACCCCTGGAGCGCTGCGCTCAT 3349
 QY 992 e----- 992
 Db 3350 AGTGAGTGTGACAGAGTGGGACAGACACCCACCTTCCCTGCCCGAGCTGTCTAT 3409
 QY 993 -----ValLeuValLeuAlaMetM 999
 Db 3410 CCTCTCTGCCAGGACCCCTCTGTGAGCCCTGTCTCTCCCTCAGGCTGTCTGTCTGCGCATGA 3469
 QY 999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProv 1019
 Db 3470 TGACAGTGGAACTCTTTGGTATCATGGGTTCCTCTGGGCTCAAGCTGAGTGCCTCCCG 3529

1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
 3530 TGTGATCTCTTGGCTCTGTAGGATTTGCGTTGAGTTTCACAGTCCACGTGCTCTGG 3589
 1039 lyPheLeuThrThrGlnGly 1045
 3590 TGAGCACGGGACCCCGGG 3609

RESULT 8
 AAD31580
 ID AAD31580 standard; cDNA; 4004 BP.
 XX
 AC AAD31580;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human patched-2 (Ptch-2) cDNA clone 3A.
 XX
 KW Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
 cytostatic; testicular cancer; hedgehog protein signalling; clone 3A; ss.
 OS Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 primer_bind 30..50
 /*tag= a
 /bound_moiety= "RACE 6 PCR primer"
 primer_bind complement(184..204)
 /*tag= b
 /bound_moiety= "RACE 5 PCR primer"
 US6348575-B1.
 19-FEB-2002.
 15-APR-1999; 99US-00293505.
 15-APR-1998; 98US-0081884P.
 (GETH) GENENTECH INC.
 De Sauvage F, Carpenter DA;
 WPI; 2002-215260/27.
 Native human patched-2 polypeptide for treating disorders caused by
 Hedgehog protein signaling such as testicular cancer, and for screening
 cDNA libraries.
 Example 1; Fig 10; 82pp; English.
 The invention relates to an isolated sequence comprising a native human
 patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
 and mediator molecules in the hedgehog (Hh) cascade which are involved in
 cell proliferation and differentiation. The isolated sequence is useful
 for the treatment of disorders which are linked to hedgehog, especially
 Desert hedgehog expression, such as testicular cancer. It may also be
 used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
 homologues, and to diagnose whether a disorder is driven by Ptch-2 or
 Hedgehog protein signalling. The present sequence is human patched-2
 (Ptch-2) cDNA clone 3A

Sequence 4004 BP; 724 A; 1330 C; 1100 G; 850 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2e-291 Length: 4004
 Score: 3955.00 Matches: 847
 Percent Similarity: 65.81% Conservative: 2
 Best Local Similarity: 65.66% Mismatches: 10
 Query Match: 63.06% Indels: 434
 DB: 6 Gaps: 10

US-09-990-046-2 (1-1203) x AAD31580 (1-4004)

Qy	101	LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
Db	:	:	:
Db	11	CGGAGAAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCACGC	70
Qy	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisGlnAlaIleu	140
Db	71	CAGGAGGAGAGAACATCCTCACACCGAAGCATTGGCTTCACCTCCAGGACGCCCTC	130
Qy	141	ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys	160
Db	131	ACTGCCAGTAAGTCCAAGTATCACTCTATGGGAAGTCTCTGGATTTGACAAAAATCTGC	190
Qy	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu	180
Db	191	TACAAAGTCAGGAGTTCCTCCCTTATTGAAAATGGAATGATTGAGCGGATGATTGAGAAGCTG	250
Qy	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200
Db	251	TTTCGCTGCGTATCCTCACCCCTCGACTCTTCTGGAGGAGCACAATCTCCAAGG	310
Qy	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220
Db	311	GGCTCCGCTACCTGCCCCT	330
Qy	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
Db	330	-----	330
Qy	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys	260
Db	330	-----	330
Qy	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
Db	331	-----	331
Qy	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly	300
Db	355	GGGGGCTGCCATGGCTTCTCCACAAATCATGCACCTGGCAGGAGGAATTGCTGTGGGA	414
Qy	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
Db	415	GGCATGGCCAGAGACCCCAAGAGAGCTGCTGAGGCGAGAGGCCCTGCAGAGCACCTTC	474
Qy	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340
Db	475	TTGCTGTAGTGTCCCGCCAGCTGTACAGAGCAATTTCCGGGGTGATCATCAGACACATGAC	534
Qy	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal	360
Db	535	ATTGGCTGGAGTGAGGACAGCCAGACAGTGTCTACAAGCCTGGCAGCGCGCTTTGTG	594
Qy	360	-----	360
Db	595	CAGTCTGTATGGACAAGGACAGGGGGTGCCCTGAGGCGCATTCCTCTCTCTGCCCTC	654
Qy	361	-----	361
Db	655	CCTATCCACCTGTTTCTCCAGCTGCCCCAGAGGCCCTCGCTGAGAACCGCTTCCACGCA	714
Qy	374	nIleHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValSer	394
Db	715	GATCCATGCCCTTCTCTCCACCACCCTGGATGCATCTCTGCATGGCTTCTCTGAAGTCAG	774
Qy	394	rAlaAlaArgValValGlyGlyTyrLeuLeuMet	405
Db	775	TGCTGCCCGTGTGTGGGAGGCTATCTGCTCATGTGTGGTCTTTGCACCTGGCACCTTGCC	834
Qy	405	-----	405
Db	835	CCCCACCCACCTCCAAACAGTGCACCCCTGGGAGGCCCTGAGAGTGCCTTTTCCCCC	894

Qy	406	----	LeuAlaTyrAlaCysValThrMetLeuArgTTrpAspCysAlaGlnSerGlnGlySe	424
Db	895	ACAGCTGGCCCTATGCTGTGTGACCAATGCTGCGGTGGGACTGCGCCAGTCCACAGGGTTC	954	
Qy	424	rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy	444	
Db	955	CGTGGGCGCTTCGCGGGGTACTGTGTGTGGGCCCTGGCGGTGCCTTCAGGCCTTGGGCTCTG	1014	
Qy	444	sAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThr	456	
Db	1015	TGCCCTGCTGGCATCATCTTCAATGCTGCACACTACCCAGGTAGCCAGGACTGCAGGGC	1074	
Qy	457	-----	-G 457	
Db	1075	AGACTAGTCCAGTCAACAGGCTTCAACGGTCTCTCAGTGCCTGCTCTGTGCCCTCC	1134	
Qy	457	lnValLeuProPheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisA	477	
Db	1135	AGGTGCTGCCCTTCTTCACTCTGGGAATCGCGTGGATGACGTATTCTCTGCTGCGCATG	1194	
Qy	477	laPheThrGluAlaLeuProGlyThr	485	
Db	1195	CCITTCAGAGGCTCTCCCTGGCACCCCTCTCCAGTGGGGCCTTGTCCCCAGGGCTCA	1254	
Qy	485	-----	-----	485
Db	1255	TCTGAGGCAGCTCAGCTTACTTGGTTAAGAGCCTCTTGGTTCAAGTGACCTTGGGCTGCTA	1314	
Qy	485	-----	-----	485
Db	1315	ATGAACCTCGTGCTCTTGTTCCTCATGTGTAAACAGGGGAAATAATAGTGTGTGCTCT	1374	
Qy	485	-----	-----	485
Db	1375	AAGGGTTATTGTTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTGAACAGCCCATCAT	1434	
Qy	485	-----	-----	485
Db	1435	ACGTACATGGTACCCTAAATGCTAGCCACTGTGTTPATGACTGCCTCCCACTCTGCACCC	1494	
Qy	485	-----	-----	485
Db	1495	CAAGTTCTTGAGCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGTGACCTGAGG	1554	
Qy	486	-----	-----	486
Db	1555	GCAGGTCCCACTCTGTCTGG-CAGAGGCGCATGGGCGAGTGCTCGAGCGCACGGGCA	1613	
Qy	500	hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValp	520	
Db	1614	CCAGTGTGTACTCACATCCATCAACAACATGCGCGCTTCTCTCATGCTGCCCTCGTTC	1673	
Qy	520	rolleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV	540	
Db	1674	CCATCCCTCGGCTGCGAGCCTTCTCC	1699	
Qy	540	alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgHisCys	559	
Db	1700	-----	-----	1700
Qy	560	GlnArgLeuAspValLeuCysPheSer	569	
Db	1731	CAGGCGCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCTGGGCCCCAGCCCCCTTCT	1789	
Qy	569	-----	-----	569
Db	1790	CCCGTGACCCAGCCAGCCTGTCCCTCAACAGCATTTCAAGGCACAGACCTGTGCATCCA	1849	
Qy	570	-----	-----	570
Db	1850	CTCTCTACCTCTTCCAGTCCCTGTCTGTCTCAGGTGATTCAGATCTCTGCCAGGAGCTG	1909	

QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
 Db 1910 GGGAGCGGACAGTACCAGTGGGATTTGCCACCTCACTGCCAGTTCAAGCTTTACC 1969
 QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
 Db 1970 CACTGTGAAGCCAGCAGCAGCATGTGTCAACATCTGCTCCCTCCCAAGCCACCTGGTG 2029
 QY 625 ProProSerSerProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
 Db 2030 CCCCCCTTCTGACCCACCTGGGCTCTGAGCTCTTCAGCCCTGGAGGGTCCACACGGGAC 2089
 QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
 Db 2090 CTTCTAGGCCAGGAGGAGGAGACAGCAGAGCCCTGCAAGTCTCCCTGCTGCTGCC 2149
 QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
 Db 2150 CGCTGGAACTTGCCTATTTGCCCGCTATCAGTTTCCCGCTGTGCTCCAGTCCACAT 2209
 QY 685 AlaLysAlaIleValLeuValPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
 Db 2210 GCCAAGCCCATGTGTGGTGCTTTTGGTGCTCTTCTGGGCTTGAGCCTCTACGGAGCC 2269
 QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
 Db 2270 ACCTTGTGCAAGAGCGCTGGCTGACGGATGTGGTGCTCGGGGACCAAGAGCAT 2329
 QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
 Db 2330 GCCTTCTGAGCCCGCCAGCTCAGTACTTCTCCTGTACAGGTGGGCTGTGACCCAG 2389
 QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
 Db 2390 GGTGGCTTTGACTACGCCCACTCCCAAGCGCCCTCTTTGATCTGCACAGCGCTTCAGT 2449
 QY 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
 Db 2450 TCCCTCAAGCGGTGTGTGCCCCACCGCCACCCAGCCAGCCCTGCTGGCTGCACTAT 2509
 QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
 Db 2510 TACCGAATCTGGCTACAGGGAATCCAGGCTGCTTTGACAGGACTGGGCTTCTGGCGC 2569
 QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeu 824
 Db 2570 ATCACCAGGCTGCTGACCGCAATGGCTCTGAGATGGGCGCTTGGCTTCAAGCTGCTC 2629
 QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer 837
 Db 2630 ATCCAGACTGGAGACGCCAGGAGCTCTGGATTTTCAGCCAGGTGGGAGGGCTGGAG 2689
 QY 837 837
 Db 2690 GGGTCCACTAGTACAGGGGCTGACGGCTCTCTGGGCCAGGCTTCAGCCCTCTCTGCCT 2749
 QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
 Db 2750 CTGCAGCTACCAACAGGAGCTGTGGAGCAGAGAGGACTGATTCACCCGAGCTCTTC 2809
 QY 857 TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla 876
 Db 2810 TACATGGGGCTGACCGTGTGGGTGAGCAGTGACGCCCTGGCTTGGCAGCTTCACAGGCC 2869
 QY 877 AsnPheTyrProProProGluTrpLeuHisAspLysTyrAspThrThrGlyGluAsn 896
 Db 2870 AACTTCTACCCCCCTCTCTGAATGGCTGCACGACAAATACGACACACAGCGGGAGAAC 2929
 QY 897 LeuArg 898
 Db 2930 CTTTGCAGTCACTTTGGGGGAGCTCGGCAAGAGCTCAGCCTCGCCCCACACAGCCCT 2989
 QY 898 898

Db 2990 GAGCTGAGGCCCTGCCCACTCTGCCCGGTGCTCACGGCCCTTCCCTCTCCCTCTTCTC 3049
 QY 899 -----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh 912
 Db 3050 CTTTCCCTCCCTCCACAGTCCCGCCAGCTCAGCCCTGGAGTTTCCCAAGTTCCCTT 3109
 QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
 Db 3110 CCTGCTGCTGGCTCCAGAGACTGACAGCTTTGTGGAGCCATCCAGGGGCGCCGGGC 3169
 QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
 Db 3170 AGCATGGCAGAGCGCGCCAGGCTGGGTGCGAGCTACCCACAGCGCTTCCCTTCT 3229
 QY 952 uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLe 972
 Db 3230 CTTCTGGAAACATATCTGGGCTTGGGGCTGCTTCTGCTGCGCCCTGCACTCTGCT 3289
 QY 972 uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuI 992
 Db 3290 GGTGTGACATTTCTGCTGTGCTGTGCTCTCAACCCCTGGACGGCTGCGCTCAT 3349
 QY 992 e----- 992
 Db 3350 AGTGAGTGTCTGAGGAGTGGGACAGACACCCACCCCTTCCCTGCCCGCTGTCTAT 3409
 QY 993 -----ValLeuValLeuAlaMetM 999
 Db 3410 CCCTCTGCCAGAGCCCTCTGTGAGCCCTGTCTCCCTCAGGTGCTGCTTGGCGATGA 3469
 QY 999 eThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProV 1019
 Db 3470 TGAAGTGGAACTCTTTGGTATCATGGGTTTCTGGGCATCAAGCTGAGTGCCATCCCG 3529
 QY 1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
 Db 3530 TGTGTATCTTGTGGCTCTGTAGGATTTGGCGTTGAGTTTACAGTCCACGCTGCTGG 3589
 QY 1039 lypheLeuThrThrGlnGly 1045
 Db 3590 TGAGCAGCGGCACCCCGGG 3609
 RESULT 9
 ID ABX15923
 XX ABX15923 standard; cDNA; 4004 BP.
 AC ABX15923;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human partial cDNA for patched-2 from brain.
 XX
 KW Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
 KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
 KW basal cell carcinoma; neurodegenerative disorder; memory deficit;
 KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
 KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
 KW bone disease; skin disease; testicular disease; ulcer; lung disease;
 KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
 OS Homo sapiens.
 XX
 PN US2002156245-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 20-NOV-2001; 2001US-00990046.
 XX
 PR 15-APR-1998; 98US-0081884P.
 PR 15-APR-1999; 99US-00293505.
 XX
 PA (GETH) GENENTECH INC.

Db	1255	TCTGAGGCGCTCAGCTTACTGGTTAAGAGCCTCTTGTTCAAGTGACCTTGGGCTGCTA	1314	Db	2270	ACCTTGTCACAGAGCGGCTTGGCCCTGACGATGTGGTGCTCGGGGACCCACAGAGCAT	2329
Qy	485	-----	485	Qy	725	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
Db	1315	ATGAACCTCGTGCTCTTGTTCCCATGTGTAAACAGGGGAAATAATAGTGTGTCT	1374	Db	2330	GCCTTCTGAGCGCCAGCTCAGTACTTCTCTGTACGAGGTGGCTGGTACCCAG	2389
Qy	485	-----	485	Qy	745	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer	764
Db	1375	AAGGGTATTGTTGGATCAGTGAAGTAACTCAAGTTGAATGCTTAGAACAGCCCATCAT	1434	Db	2390	GTTGGCTTTGACTACGCCCACTCCCAACGGCCCTCTTTGATCTGCACCGCGCTTCACT	2449
Qy	485	-----	485	Qy	765	SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr	784
Db	1435	ACGTACATGTTACCAATAAATGCTAGCCACTGTGTATGACTGCCCCACCTCTGCACCC	1494	Db	2450	TCCCTCAAGCGGTGTCTGCCCCACCGGCCACCCAGGCACCCCGCACTGGCTGCACTAT	2509
Qy	485	-----	485	Qy	785	TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg	804
Db	1495	CAAGTTCTCGAGCTCCCTTCACTCCACTTTTGACAGCGGCCCTTCCCTTGTGACTGAGG	1554	Db	2510	TACCGCAACTGGGTACAGGAATCCAGGCTGCCCTTGACGAGGACTGGGCTTCTGGGCGC	2569
Qy	486	-----ProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyT	500	Qy	805	IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu	824
Db	1555	GCAGGTCCCACTCTGCTCTGG-CAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCA	1613	Db	2570	ATCACCGCCCACTCGTACCGCAATGGCTCTGAGGATGGGCGCCCTGGGCTACAGCTGCTC	2629
Qy	500	hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValp	520	Qy	825	IleGlnThrGlyAspAlaGlnGluProLeuAspPheSer	837
Db	1614	CCAGTGTGTACTCACATCCATCAACAACATGGCCGCTTCTCTCATGGCTGCCCTCGTTC	1673	Db	2630	ATCCAGACTGGAGAGCGCCAGGAGCCTCTGGATTTCAGCCAGGTTGGAGAGGGCTGGAG	2689
Qy	520	rolleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV	540	Qy	837	-----	837
Db	1674	CCATCCCTGCTGCGAGCCTTCTCC	1699	Db	2690	GGGTCCACTAGTACAGGGGCTGCAGGCTCTCTGGGCCAGGCTTACGCCCTCTCTGCCT	2749
Qy	540	alAlaValMetLeuValPheProAlaIleLeu-SerLeuAspLeuArgArgArgHisCys	559	Qy	838	---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe	856
Db	1700	-----CTACAGCCTGACCTACGGCGCGCCACTGC	1730	Db	2750	CTGCAGCTGACCAAGAGAGCTGGTGGACAGAGAGGACTGATTCACCCGAGCTCTTC	2809
Qy	560	GlnArgLeuAspValLeuCysCysPheSer	569	Qy	857	TyrMetGlyLeuThrValTrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAla	876
Db	1731	CAGCGCTTGATGTGCTCTGCTGCTTCTC-CAGGTACTGCTGCGCCCGCCAGCCCTTCT	1789	Db	2810	TACATGGGCTGACCGTGGTGGTGGAGTGCACCCCTGGGCTTGGCAGGCTCACAGGCC	2869
Qy	569	-----	569	Qy	877	AspPheTyrProProProGluTyrLeuHisAspLysTyrAspThrThrGlyGluAsn	896
Db	1790	CCCGTGACCACCGCCAGCTGTCCCTCACAGCATTTCAAGGCACAGACCTGTATCCA	1849	Db	2870	AACCTTACCCCCACCTCTCTGAATGGCTGCAGACAAATACGACACACCGGGGAGAAC	2929
Qy	570	-----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu	584	Qy	897	LeuArg	898
Db	1850	CTCTTACTCTTCCAGTCCCTGCTCTGCTCAGTGAATTCAGATCTGCCCGCAGGAGCTG	1909	Db	2930	CTTCGAGTGTCTTGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCACACAGCCCT	2989
Qy	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604	Qy	898	-----	898
Db	1910	GGGACCGGACAGTACAGTGGGCATTTGCCACCTCACTGCACAGTTCAGGCCTTTTACC	1969	Db	2990	GAGCCTGAGGCTCTGCCACTCTGCCCGGTGCTCACCGCCCTGTCTCCCTCTTCTC	3049
Qy	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal	624	Qy	899	-----IleProProAlaGlnProLeuGluPheAlaGlnPheProPh	912
Db	1970	CACGTGAAGCCAGCAGCAGCATGTGTGCACCATCTGCTCTCCCAAGGCCACCTGGTG	2029	Db	3050	CTTCCCTCCCTCCCTCCACAGTCCCGCAGCTCAGCCCTTGAGTTTGCCAGTTCCCTT	3109
Qy	625	ProProSerSerProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644	Qy	912	eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl	932
Db	2030	CCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGTTCCACACGGGAC	2089	Db	3110	CTGTCTGCTGGCTCCAGAAAGCTGCAGACTTGTGGAGGCCATCGAGGGGCGCGGCG	3169
Qy	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664	Qy	932	alaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe	952
Db	2090	CTTCTAGGCCAGGAGGAGGACAAAGCAGAGGACGCTGCAAGTCCCTGCCCTGTGCC	2149	Db	3170	AGCATGCGCAGAGGCGCGGCTGGGGTGGCAGCCCTACCCAGCGGCTCCCTCTCTCT	3229
Qy	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684	Qy	952	uPheTrpGluGlnTyrLeuGlyLeuArgArgCysPheLeuAlaValCysIleLeuLe	972
Db	2150	CGCTGGAATCTTGCCCAATTTGCCCGGTATCAGTTTGCCTGCTGCTGCTGCTGCTGCT	2209	Db	3230	CTTCTGGGAACAGTATCTGGGCTTGGGCGCTGCTCTCTCTGCGCGCTCTGCACTCTGCT	3289
Qy	685	AlaLysAlaIleValLeuValPhePheAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704	Qy	972	uValCysThrPheLeuValCysAlaLeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIle	992
Db	2210	GCCAGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2269	Db	3290	GGTGTGCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3349
Qy	705	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis	724	Qy	992	e	992
				Db	3350	AGTGAGTGTTCAGAGGAGTGGGGACAGACACCCACCTTCCCTGCCCCAGCCTGTGAT	3409

```
QY 993 -----ValleuValleuAlaMetM 999
Db 3410 CCCTCTGCCAGGAGCCCTCTGTGAGCCCTGTCCTCCCTCAGGTGCTGCTGCTGCGGATGA 3469
QY 999 etThrValGluLeuPheGlyIleMetGlyPheLeuGlyIleLeuLeuSerAlaIleProV 1019
Db 3470 TGACAGTGGAACTCTTTGATATCATGGGTTTCTGGGCATCAAGCTGAGTGCCATCCCG 3529
QY 1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
Db 3530 TGGTGATCCTTGTGGCCCTCTGTAGGCATTGGGTTGAGTTCACAGTCCACGTCGGCTCTGG 3589
QY 1039 lyPheLeuThrThrClnGly 1045
Db 3590 TGAGCAGGGGACCCCGGGG 3609

RESULT 10
ID AA231729
ID AA231729 standard; DNA; 2082 BP.
AC AA231729;
XX 19-JAN-2000 (first entry)
XX Human patched-2 coding sequence partial clone 16.1.
KW Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
KW cell proliferation; cell differentiation; testicular cancer; gut disease;
KW degenerative disorder; nervous system disorder; Parkinson's disease;
KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
KW therapy; ss.
XX
OS Homo sapiens.
XX
XX WO9553058-A1.
XX
XX 21-OCT-1999.
XX
XX 02-APR-1999; 99WO-US007417.
XX
XX 15-APR-1998; 98US-00060939.
XX
XX (GETH ) GENENTECH INC.
XX
XX De Sauvage FU, Carpenter DA;
XX
XX WPI; 1999-620428/53.
XX
XX New isolated human patched-2 gene, used to develop products for treating,
XX e.g. cancer and Alzheimer's disease.
XX
XX Example 1; Page 96-97; 124pp; English.
XX
XX This sequence is a partial clone of DNA encoding the human patched-2
XX (ptch-2) protein of the invention. The patched-2 polypeptides are
XX signalling molecules, specifically for signalling and mediator molecules
XX in the hedgehog (hh) cascade which are involved in cell proliferation and
XX differentiation. They can be used for the treatment of disorders which
XX are mediated at least in part by hh, especially Bhh, e.g. testicular
XX cancer. They can also be used for treating degenerative disorders of the
XX nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's
XX disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,
XX stroke and drug addiction. Patched-2 agonists can be used to treat gut
XX diseases, bone diseases, skin diseases, diseases of the testis (including
XX infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,
XX and osteoporosis. Antagonists or agonists of patched-2 may be used for
XX treating disorders or creating a desirable physiological condition
XX effected by blocking hh signalling, especially Bhh signalling, e.g.
XX contraception or infertility treatment. The products can also be used for
XX detection, diagnosis, drug screening and production of transgenic animals
```

```
XX SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.82e-248 Length: 2082
Score: 3387.00 Matches: 656
Percent Similarity: 96.33% Conservative: 1
Best Local Similarity: 96.19% Mismatches: 3
Query Match: 54.00% Indels: 23
DB: 2 Gaps: 2
US-09-990-046-2 (1-1203) x AA231729 (1-2082)
QY 1 MetThrArgSerProProLeuArgGluLeuProSerTyrThrProProAlaArgThr 20
Db 8 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCGAGTTACACACCCCGAGTCGAACC 67
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 68 GCAGACCCAGATCCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTCTTACTTC 127
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 128 CAGGCGCTGCTCTTCTCTGGGATGGGGATCCAGAGACATTGTGGCAAGTGTCTTT 187
QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleLthr 80
Db 188 CTGGGACTGTGGGCTTTGGGGCTTGGCATTAGGTCTCCGATGGCCATTATTGAGACA 247
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 248 AACTTGAACAGCTCTCTGGGTAGAAAGTGGGACCGGGTGAGCCAGGAGTGCATTACACC 307
QY 101 LysGlyLysLeuGlyGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 308 AAGGAGAGCTGGGGGAGGAGGCTGCATACACTCTCAGATGCTGATACAGCCGACGC 367
QY 121 GlnGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db 368 CAGGAGGAGAGAACATCTCTCACCCGAGACCTTGGCCCTCCACCTCCAGGAGCCCTC 427
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 428 ACTGCCAGTAAAGTCCAAAGTATCATCTATGGGAAGTCTTGGGATTTGAACAAATCTGC 487
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
Db 488 TACAAGTCAGAGATTCCCTTTTGAANAATGGAATGATTGAGTGGATGATTGAGAAGCTG 547
QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 548 TTTCCGTGCGTGATCTCTCACCCCTCGACTGCTTCTGGGAGGAGGAGCAACTCCAAGG 607
QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 608 GGCTCCGCTTACCTGCGCCCGCCCGGATATCAGTGGACCAACTCTGGATCCAGAGCAG 667
QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
Db 668 CTGCTGGAGAGCTGGGTCTCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC 727
QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys 260
Db 728 GCACAGTGGGCCAGGCTACGTGGGGGGCCCTGTCTGTCACCTGATGACCTCCACTGC 787
QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
Db 788 CCACCTTAGTGGCCCCCAACCATCATCAGCAGCAGGCTCCCAATGTGGCTCAGAGCTGAGT 847
QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly 300
Db 848 GGGGGCTGCCATGGCTCTTCCCCCAAAATTCATGCACTGGCAGGAGGAATGTGCTGGGGA 907
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QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
 Db 128 CAGGGCCCTGCTCTCTCTGGGATGGGGATCCAGAGACATTGTGGCAAAAGTGCTCTTT 187
 QY 61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
 Db 188 CTGGGACTCTGGCCCTTTGGGGCCCTGGGCATTAGGTCTCCGATGGCCATTATTAGACA 247
 QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
 Db 248 AACTTGGAAACAGCTCTGGGTAGAGTGGCAGCCGGGTGAGCAGAGCTGCATTACACC 307
 QY 101 LysGluLysLeuGlyGluGluAlaIleTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
 Db 308 AAGGAGAAGCTGGGGAGGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCAGC 367
 QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
 Db 368 CAGGAGGAGAGAACATCTCTCACACCCGAAGCACTTGGCCCTCCACCTCCAGGAGGCCCTC 427
 QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
 Db 428 ACTGCCAGTAAGTCAAGTATCACTCTATGGGAGTCTCTGGGATTTGAACAAATCTGC 487
 QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
 Db 488 TACAAGTCAGAGTTCCCTTTATTGAAATATGGAATGATTGAGTGGATGATTGAGAAGCTG 547
 QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
 Db 548 TTTCCGTGCGTGTATCTCACCCCTCTGCTGCTGCTGAGGAGGAGCAAACTCCAAAGGG 607
 QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpAsnLeuAspProGluGln 220
 Db 608 GGTCTCCGCTACCTGCCCCGCGCCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG 667
 QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
 Db 668 CTGCTGAGGAGCTGGGTCTCTTGCCTTCTGAGGGCTTCGGGAGCTGCTAGACAAG 727
 QY 241 AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys 260
 Db 728 GCACAGTGGGCCAGGCTACGTGGGCGGCCCTGTCTGCACCTGTATGACCTCCACTGC 787
 QY 261 ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer 280
 Db 788 CCACCTAGTCCCCCAACCATCACAGCAGCAGGCTCCCAATGTGGCTCAGGAGCTGAGT 847
 QY 281 GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluLeuLeuLeuGly 300
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 QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
 Db 968 TTGCTGTATGATGCTCCCGCCAGCTGTACAGAGCATTTCCGGGGTGACTATCAGACACATGAC 1027
 QY 341 IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal 360
 Db 1028 ATTGCTGAGTGGAGGAGCAGCCAGCAGCAGTGTCTACAAAGCTGCAGGCGGTGCTTGTG 1087
 QY 361 GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer 380
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 QY 381 ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly 400
 Db 1148 ACCACCTGGATACATCTCTGATGCGTCTCTGAAGTCAGTGTGCTGCTGGTGGGA 1207

QY 401 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln 420
 Db 1208 GGCTATCTGCTCATGCTGCGCCTATGCTCTGTGTGACCATGCTCGGTGGGACTGCGCCAG 1267
 QY 421 SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly 440
 Db 1268 TCCAGGGTTCCGTGGGCTTGGTGGGCTGCTGCTGGTGGGCTGCTGCGGCTGCGCTCAGGC 1327
 QY 441 LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro 460
 Db 1328 CTTGGGCTCTGTGGCCCTGCTCGGCATCACCTTCATGTCTGCCACTACCCAGGCTGCTGCC 1387
 QY 461 PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu 480
 Db 1388 TTTCTTGGCTCTGGGAATCGCGCTGGATGACGTATTCTCTGCTGGCGCATGCCCTTCACAGAG 1447
 QY 481 AlaLeuProGlyThrProLeuGlnArgMetGlyGluCysLeuGlnArgThrGlyThr 500
 Db 1448 GCTCTGCTGGCACCCCTCTCCAGGAGCGCATGGGCGAGTGTCTGCAGCGCACGGGCACC 1507
 QY 501 SerValValLeuThrSerIleAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro 520
 Db 1508 AGTGTCTGTACTCACATCCATCAACATGGCGCCCTTCTCATGGCTGCCCTCGTCTCC 1567
 QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 Db 1568 ATCCCTGCGCTGGAGCCTTCTCTTACAGCC----- 1599
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 Db 1600 -----ATCCTCAGCCTGGACCTACGGCGGGCGCACTGCCAG 1635
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 Db 1636 CGCTTGTATGTCTGTCTGCTTCTCCAGTCCCTGCTGCTGCTCAGGTGATTCAGATCTCG 1695
 QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 Db 1696 CCCCAGGAGCTGGGGAGCGGAGCAGTACCAGTGGCATTCGCCACCTCTCAGTCCACAGTT 1755
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
 Db 1756 CAAGCCTTTACCACTGTGAAGCAGCAGCAGCATGTGTGTGCTCACCATCTGCTGCCCTCCCAA 1815
 QY 621 AlaHisLeuValProProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 Db 1816 GCCACCTGTGGCCCCCACCCTTTCACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGGG 1875
 QY 641 SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer 660
 Db 1876 TCCACAGCGGACCTTCTTAGCCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1935
 QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
 Db 1936 CTGCGCTGTGCGCGCTGGAATCTTGGCCAT-----TTGCGCCCCGGAATTC 1980
 QY 581 LeuGln 682
 Db 1981 CTGCAG 1986
 RESULT 12
 ABX15924
 ID ABX15924 standard; cDNA; 2082 BP.
 XX AC ABX15924;
 XX AC
 XX 02-APR-2003 (first entry)
 XX DE Human partial cDNA for patched-2 from testis.
 XX Human; patched-2; Dhh signalling; proliferation; differentiation; ss;
 KW chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
 KW basal cell carcinoma; neurodegenerative disorder; memory deficit;

KW Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease; gene;
 KW Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;
 KW bone disease; skin disease; testicular disease; ulcer; lung disease;
 XX pancreatic disease; diabetes; osteoporosis; desert hedgehog.

OS Homo sapiens.

XX US2002156245-A1.

XX 24-OCT-2002.

XX 20-NOV-2001; 2001US-009900046.

XX 15-APR-1998; 98US-0081884P.

XX 15-APR-1999; 99US-00293505.

XX (GETH) GENENTECH INC.

XX De Sauvage FJ, Carpenter DA;

XX WPI; 2003-182650/18.

XX New nucleic acid, useful for manufacturing a medicament for diagnosing or
 PT treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
 PT e.g., testicular cancer.

XX Example 1; Fig 11; 85pp; English.

XX The invention relates to a new isolated nucleic acid encoding a
 CC polypeptide having patched-2 biological activity, comprises DNA having at
 CC least 95% sequence identity with a DNA molecule or its complement
 CC encoding: (a) a human patched-2 polypeptide comprising the sequence
 CC ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
 CC Deposit No. 209778 designation). Also included are a vector comprising
 CC the nucleic acid, a host cell transformed with the vector, a process for
 CC producing patched-2 polypeptides, an isolated native sequence of human
 CC patched-2 polypeptide, a chimeric molecule comprising the vertebrate
 CC patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
 CC hedgehog (Dhh) function in the Dhh signalling pathway, an agonist of
 CC patched-2 that stimulates or enhances the normal functioning of patched-2
 CC in the Dhh signalling pathway, screening for ant/agonists of patched-2
 CC and diagnosing to determine whether a particular disorder is modulated
 CC The nucleic acid is useful for manufacturing a medicament for diagnosing
 CC or treating a disorder that is modulated by Dhh signalling e.g. tumour,
 CC basal cell carcinoma, neurodegenerative disorders, memory deficit,
 CC Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
 CC Huntington's disease, schizophrenia, stroke, drug addiction, gut
 CC diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
 CC diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
 CC Patched-2 may also be used to develop male contraceptives. The gene for
 CC Patched-2 is located on human chromosome 1p33-34. The present sequence is
 CC a Human partial cDNA for patched-2 from testis

XX SQ Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,82e-248	Length:	2082
Score:	3387.00	Matches:	656
Percent Similarity:	96.33%	Conservative:	1
Best Local Similarity:	96.19%	Mismatches:	3
Query Match:	54.00%	Indels:	23
DB:	8	Gaps:	2

US-09-990-046-2 (1-1203) x ABX15924 (1-2082)

QY	1	MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProAlaArgThr	20
DB	8	ATGACTCGATCGCCGCCCTCAGAGAGCTGCCCGAGTTACACACCCCGAGCTCGAAC	67
QY	21	AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe	40
DB	68	GCAGCACCCAGATCTTAGTGGAGGCTGAAGGCTCCACTCTGGCTTCGTCTTACTTC	127

QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe	60
DB	128	CAGGGCCCTGCTCTTCTCTGGGATCGGGATCCAGAGACATTTGGGAAAGTGTCTTT	187
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleLeuThr	80
DB	188	CTGGGACTGTTGGCCCTTTGGGGCCCTAGTCTCCGATGCCCATTTATTGAGACA	247
QY	81	AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr	100
DB	248	AACITGGAAACAGCTCTGGTAGAAGTGGGAGCCGGGTGAGCCAGAGCTGCAATTACAC	307
QY	101	LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120
DB	308	AAGGAGAGCTGGGGAGGAGGCTGCATACCTCTCAGATGCTGATACAGACCCAGC	367
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu	140
DB	368	CAGGAGGAGAGAAATCCTCACACCCGAAACACTTGGCCCTCCACCTCCAGGAGCCCTC	427
QY	141	ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys	160
DB	428	ACTGCCAGTAAAGTCCAAAGTATCACTCTATGGGAAGTCCCTGGGATTTGAAACAAATCTGC	487
QY	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu	180
DB	488	TACAAAGTCAGAGTTCCTTATTGAAATGGAATGATTGATGATGATGATGATGATGATG	547
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200
DB	548	TTTCCGTGGGTGATCTTACCCCTCGACTGCTTCTGGGAGGAGGAGCAAACTCAAAGG	607
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220
DB	608	GGCTCCGCTACCTGCCCGCCCGCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG	667
QY	221	LeuLeuGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240
DB	668	CTGCTGAGGAGCTGGGTCTCTTGGCTTCTTGGGGCTTCCGGGAGCTGTAGACAAG	727
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys	260
DB	728	GCAAGGTGGGCGAGGCTTACGTGGGGCGGCCCTGTCTGCACCTCTGATGACCTCCATGC	787
QY	261	ProProSerAlaProAsnHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280
DB	788	CCACCTAGTGGCCCAACCATCACAGAGGAGCTCCCAATGTGGCTACAGAGCTGAGT	847
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly	300
DB	848	GGGGGTGCTCATGGCTTCTCCCAAAATTCATGCTGCGAGGAGGAATGTCTGTGGGA	907
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320
DB	908	GGCATGGCCAGAGACCCCAAGAGAGCTGTGAGGGCAGAGGCCCTTGAGAGACCTTC	967
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340
DB	968	TTGCTGATGAGTCCCGCCGAGCTGTACGAGCATTTCCGGGGTGACTATCAGACACATGAC	1027
QY	341	IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal	360
DB	1028	ATTGGCTGGAGTGGAGGAGGAGCCAGAGTGTCTACAAAGCTGGCAGCGGGCTTTGTG	1087
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380
DB	1088	CAGCTGGCCAGAGGAGCCCTGCCTGAGAACGCTTCCAGAGCATCCATGCTCTCTCTCC	1147
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400
DB	1148	ACCACCTGGATAACATCTGCTGCTGCTTCTCTGAAGTCAGTGTGCGCGCTGTGTGGGA	1207

QY 129 ProGluAlaLeuGlyLeuHisLeuGlnAlaLeuThrAlaSerLysValGlnValSer 148
Db 897 ACAGAGCGCTCTTACACACCTTGGAGCTCGGACCTCCAGGCGCAGCCGTGCTATATAC 956
QY 149 LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle 168
Db 957 ATGTACACAGGAGTGGAAATTGGACATTGGTTACAAATCAGAGAGCTTATCACA 1016
QY 169 GluAsnGlyMetIleGluTrpMetIleGluLysLeuPheProCysValIleLeuThrPro 188
Db 1017 GAAACAGGTTACATGGATCAGATAAGATAATCTTACCTTGGTTGATTAATACACCT 1076
QY 189 LeuAspCysPheTrpGluGlyAlaLeuGlnGlyGlySerAlaTyrLeuProGlyArg 208
Db 1077 TTGACTGCTTCTGGGAAGGGCGAAATACAGTCTGGGACAGATACCTCTAGGTAAA 1136
QY 209 ProAspIleGlnTrpAsnLeuAspProGluGlnLeuLeuGluLeuGlyProPhe 228
Db 1137 CCTCCTTGGGTGGACAACTTCGACCTTGGAAATCTCGGAAGATTAAAGAAATA 1196
QY 229 ---AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlnAlaTyr 247
Db 1197 AACTATCAAGTGGACAGCTGGGAGAAATGCTGAATAAGGCTGAGTTGGTTCATGGTTAC 1256
QY 248 ValGlyArgProCysLeuHisProAspLeuHisCysProProSerAlaProAsnHis 267
Db 1257 ATGACCGCCCTGCTCAATCCGCGCGATCCAGACTGCCCGCCGACACAGCCGCCCAAAA 1316
QY 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACCAACCTCTTGATATGGCCCTGTTTGAATGGTGAATGCTCATGGTTATCC 1376
QY 288 HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAGATATATGCACTGGCAGGAGGAGTTGANTGGGTGGCGCACAGTCAAGAACAGCACT 1436
QY 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAACCTGCTAGCGCCATGCTCCGACACCATGTTCCAGTTAATGATCTCCCAAGCAA 1496
QY 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATGTACGAGCACTTCAAGGGGTACGAGTATGTCTCACAC--ATCAACTGGAACGAGGAC 1553
QY 347 GlnAlaSerThrValLeuGlnAlaTrpGlnArgPheValGlnLeuAlaGlnGluAla 366
Db 1554 AAGCGCGACGACCTCTCGAGGCGCTGCGAGGACACATATGAGGTGGTTCATCAGAGT 1613
QY 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle 386
Db 1614 GTGCGACAGACTCCACTCAAAAGGTGCTTCTTCCACACGACGACCTCGGACGATC 1673
QY 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
Db 1674 CTGAAATCCTCTCTGACGTGAGTGTATCGCGTGGCCGACGAGCTTACTTACTCATGCTC 1733
QY 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCTCTTAACCATGCTGCGTGGGAGTGTCTTCCAGTGGGCTCCAGGCGTGGGG 1793
QY 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCTGCTGGTTGACTGTAGTGGCTGAGACTGGGCTTGTCTCATTTG 1853
QY 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
Db 1854 ATCGGAATTCCTTAACTGCTGCAACACTCAGGTTTTGCAATTTCTCGCTCTTGGTGT 1913
QY 467 GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----- 484
Db 1914 GGTGTGATGATGTTTTCTTCTGGCCCGCCCTTCAAGTGAACAGGACAGATAAAGA 1973

QY 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTTCAGGACGAGACCGGGAGTGTCTGAAGCGCACAGGACGCGTGGCCCTC 2033
QY 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
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QY 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
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QY 565 LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
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QY 585 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
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QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
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QY 609 SerSerGlnHisValThrIleLeuProProGlnAlaHisLeuValProPro--- 627
Db 2394 CACACGACGCTGATACACACCGCTGACCGCGCTCCGAGATCTCTGTGACGCGCTC 2453
QY 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGACACACCTCAGCTGCCAGAGCCGACGAGACACAGCTCCACAAAGGAC 2513
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QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
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QY 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyValHis 943
Db 3345 GTGGAGGCAATTGAAAAGTAAAGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
QY 944 AlaTyrProSerGlySerProPheLeuPheTrrpGlnTyrLeuGlyLeuArgArgCys 963
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QY 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
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Db 3885 CTGGTTTCTCCCGTCTTGTCTTCTTGTGGACCATATCTCAGGTGTCTCAGCC 3944
QY 1123 tTyrLys-----GluSerProGluIleLeuSerProAlaProGlnGlyG1 1139
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Db 3994 -----TGTTCGCGTTCGCGATGCGCGCG-----GCCAC 4022
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Db 4023 ACCCAGCGGGTCTGATCTCTCCGACTCGGAGTATAGTTCACAGACGAGTGTGAGGC 4082
QY 1168 -----ProLeuProGlyAlaTyrIleHisProAlaProAspG1 1180
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Db 4083 CTCAAGCAGAGAGCTTCGGCACTAGAGCCAGCAGGGCGGGAGGCCCTGCCCCACAA 4142
QY 1180 uProProTrrpSerProAlaAlaThrSerSer 1190
Db 4143 GTGATCGTGAAGCCACAGAAAACCCCGTCT 4173

RESULT 14
AAV64093
ID AAV64093 standard; cDNA; 5288 BP.
XX AAV64093;
AC AAV64093;
DT 26-JAN-1999 (first entry)
XX Human patched gene.
XX Human; patched gene; diagnosis; treatment; developmental disorder;
XX cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
XX sperm production; gene therapy; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 384..4727
FT /*tag= a
XX
FN US5837538-A.
XX
PD 17-NOV-1998.
XX
PF 06-OCT-1995; 95US-00540406.
XX
PR 07-OCT-1994; 94US-00319745.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX P-PSDB; AAW72969.
DR WPI; 1999-023461/02.
DR
XX Nucleic acid encoding vertebrate patched protein and related
XX transformants - used to express poly:peptide(s), useful for diagnosis and
XX treatment of developmental disorders or cancer, and in healing of injured
XX tissue.
XX Claim 1; Col 59-64; 38pp; English.
XX
XX The present sequence represents the human patched (ptc) gene. Cells
XX containing and expressing the ptc gene are used for the recombinant
XX production of the protein. These in turn are useful: (i) for generating
XX antibodies (Ab); and (ii) to screen for specific-binding ligands
XX (potential therapeutic agonists and antagonists). The ptc gene, or its
XX fragments, are used to isolate related sequences from other mammals; to
XX identify mutations (particularly those associated with genetic diseases
XX such as spina bifida and other developmental disorders); to monitor
XX expression levels in testis (to determine relationship with sperm
XX production) and to isolate 5'-non-coding sequences (used to study
XX embryonic development and to provide regulated expression of proteins).
XX The complete gene can be used in gene therapy, including expression of
XX antisense molecules, and to generate transgenic animals for studies of
XX embryonic development. Ab are used diagnostically to determine the ptc
XX protein on cell surfaces and as competitive inhibitors of signal
XX transduction through the ptc ligand. Cells that have been engineered to
XX express the ptc protein can be used to promote regrowth and healing of
XX damaged tissue (e.g. growth of new teeth) and regulation of the ptc
XX protein expression may be useful in cancer treatment (it may control the
XX Wnt-1 oncogene)
XX
SQ Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 U; 0 Other;
Alignment Scores: 5.29e-245 Length: 5288
Pred. NO.: 5288
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 Db 4083 CTGACGAGGAGGCTTGGCACTACGAGGCCACAGCGGCGCGGAGGCCCTGCCCCACAA 4142
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 Db 4143 GTGATCGTGGAGCCACAGAAAACCCCGTCT 4173

RESULT 15

ID AAF32185
 ID AAF32185 standard; DNA; 5288 BP.

AC AAF32185;

DT 12-APR-2001 (first entry)

DE Human patched gene.

XX Human; patched; PTC; segment polarity; limb patterning; development;

XX hedgehog; antibody; mouse; ds.

OS Homo sapiens.

XX US6172200-B1.

PN 09-JAN-2001.

PF 20-OCT-1997; 97US-00954668.

PR 07-OCT-1994; 94US-00319745.

PR 06-OCT-1995; 95US-00540406.

PA (STRD) UNIV LELAND S STANFORD.

XX Scott MP, Goodrich LV, Johnson RL;

DR WPI: 2001-136884/14.

XX P-PSDB; AAB67163.

PT Novel monoclonal antibody useful in diagnostic assays for detection of
 PT presence of protein on surface of cells specifically binds to naturally
 XX occurring patched protein, other than Drosophila patched protein.

PS Disclosure; Col 57-62; 39pp; English.

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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:57:40 ; Search time 327 Seconds
(without alignments)
1302.800 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA: *

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6248	99.6	1203	9	US-09-909-280A-2
3	5599	89.3	1182	9	US-09-990-046-7
4	3348	53.4	1447	8	US-08-954-701A-19
5	3348	53.4	1447	9	US-09-898-533-5
6	3348	53.4	1447	10	US-09-754-032-19
7	3348	53.4	1447	14	US-10-421-446-19
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12	2235	35.6	1311	8	US-08-954-701A-4
13	2235	35.6	1311	10	US-09-754-032-4

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15	1992	31.8	1286	9	US-09-898-533-3	Sequence 3, Appli
16	1961.5	31.3	1299	8	US-08-954-771-48	Sequence 48, Appl
17	1961.5	31.3	1299	17	US-10-647-654-48	Sequence 48, Appl
18	1936.5	30.9	1285	8	US-08-954-701A-6	Sequence 6, Appli
19	1936.5	30.9	1285	10	US-09-754-032-6	Sequence 6, Appli
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22	992	15.8	714	14	US-10-369-493-5410	Sequence 2, Appli
23	640	10.2	1278	14	US-10-208-731-2	Sequence 4, Appli
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26	600.5	9.6	1359	15	US-10-621-758A-44	Sequence 44, Appl
27	600.5	9.6	1359	16	US-10-663-208A-44	Sequence 44, Appl
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34	590	9.4	1332	14	US-10-239-316-9	Sequence 9, Appli
35	584	9.3	1332	15	US-10-621-758A-4	Sequence 4, Appli
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37	584	9.3	1332	16	US-10-646-301A-4	Sequence 4, Appli
38	584	9.3	1332	16	US-10-736-769-4	Sequence 4, Appli
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40	557.5	8.9	1333	16	US-10-663-208A-12	Sequence 12, Appl
41	557.5	8.9	1333	16	US-10-646-301A-12	Sequence 12, Appl
42	557.5	8.9	1333	16	US-10-736-769-12	Sequence 12, Appl
43	444	7.1	933	15	US-10-415-934-3	Sequence 3, Appli
44	434	6.9	1061	15	US-10-415-934-9	Sequence 9, Appli
45	413.5	6.6	934	14	US-10-060-756A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-990-046-2
; Sequence 2, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990, 046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-046-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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; Sequence 2, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THEREETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2
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Query Match 99.6%; Score 6248; DB 9; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSPYTPPARTAAPQILAGSLKAPILWLRAYFCGLLFSLCGCIQRHCXKVL 60
Db 1 MTRSPPLRELPSPYTPPARTAAPQILAGSLKAPILWLRAYFCGLLFSLCGCIQRHCXKVL 60
QY 61 LGLAFGALGALGRMAIETNLQWLVEVGRSVRSQELHYTKELGEEAAVTSQMLIQTAR 120
Db 61 LGLAFGALGALGRMAIETNLQWLVEVGRSVRSQELHYTKELGEEAAVTSQMLIQTAR 120
QY 121 QEGENILTPALGHLQAALTASKVQVSLYKGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPALGHLQAALTASKVQVSLYKGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLFCFWEKALQGGSAIYLPGRDPIQWNTLDPQELLBELGPFASLEGPRELLDK 240
Db 181 FPCVILTPDLFCFWEKALQGGSAIYLPGRDPIQWNTLDPQELLBELGPFASLEGPRELLDK 240
QY 241 AQVQAVVGRPCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
Db 241 AQVQAVVGRPCPLHPPDLHCPSPAPNHHSRQAPNVAHELSCGGCHGFSHKFMHMQEELLG 300
QY 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
QY 361 QLAQEALPENASQOIHAFFSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWPCAQ 420
Db 361 QLAQEALPENASQOIHAFFSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWPCAQ 420
QY 421 SQSVGLAGVLLVALAVASGLGICALLGITFNATTOVLPFLALGIGVDDVFLLAHAFFE 480
Db 421 SQSVGLAGVLLVALAVASGLGICALLGITFNATTOVLPFLALGIGVDDVFLLAHAFFE 480
QY 481 ALPGTPLQERMGECLQRTGTSTSVLTSINNMAAFIIPALRAFSLOAAIIVGCTFV 540
Db 481 ALPGTPLQERMGECLQRTGTSTSVLTSINNMAAFIIPALRAFSLOAAIIVGCTFV 540
QY 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSSPCSAQVIQILPOELGDCGTVPVGIHAHLTATV 600
Db 541 AVMLVFPAILSLDLRRRHQCORLDVLCFSSPCSAQVIQILPOELGDCGTVPVGIHAHLTATV 600
QY 601 QAETHCEASSQHVVTILPPQAHVLPSPDPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
Db 601 QAETHCEASSQHVVTILPPQAHVLPSPDPLGSELFSFGGSTRDLLGQEEETROKAAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
```

Db 661 LPCARNLAHFARYQFAPLLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSSLKAVLPPPTAQART 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSSLKAVLPPPTAQART 780
Qy 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAAQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAAQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQFELRLGQKTADFVEAIEGABAAACAEAGQAGVHAYPSGSPFLFWEYVGL 960
Db 901 PAQPLEFAQFELRLGQKTADFVEAIEGABAAACAEAGQAGVHAYPSGSPFLFWEYVGL 960
Qy 961 RRCFLAVCILLVCTFLVALLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVALLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Qy 1021 ILVASGIGVEFTHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALT VTLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Db 1081 FDFIVRYFFAALT VTLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Qy 1141 LRWGASSLPSQSFARVTTSMVAIHPPPLPGAYIHPAPDEPPSPAAATSSGNLSSRGPG 1200
Db 1141 LRWGASSLPSQSFARVTTSMVAIHPPPLPGAYIHPAPDEPPSPAAATSSGNLSSRGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
US-09-990-046-7
; Sequence 7, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: PI405R1
; CURRENT APPLICATION NUMBER: US/09/990, 046
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-990-046-7

Query Match 89.3%; Score 5599; DB 9; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

Qy 1 MTRSPRLPSPYTPPARTAQAQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCKVLF 60
Db 1 MTRSPRLPSPYTPPARTAQAQIILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCKVLF 60
Qy 61 LGLAFGALALGRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIOTAR 120
Db 61 LGLAFGALALGRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIOTAR 120
Qy 121 QGENILTPALGLHLQAALTASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIERIEKL 180
Db 121 QGENILTPALGLHLQAALTASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIERIEKL 180

Db 121 QEGNVLTPEALDHLHQAALTASKVQVSLYSGKSWDLNKICYKSGVPLIENGMIERIEKL 180
Qy 181 FPCVILTPDLCFWEGAKLQGSAYLPGRPDIQTWNLDPEQLLEELGPPFASLEGRELLDK 240
Db 181 FPCVILTPDLCFWEGAKLQGSAYLPGRPDIQTWNLDPEQLLEELGPPFASLEGRELLDK 240
Qy 241 AQVCQAVGRPCLPDHDHCPSPAPNHHRSQAPNVAHELSSGGCHGFSKFMHWQBELLLG 300
Db 241 AQVCQAVGRPCLPDHDHCPSPAPNHHRSQAPNVAHELSSGGCHGFSKFMHWQBELLLG 300
Qy 301 GMARDPOGELLARABALOSTFLLMSPROLYEHFRGDYQTHDIGHSEEQASTVLOAWORRFV 360
Db 301 GTARDLQQLLRABALOSTFLLMSPROLYEHFRGDYQTHDIGHSEEQASTVLOAWORRFV 360
Qy 361 QLAQALPENASQIHAFFSTTLLDDIILHAFSEVSAARVWGGYLLMLAYACVTMLRWBCAQ 420
Db 361 QLAQALPENASQIHAFFSTTLLDDIILHAFSEVSAARVWGGYLLMLAYACVTMLRWBCAQ 420
Qy 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPPLALGIGVDDVFLLAHAFTE 480
Db 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPPLALGIGVDDVFLLAHAFTE 480
Qy 481 ALPCTPLQERMGECLORTGTSVVLTSINNMAAFILMAALVPIPALRAESLQAAIYVGCFTV 540
Db 481 APDPTPLPERMGECLRTSTGTSVALTSVNNWVAFFMAALVPIPALRAESLQAAIYVGCFTV 540
Qy 541 AVMLVFPAILSLDLRRHRQRDLVLCFSSPCSAQVIQILPQELGDCGTVPGVIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRQRDLVLCFSSPCSAQVIQILPQELGDCGTVPGVIAHLTATV 600
Qy 601 QATHCEASSQHVVTILPPOAHVPPSDPLGSELSPGSGTRDLLQGEETRQKAAACKS 660
Db 601 QATHCEASSQHVVTILPPOAHVPPSDPLGSELSPGSGTRDLLQGEETRQKAAACKS 660
Qy 661 LPCARNLAHFARYQFAPLLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Db 661 LPCARNLAHFARYQFAPLLQSHAKAIVLVIFGALLGLSLYATLVQDGLATDVVPRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSSLKAVLPPPTAQART 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSORALFDLHORFSSSLKAVLPPPTAQART 780
Qy 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIQAAFDQDMSAGRIITRHSYRNGSDGALAYKLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAAQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAAQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQFELRLGQKTADFVEAIEGABAAACAEAGQAGVHAYPSGSPFLFWEYVGL 960
Db 901 PAQPLEFAQFELRLGQKTADFVEAIEGABAAACAEAGQAGVHAYPSGSPFLFWEYVGL 960
Qy 961 RRCFLAVCILLVCTFLVALLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVALLNPNWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPV 1020
Qy 1021 ILVASGIGVEFTHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTHVALGFLTTQGSRNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALT VTLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Db 1081 FDFIVRYFFAALT VTLTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGG 1140
Qy 1141 LRWGASSLPSQSFARVTTSMVAIHPPPLPGAYIHPAPDEPPSPAAATSSGNLSSRGPG 1181
Db 1141 LRWGASSLPSQSFARVTTSMVAIHPPPLPGAYIHPAPDEPPSPAAATSSGNLSSRGPG 1181

Sequence 19, Application US/08954701A
Publication No. US20030032085A1
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
FILING DATE: 20-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36709
REFERENCE/DOCKET NUMBER: SUV-003.08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 8; Length 1447;
Best Local Similarity 49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLMRAYFQGLLFLSLGCGIQHCHGKULFLGLAFA 68
DB 53 PSYC-DAFALEQISKGATGRKAPLWLRKAFQRLFLKLCYIQKNCGLFVWGLLIFGA 111
QY 69 LAIGLRMAITETMLEQLWVEGSRVSOELHYTKELGEEAAYTSOMLIQTARQGENILT 128
DB 112 FAVGLKAANLETNVEELWVEGSRVRELNTYRQKIGEEAAYTSOMLIQTARQGENILT 171
QY 129 PEALGLHQAALTASKQVSLYKGSWDINKICYKSGVPLIENGMIEMWIEKLFECVILTP 188
DB 172 TEALLQHLDSALQASRVHYVYNNQWKLHLCYKSGELITETGYMDQIIEVLYECLLIPT 231
QY 189 LDCFWEGAKQGGAYLPGRPDIQWNLDPQLLELGPFF-ASLEGFRELDDKQVQAY 247
DB 232 LDCFWEGAKLQSGTAYLLGKPLRWTFNDFPLEFLEELKKNYQVDSWEMLNKAUEVGHY 291
QY 248 VGRPLHPDDLHCPPSPNHHROAPNVAHLSGCHGSKHFMHWOBEILLGGWARPDPQ 307
DB 292 MDRECLFPADPDCCATAPNKNSTKPLDVALVINGGCHLSKRYMEHQEELIVGTVKNST 351
QY 308 GELLEAEALQSTFLIMSPPQYEHFRG-DYQTHPDIGMSEBOASTVLOAQRFFVOLAQEA 366
DB 352 GKLVSAHALQTMFQMLTPKQYEHFKGYEYVSH-INNWEDKAAALIEAWQRTYVEVHQ 410
QY 367 LPENASQOIHAFSPTLDDILHARSEVSAARVVGYYLIMLAYACVTMLRWDCASQSGVG 426
DB 411 VAQNSTQVLSTFTTLLDILKSDSVIRVAGYLLMLAYACVTMLRWDCSKSQGAVG 470
QY 427 LAGVLLVALVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFFILAHAFTEALPG-- 484

DB 471 LAGVLLVALVASAGLGLCSLIGISFNAATTQVLPFLALGIGVDDVFFILAHAFSETQNK 530
QY 485 TELQERMGECLQRTGTSVLTSTNNVAAFLMAALDIPALRAFSLQAAIVVGCTFVAVML 544
DB 531 IPEEDRTGECLKRTGASVALTSISNVTAFMAALDIPALRAFSLQAAIVVFNFAVLL 590
QY 545 VPAIILSLDLRRHRCORLDVLCFSSPCSAQVQIQLPQELGD-----GTVPVGAH-- 595
DB 591 IFFAILSMOLYRRREDRLDIFCCFTSPCVSRVLOVEPQAYTHTDNRXSPFPYSHSF 650
QY 596 -----LATATQAFTHCEASSQHVVTILPQAHVPPP-----SDPLGSELFPGGSTRD 644
DB 651 AHETQITMQSTVOLRTXDHPHTHYVTTAEPRSEISVQPVVTTQDTLSCQPESTSTRD 710
QY 645 LLQBEETROKAAACKSLPCARWNLAHARYQFAPILLQSHAKAIVLVFALLGLSLYGA 704
DB 711 LLSQFSDS--SLHCLPEPCTKWTLSFAEKYAFLLKPKAKVVVFLFLGLLGLSVLYGT 768
QY 705 TLVQDGLALTDVVPRTGKEHAPLSAOLRYPFLSYEVALVTQGGFDYAHSQRALFDLHORFS 764
DB 769 TRVRDGLDLTDIVPRETREVDFAAQKFYSFYNNWIVTQKA-DYPNIQHLLVLDLHRSFS 827
QY 765 SLKAVLPPPATQAPRTWMLHYRNWLOGIQAAFQDQWASGRITRHSYRNGEDGALAYKLL 824
DB 828 NVKYVMLEENKQLPKMWLHYFRDMLQGLQDAFDSWETGKIMPNYKNGSDGVLAYKLL 887
QY 825 IQGDAQEPFLDFSLQITRKLVDREGILPPELFYMGTLVWVSSDPLGLAAQANFYPPPE 884
DB 888 VQTGSRDKPIDISQLTKQRLVDADGINSFAFYIYLTAWVSDNDFVAYAAQANIRPERPE 947
QY 885 WLHDKYDTTGE-NLRIPPAQPLEFAOPFLLRLGKLTADFEATEGARAACAQAGVH 943
DB 948 WHDKADYMPETRLRIPAEPIHYAQFPFYNGLRDTSDFEAELEKVRTICSNVTSLSLS 1007
QY 944 AYPGSPFLEWQYGLRRCFLLAVALCILLVCTFLVOCALLLLNPTAGLIVLVLAMMTVEL 1003
DB 1008 SYPNGYFLEWQYGLRHWLLFISVLACTFLVCAVFLINPWTAGIIVWLALMTVEL 1067
QY 1004 FGIMFLGKILSAIPVVLIVASVIGVEFTVHVALGFLTTQGSNRAAHLAHTFAPVT 1063
DB 1068 FGIMFLGKILSAIPVVLIVASVIGVEFTVHVALGFLTTQGSNRAAHLAHTFAPVT 1127
QY 1064 DGAISTLLGLLAGSHDFIVRYFFAALTATLTLGLLHGLVLLPVLSSILGPPPEVI-- 1121
DB 1128 DGAISTLLGLLAGSHDFIVRYFFAALTATLTLGLLHGLVLLPVLSSILGPPPEVI-- 1187
QY 1122 ---QMYKESPE-----ILSP-----APOGG 1139
DB 1188 NGLNRLTPSPPEPPSVVRFAMPBGHTHSGSDSDSEYSSQTTVSGLSGLSELRHYEAQGA 1247
QY 1140 G-----LRWG-----ASSSLPQSFA 1155
DB 1248 GPPAHQVIVEATENPVFAHSTVHVHPSRHHPPSPNROOHLDSGLPPGROGQPRDPP 1307
QY 1141 -----SMTVAIHPPLPGAYIHP 1176
DB 1308 REGIWPPLYRPRDADFISTEGHSGPSNRARWGRGARSHNPNRNPASTAMGSSVPGYQCP 1367
QY 1156 VTT-----SMTVAIHPPLPGAYIHP 1176
DB 1368 ITTVTASVTVAVHPPPPVPGGRNP 1393

RESULT 5
US-09-898-533-5
Sequence 5, Application US/09898533
Patent No. US20020106656A1
GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: ITC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
TITLE OF INVENTION: PATCHED

```

; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/898,533
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: US/09/268,140
; PRIOR FILING DATE: 2000-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-898-533-5

Query Match      53.4%; Score 3348; DB 9; Length 1447;
Best Local Similarity 49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAQAQILASGL---KAPLMRAYFOGLFLSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAFALEQISKGKATGRKAPLWLRKAFORILLFKIGCYIQKNCCKFLVGLLIFGA 111
QY 69 LALGLRMAITETNLEQLWVEGSRVSOELHYTKELGEEAAYTSOMLIQTARQGENILT 128
Db 112 FAVGLKAAITETNVEELWVEGGRVSRRELNYTRQKIGEEAMPNQLMIQTPEEGANVLT 171
QY 129 PEALGLHQAALTAASKVQSVLYGKSWDLNKIKCYSGVPLIENGMIENWIEKLPPCVILTP 188
Db 172 TEALLQHLDSALQASRVHVMYNEQWLEHLKCYSGELITETGYMDQIIEVLYPCLLIITP 231
QY 189 LDCFWEGAKLQGSAYLPGRPDITOWNLDPQLLEELGPF-ASLEGPRELLDKAQVQAY 247
Db 232 LDCFWEGAKLQSGTAYLLGKPLRWTFNDFLEFLKELKKNYQVDSWEENLNAEVGHY 291
QY 248 VGRPCLHPDDLHCPSPAPNHSQAPNAVAHELSCGCHGFSGHKPMHWOEILLGGMARDPQ 307
Db 292 MDRPCLNPADPCPATAPNNKNTKPLDMALVNLGCGCHGLSRKYNHWOEEELVIGTVKNST 351
QY 308 GELLRAEALQSTFLMSPROLYEHRFG-DYQTHDIGMSEBOASTVLQAWQRRFVOLAQEA 366
Db 352 GKLVSAAHALQTMFLQMTFKQMYEHFKGYEVSH-INWNEKAAALIEAWORTTVEVHHQS 410
QY 367 LPNASSQOIHAFSTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQSQSVG 426
Db 411 VAQNSTQKVSFTTTTLLDILKFSFSDVSVIRVASGYLLMLAYACVTMLRWDCKSKQAVG 470
QY 427 LAGVLLVALAVASGLGCLLGTENAAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAGLGLCLGSLIGISFNAATTQVLPFLALGIGVDDVFLLAHAFSETQNK 530
QY 485 TPLQRMGECLQRTGTSVVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db 531 IFFEDRTGELKETGASVALTSISNTAFMAALIIPIPALRAFSLQAAVVVFNFAVLL 590
QY 545 VFPAILSLDIRRHORLORLVLCFSSPCSAQVLIQILPQELG-----GTVPVGIAH-- 595
Db 591 IFFAILSMDLRYRDRRLDIFCCFTSPCVSRVIVQEPQAYTDHNTNRYSPPPPYSSHFP 650
QY 596 -----LTAIVQAFTHCEASSQHVVTILPQAHVPPP-----SDPLGSELSPGSGSTRD 644
Db 651 AHETQITMOSTVQLRTEYDPHTHYTTAEPRESEISVQPVTVTQDTLSCQSPESSTRD 710
QY 645 LLGQBEETRQKAAKSLPCARNLNAHAFARYQAPILLOSHAKAIVLFLGALIGLSLYCA 704
Db 711 LLSQFSDS--SLHCLPEPCTKTLTSFAEKHYAPFLKPKAKVVVIFLFLGLGVSlyGT 768
QY 705 TLVQDGLALTVDVPRGTKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHOREP 764
Db 769 TRVRDGLDLDIVPRETRYDFIAQKFVFSFYNMYIVTQKA-DYPNIGHLYDLHRSFS 827
QY 765 SLKAVLPPATQAPRTLWLYHYNRWLOGIOAAFDQDQWASGRIITHRSYRNGSEDALAYKLL 824
Db 828 NVKYVWLEENKQLPKMWLHYFRDWTQLGLQDAFDSOWETGKIMPNYKNYKNGSDGVLAYKLL 887

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RESULT 6

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US-09-754-032-19
; Sequence 19, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;                GOODRICH, LISA V
;                JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

```

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; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-754-032-19

Query Match 53.4%; Score 3348; DB 10; Length 1447;
Best Local Similarity 49.9%; Pred. No. 9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAQAQILAGSL---KAPLWRAYPGCLLFSLGCGTORHCGKVLFLGLAFA 68
Db 53 PSYC-DAAPALEQISKGATGRKAPLWRAKFORLLFKLGYIQKNGKFLVVGLLIFGA 111
QY 69 LALGLRMAITETNLEQLWVEGVSQELHYVTKELGEEAAYTSQMLIOTARCEGENILT 128
Db 112 FAVGLKAANLEITNVEELWVEGVSRELNYTRQKIGEEANFPQLMIQTPKEEGANVLT 171
QY 129 PEALGLHLAALTASKVQVSLYKGSWDLNKIKYKSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVVMYNRQWKLHLKYSGLELITETGYMDQIIEVLYPCLITP 231
QY 189 LDCFWGAKLOGGSAYLPGRPDIOWTNMLDPEQLLELGPFF-ASLEGPRELLDKAUVQAY 247
Db 232 LDCFWGAKLOGGSAVLLGKPLRWTFNDFLEFLEELKKNYQVDSWEEMLNKAEVGHGY 291
QY 248 VGRPCLPDHLHCPSPANHSQAPNVAHELSGCHGFHMKPMHWOEEILLGGMARDPQ 307
Db 292 MDRPCLNPADPCPATPANKNSTKPLDMALVNGCGHGLSKRYMHWQEEILVGGTVKXST 351
QY 308 GELLRAALQSTFLMSPROLYEHFRG-DYQTHDIGWSEEQASTVLAQWQRRFVQLAQEA 366
Db 352 GKLVSAHALQTMQLMTPKQMYEHFKYEVVSH-INNEDKAAALEAMQRTYVEVWHQS 410
QY 367 LPENASQIHFAGSTTLDDILHAFSEVSAARVVGYYLLMLAYACTVMLRWDCQSQSVG 426
Db 411 VAQNSTQKVLSTFTLLDDILKSPSDSVIRVASGYLLMLAYACTVMLRWDCSKSQGAVG 470
QY 427 LAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIVDDVDELLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGSLGICSLGISFNAAATQVLPFLALGIVDDVDELLAHAFSTGQNR 530
QY 485 TPLQRMGEICQRTGTGTVLTSINNMAAFMAALVPIPALRAFSLOAAIVVCGTTFVAVML 544
Db 531 IPPEDRTGECLKRTGASVALTSISNVTAFTFAALIPALRAFSLOAAIVVVFVNFAMVLL 590
QY 545 VFPAILSLDRRHRCQRLDVLCCFSSPCSAQVIQILFQELGD-----GVTPVGVIAH-- 595
Db 591 IFFAILSMGLYRREDRLDIPCCFTSPCVSRVIOVEFAQYTDTHNTRYSPPPYSSHSF 650
QY 596 -----LTAIVQAFTHCEAASSQHVVTILPQAHVLEPP-----SDPLGSELFSFGGSTR 644
Db 651 AHETQITMQSTVQURTEYDPHTHYVYTTAEPSISVQPVTVTQDTLSCQPESTSTRD 710
QY 645 LLQGEETROKAAKSLPCARWNLHAFARYQAFLLQSHAKAIVLVFLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLEPPCTKWTLSFPAEKHYAPFLPKAKVAVVFLFLGLGVSLEYGT 768
QY 705 TLVQDGLALTDPVPRGKTEHAFSLAQLRYFSLYVALVTCGGFDYAHSORALFDLHQRES 764
Db 769 TRVRDGLDITDIPRETRYEDFIAAQFKYFSYNNYIVTQKA-DYFNIOHLLLYDLHRSFS 827
QY 765 SLKAVLPPATQAPRTLHYVRNWLQIQAADFQDQWASGRITRHSYRNGSDGALAYKLL 824
Db 828 NVKYVLEENKQLPKWMLHYFRDMLQGLQDAFSDSWETGKIMPNNYKNGSDGVLAYKLL 887
QY 825 IQTGDAQBPPLPFSQLTTKLVDRREGLIPELFPYMGLTWVWSSDPLGLAASQANFPYPPPE 884
Db 888 VQTGRDRKPIDISQLTQKRLVDADGIINPFAFYIYLTAWVNSDPVAYAAASQANIRPHRPE 947
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RESULT 7

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US-10-421-446-19
; Sequence 19, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;                GOODRICH, LISA V
;                JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
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Db	888	VQTGSRDKPIDISQTLKQRLVDADGIINPSAFYIYLTAWVSNDFVAAASQANIRPHRPE	947
Qy	885	WLHKDYTTTGC-NLRIIPPAQPLEFAQPFLLRGLQKTFADFEATEGARAAACAAGQGVH	943
Db	948	WHDKADYMPETRURIPAAEFIEYAQPFYFYLNGLRDTSDFEATEKVRTTICSNYTSIGLS	1007
Qy	944	AYPSGSPFLFEWQYGLGRRCFLLAVCAIIVCTFLVCALLLNPMWTAGIIVLVLAMMTVEL	1003
Db	1008	SYPNGYFPLFEWQYGLRHWMLLFISVVLACTFLVCVAFLLNPWTAGIIVVLALMTVEL	1067
Qy	1004	FGIMGFYGIKLSAIPVIVILVASVIGVFEVTHVALGFLTTCGSRNLRAAAHLEHTFAPVT	1063
Db	1068	FGMGLIGIKLSAVPVVILIASVIGVFEVTHVALAFLTAIDKNRAVLALEHMPAPVL	1127
Qy	1064	DGATSTLLGLMLAGSHDFIVRYFFAALTIVLTLLGLHGLVLLPULLSILGPPPEVI--	1121
Db	1128	DGAVSTLLGLMLAGSEDFIVRYFFAVLAITLILGVINGLVLLPULLSFFGYPEVSPA	1187
Qy	1122	---QMYKESPE-----ILSP-----APQGG	1139
Db	1188	NGLNRLPTSPPEPPSVVRPAMPGHTHSGDSSDSEYSSQTTVSGLSEBLRHYEAQQGA	1247
Qy	1140	G-----	1140
Db	1248	GGAHQVIVEATENPVFAHSTVVHPESRHPPSNPRQQPHLDSGLPPCGRQGOQPRDPP	1307
Qy	1141	-----LRWG-----ASSSLPOSFAR	1155
Db	1308	REGIMPLYLRPRDAFEISTEGHSGPSNRARMGPRGARSHNPRNPASTAMGSSVFGYQCP	1367
Qy	1156	VTT-----SMTVAIHPPPLPGAYIHP	1176
Db	1368	ITTVTASVTVAVHPHPVPGGRNP	1393
RESULT 8			
US-08-954-701A-10			
; Sequence 10, Application US/08954701A			
; Publication No. US20030032085A1			
; GENERAL INFORMATION:			
; APPLICANT: SCOTT, MATHEW P			
; APPLICANT: GOODRICH, LISA V			
; APPLICANT: JOHNSON, RONALD L			
; TITLE OF INVENTION: Patched Genes and their Use			
; NUMBER OF SEQUENCES: 19			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Foley, Hoag & Eliot			
; STREET: One Post Office Square			
; CITY: Boston			
; STATE: MA			
; COUNTRY: USA			
; ZIP: 02109			
; COMPUTER READABLE FORM:			
; MEDUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: ASCII(text)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/954,701A			
; FILING DATE: 20-OCT-1997			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Vincent, Matthew P.			
; REGISTRATION NUMBER: 36709			
; REFERENCE/DOCKET NUMBER: SUY-003.08			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 617-832-1000			
; TELEFAX: 617-832-7000			
; INFORMATION FOR SEQ ID NO: 10:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1434 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			

20:

28 RAAPDEDYLRHSYC-DAAFALQISKGKATGRKAPLMLRAKFORLLFLKGLCVIQKNCCK 86
58 VFLGALLAFALGALURMAIETNLEQLWVEGSRVSQELHYTKELGEBAAYSQMLIQ 117
87 FLVGLLIFGAFVGLKAANLETNVBEELWVEGSRVREINLYTRQIGBEAMFNQMLIQ 146
118 TARQEGENILTPALGHLQAALTASKVQSVLKGKSWDLNKKICKYSGVPLIENGMEIEM 177
147 TPKEGANVLTTEALLQHLSDLAQGRVHVYMTNRQMKLEHLCKYSGELITETGYMDQII 206
178 EKLFPVCVILTPDLFCWEGAKLOGGSAYLPGRPDIQNTLNDPEQLLELGP-ASLEGPRE 236
207 EYLYPCLIITPLDCWEGAKLOGSTAYLLGKPLRWTFDLFLBELKKINQVDSWEE 266
237 LLDKAQVQAYVGRPCILHDDDLHCPSPAPNHHGRQAPNVAHELSCGCHGSHKPMWQEE 296
267 MLNKAEGVGHYMDRCPCLNPADPCPATAPNKNSTKPLDVALVNGGCGGLSRKYMWQEE 326
297 LILGGMARDPOGELLRAEALQSTFLLMSPROLYEHFEG-DYQTHDIGWSEQASTVILQAW 355
327 LIVGGTVKNTGKLVSAHALQTFQMLTPKQMYEHFEGYDVSH-INWEDRAAAILLEAW 385
356 QRRFVOLAQBALPENASQQIHAFSSTLDDILHAFSEVSAARVVGGYLLMLAYACVMTLR 415
386 QRYVEVHVQSVAPNSTQKVLPTFTTLLDILKSPSDSVIRVASGYLLMLAYACVMTLR 445
416 WDCAQSGVGLAGVLLVALAVASGLGLCALLGITENAAQTQVLPFLALGIGVDDVLELLA 475
446 WDCSKSQAGVGLAGVLLVALSVAAGLGLSLIGISFNAATQVLPFLALGIGVDDVLELLA 505
476 HATEALPG--TPOERMGECLORTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAI 533
506 HAFSETQCNKRIPEFTGTGCLKRTGASVALTSISNVTAFMAALIPALRAFSLQAAV 565
534 VVGCTFVAVMLVFPAILSLDRRRHQRDLVLCFCSSPCSAQVILQIPBELGD----- 586
566 VVFNFAVMLIIPAILSMDLXREDRLDIFCCFTSPCVSRVIOVEPQAYTEPHSNTRY 625
587 GTVPVGIAGH-----LFAVQAFTHCEASSQHVITLPPQAHVPPP-----SDPLGS 633
626 SPPTPYTSHSFAHETHITMOSTVQLRTYDPHTHVYTTAEPRSEISVQPVVTQDNLSC 685
634 ELSPGSGSTRDLGQEBETKQACKSLPCARNLAHFAFYQAPLQLQSHAKAIVLVLF 693
686 QSPBSTSTDLQLSQFSDS--SLHCLPPTCKWTLSFAEKHYAFPLKPKAKVVILLF 743
694 GALLGLSLYGATLVQDGLALTVDVPRGTKEHAFSLAQLRYSLEYVALVTQGGFDYAHSQ 753
744 LGLLGLVSLYGTTRVRDGLDLDIIVPRETREYDFIAAQFKYFSFYNNVIVTOKA-DYFNIQ 802
754 RALEDLHORFSSLKAVLPPATQAPRTWLHYRNWLOGIQAAPQODWASGEITHRSYRNG 813
803 HLLYDLHKFSFNKVMLEENKQLPQMWLHYFRDMLQGLQDAPSDMETGRIMPNNYKNG 862
814 SEDCALAYKLLIQDGAQEPDLDFQSOLTRKLVDRGLIPPLBYFMYGLTWVWSSDPLGLAA 873
863 SDDGVLAYKLLVQIGSRDKPIDISQLTKQLRVADAGIINPFAFYLYLTAWVNDPVAIA 922
874 SQANFYPPPEWLHDKYDTTGE-NLRIPPAQPLEFAFPFLRLGLOKTDADFEVAIEGARA 932
923 SQANIRPHRPEVWHDKADYMPETRLRIPAAEPYEAQPPFYINGLRDTSDFEVAIEKVRV 982
933 ACAEAGQGVHAYPSGPFWEQYGLRRCFLAVCTILVCAALLLNPTWAGLI 992
983 ICNNYTSIGLSSYPNGPYFWEQYISLRHMLLSISVVLACTFLVCAVFLNPTWAGLI 1042
993 VLVAMTVLFGIMGFLGKLSAIPVVLVASVIGVEFTVHVALGELTTQGSNRLFAA 1052
1043 VVVLAMTVLFGIMGFLGKLSAIPVVLVASVIGVEFTVHVALGELTTQGSNRLFAA 1102
1053 HALEHTFAPVTDGAIISTLLGLMLAGSHDFIVRYFFAALTIVTLGLLHGLVLLPVLLS 1112
1103 LALEHMFAPVLDGAVSTLLGLMLAGSDFIVRYFFAALTIVTLGLVGLVLLPVLLS 1162

1113 ILGPPPEVI-----OMYKESPEILSPP-----APOGGGLRWGASSSLFPQSFAVTVTS-- 1159
1163 FGPCPEVSPANGLNPLTPSP--PPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGI 1220
1160 -----MTVALHPPPLPCAYIHP-APDEPPWSPAA-----TSSGNLS 1194
1221 SEELRQYEAQAGGAGHQAQVIVEATENPVFAKSTVVHPDSRHQPPLTPRQQPHLDGSL 1280
1195 SRGPG 1199
1281 ---PG 1282

RESULT 11
US-10-302-279-60
; Sequence 60, Application US/10302279
; Publication No. US20030171566A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael Carlton
; Hahn, Heidi Eve
; Wicking, Carol
; Christiansen, Jeffrey
; Zaphiropoulos, Peter G.
; Gailani, Mae R.
; Shanley, Susan Mary
; Chidambaram, Abirami
; Vorechovsky, Igor
; Holmberg-Lindstrom, Erika
TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10302,279
FILING DATE: 22-No. US20030171566A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/857,636
FILING DATE: 16-MAY-1997
APPLICATION NUMBER: US 60/017,906
FILING DATE: 17-MAY-1996
APPLICATION NUMBER: AU P00011
FILING DATE: 21-MAY-1996
APPLICATION NUMBER: AU P00363
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 60/019,765
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35, 551
REFERENCE/DOCKET NUMBER: 015280-278200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

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Db      898 NPWTAGIIVVVLMTVELFGMGLIGIKLSAVPVVIIASVGIGVEFTVHVALAFLTAI   957
QY      1045 GSRNLRAHALEHTFAPVTGAI STLGLLMLAGSHFDIVRYFFAAALTVLTLLGLHLGL 1104
Db      958 SDKNRRAVLALEHMFAVLDGAVSTLLGVLMLAGSEDFDIVRFFAVLALTILGVNGL 1017
QY      1105 VLPVLISILGPPEV----- 1120
Db      1018 VLLEVLLSFGPYPEVSPANGLNRLPTSPPPPPVVRFAMPPEGHTHSGSDSDSEYSQ 1077
QY      1121 -----IQWY-----KESPEI 1130
Db      1078 TTYSGLSEELRHVEAQOAGGPAHQVIVEATENPFVAHSTVVHPESRRHHPPNPKKOQPHL 1137
QY      1131 LS---PPAPQG-----GGU-----RWG----- 1144
Db      1138 DSGSLPEGRCQQPRDRPKRGWLPLYPXLRDAFEISTEGHSGPSNRARWGPRGARSHN 1197
QY      1145 -----ASSSLPQSFCARVTT-----SMTVAIHPPPLEGAYIHP 1176
Db      1198 PRAPTSTAMGSSVPGYCQPITTTVTSASVTVAHVHPPVPVFGGRNP 1242

RESULT 12
US-08-954-701A-4
; Sequence 4, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-701A-4

Query Match          35.6%; Score 2235; DB 8; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

QY      18 ARTAAPQLIAGSL---KAPLWLRAYFOGLLFSLGCGIQRHCQKVFLGLIAFGALALGLR 74
Db      41 AVALALELYEYNICGGTSTSWIPAWQEQVPIYCCVGCSTL----- 111

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QY 1137 Q-----GGGLRWGASSSLPOSFARVTTTMT 1161
Db 1122 KCSHPHPRXSSSSGGGKSSRTSKSAPRCPASLTIT 1160
RESULT 13
US-09-754-032-4
; Sequence 4, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fiehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-754-032-4
Query Match 35.6%; Score 2235; DB 10; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

QY 75 MAIETNLQWVEGSRVSVQELHYTKELGEEAAYTSQMLIQARQEGENILTPALGL 134
Db 101 SAQHTRVQWVQEGRLAEALKYTAQALGEADSTHQLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLOALATASKVQVSLYKGSWDLNKIKYKSGVPLIEN-GMIEWMIKLFPCVILTPDLCFW 193
Db 161 HLKVVHAATRVTHMYDIEMRLKOLCYSPIPDFEGYHHIESIDNVIPCAIITPDLCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNLDPDLEQLLEELG-----PFASLEGFRELDDKAQVG 244
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
QY 75 MAIETNLQWVEGSRVSVQELHYTKELGEEAAYTSQMLIQARQEGENILTPALGL 134
Db 101 SAQHTRVQWVQEGRLAEALKYTAQALGEADSTHQLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLOALATASKVQVSLYKGSWDLNKIKYKSGVPLIEN-GMIEWMIKLFPCVILTPDLCFW 193
Db 161 HLKVVHAATRVTHMYDIEMRLKOLCYSPIPDFEGYHHIESIDNVIPCAIITPDLCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNLDPDLEQLLEELG-----PFASLEGFRELDDKAQVG 244
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
QY 75 MAIETNLQWVEGSRVSVQELHYTKELGEEAAYTSQMLIQARQEGENILTPALGL 134
Db 101 SAQHTRVQWVQEGRLAEALKYTAQALGEADSTHQLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLOALATASKVQVSLYKGSWDLNKIKYKSGVPLIEN-GMIEWMIKLFPCVILTPDLCFW 193
Db 161 HLKVVHAATRVTHMYDIEMRLKOLCYSPIPDFEGYHHIESIDNVIPCAIITPDLCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNLDPDLEQLLEELG-----PFASLEGFRELDDKAQVG 244
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
QY 75 MAIETNLQWVEGSRVSVQELHYTKELGEEAAYTSQMLIQARQEGENILTPALGL 134
Db 101 SAQHTRVQWVQEGRLAEALKYTAQALGEADSTHQLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLOALATASKVQVSLYKGSWDLNKIKYKSGVPLIEN-GMIEWMIKLFPCVILTPDLCFW 193
Db 161 HLKVVHAATRVTHMYDIEMRLKOLCYSPIPDFEGYHHIESIDNVIPCAIITPDLCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNLDPDLEQLLEELG-----PFASLEGFRELDDKAQVG 244
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304
Db 221 EGSKLGLPDYPIYVPHLKHKLQWHLNPLEVVEVKLKFQFPLSTIEAY---MKRAGIT 277
QY 245 QAYVGRPCILHPDDLHCPSPSANHHRSQAPNTVAHELSGCHGSHKFMHWQELLGGMAR 304

Db 278 SAYMKKPCLDPTDHPCHPATAPKKSCHTIPDVAELSHGCGYFAAAAYMEWPEQLIVGGATR 337
Qy 305 DPQGLLRAEALQSTFLMSPROLYEHFRGDYQTHDIGWSEQASTVLOAWQRFVQLAQ 364
Db 338 NSTSALRKARXLQTVVQUMGERMEYKADHYKHQICWNOEKAADVADAWQRFVAAEVR 397
Qy 365 BALPE--NASSQIHAFSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRW-DCAQ 420
Db 398 KITTSAGVSSAYSFYFPTSTLNDILGKFEVSLKNILGYMFLIYVAVTILQWRDIR 457
Qy 421 SOGSVGLAGVLLVALAVASGLGCLGALGITNAATQVLPFLAIGIGVDDVFLLAHAFTE 480
Db 458 SOAGVGIAGVLLSITVAAGLGFALGIPENASSTQVPELALGLGVQDMFLTHITVE 517
Qy 481 ALPGTQERMEGECLORTGTSVLTSTNNMAAFMAALVPTPALRAFSLQAAIVVGGTFV 540
Db 518 QAGDVPEERTGLVVKSGGLSVLASCNVMAFLAAALLPAPFRVFCLOQAAILLFLNLG 577
Qy 541 AVMLVFPAILSLDRRHRCORLDVLCFF--SSPCSAQVIQLPOBLGDTGTPVGVIAHLTA 598
Db 578 SILLVFPAMISLDRRSARADLLCCLMPESP-----LPKK-----KIP----- 617
Qy 599 TVQAFTHCEASSQHVITLPPQAHVPPSPDPLSELFPSCGSTRDLGQEEETRKAAC 658
Db 618 -----ERAKTRKNDKTHRIDTTPROLDPDV-----SENVTKTC 651
Qy 659 KSLPCARWLAHAFARYOPAPILLQSHAKAIVLVLFGLLGLSLYGATLVQDGLALTDPVP 718
Db 652 LSVSLTKW-----AKNOYAFIMKPAVKVTSMLALIAVILTSVWGATKVKDGLDITVP 706
Qy 719 RGTKEHAFSLAQRYFSLYEVALVTOGGFYAHQSQRALFDLHORFSSLKAVLPPATQAP 778
Db 707 ENTDEHEFLSKQEKYFGFYNNYVATQNFYPTNQKLLYEHDFVPIPIIKNNDGGLT 766
Qy 779 RTWLHYRNWLOGIQAADFQDQWASGRITRHSY-RNGSEDGALAYKLLIQTGDAQEPDLS 837
Db 767 KFWLSUFRDWLLDQVAFDREVASGCTQBYWCKNASDEGLAYKLMVQTHVDNPDKS 826
Qy 838 QLTTR-KLVDREGLIPPELFVGMGLTVWVSSDPLGLAASQANFYPPPEWHLHDKYDITGN 896
Db 827 LIITAGHLVDKGLIINPKAFYNLSAWATNDALAYGASQGNLKPQQRWTHSPEDV---H 883
Qy 897 LRIPPAQPLEFAQFPFLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSPFLFWEQ 956
Db 884 LEIKSSPLIYTLQPFVLSGLSDTXSITKLIRSVRDLCLYEAKEGPNFSPGIPFLFWEQ 943
Qy 957 YLGLRCFILLAVCILVCTFLVCALLLNPNWTAGLIVLVLMVMTVELFGIMFLGKLSA 1016
Db 944 YLYLRTSLALACALAAAFVIAVMVLLNAAVAIVTLALATLVQLLGVALLGVKLSA 1003
Qy 1017 IPVILVASVIGVEFTVHVALGFLTTQGSNRLRAHALEHTAPVTDGAI STLGLLML 1076
Db 1004 MEAVLLVLAIGRVHTVHLCGLFVTSIGCKRRRASLALESVAPVVGALAAALASML 1063
Qy 1077 AGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAP 1136
Db 1064 AASECGFARFLRLLDIVFLGLIDGLFFPILVLSILGPAEVRPI--EHPRLSTSP 1121
Qy 1137 Q-----GGGRWAGASSLPQSFAKVTTSMT 1161
Db 1122 KCSPIHPRKSSSSGGGKSSRTSKSAPRPCAPSLTIT 1160

RESULT 14

US-10-421-446-4
; Sequence 4, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421.446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724.631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656.055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540.406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-421-446-4

Query Match 35.6%; Score 2235; DB 14; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.5e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;
Qy 18 ARTAAPQIILAGSL---KAPLWRAFYQGLLFLSGCGIQRHCGKVLFLGLAFGALALGLR 74
Db 41 AALALSELEKNEGRTSLIRAWLQEQFLILGCFQGDAGKVLFAVLVLTFCVGLK 100
Qy 75 MAIETNLEQLWVEGSRVSOELHYTHKEKLGEAAVTSQMLIQARQEGENILTPALGL 134
Db 101 SAQIHTRPDQLWVQEGRLAEALKYTAQALGADSTHQLVIQAKDPDVSLLHPGALLE 160
Qy 135 HLQAAALTSKQVSVLSYKSGMDLNLKCYKSGVPLIEN-GMIEMWIEKLPFCVILTPDCCFW 193
Db 161 HLKVVHAAATVTHMDIENRDLKDCYSPISDFEGYHHIESIIDNVICAITPLDCCFW 220
Qy 194 EGAKLQGGG--AYLPQ-RPDIQNTNLDLPQLLEELG-----PFASLEGFRELDKAQVG 244
Db 221 EGSKLLGPDYPIYVPHLKHKLQWTHLNPLEVVEVKLKFQFPLSTIAY---MKRAGIT 277
Qy 245 QAYVGRPCLPDLDLHCPSPAPNHHSRQAPNVAHEISGGCHGFSHKPMHWEELLGGMAR 304
Db 278 SAYMKKPCLDPTDHPCHPATAPKKSCHTIPDVAELSHGCGYFAAAAYMEWPEQLIVGGATR 337
Qy 305 DPQGLLRAEALQSTFLMSPROLYEHFRGDYQTHDIGWSEQASTVLOAWQRFVQLAQ 364
Db 338 NSTSALRKARXLQTVVQUMGERMEYKADHYKHQICWNOEKAADVADAWQRFVAAEVR 397
Qy 365 BALPE--NASSQIHAFSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRW-DCAQ 420
Db 398 KITTSAGVSSAYSFYFPTSTLNDILGKFEVSLKNILGYMFLIYVAVTILQWRDIR 457
Qy 421 SOGSVGLAGVLLVALAVASGLGCLGALGITNAATQVLPFLAIGIGVDDVFLLAHAFTE 480

Db	458	SOAGVGIAGVLLSITVAAGLGCALGIPFNASSITQIVFFLALGVQDMFLTTYVE	517
Qy	481	ALPGTQLQRMGECLORTGTSVLTISINNAAFMAALVPIPALRAFSIQAAIIVGCTFV	540
Db	518	OAGDVPREERTGLVKXSGSLVSLASUCNMAFLAAALPPIPAFVFCQAALLFLNLG	577
Qy	541	AVMLVFPAILSLDLRRHQRDLVLCF--SSPCSAQVITQILPQELGDGTVPVGIHLTA	598
Db	578	SILLVFPAMISLDLRRRSARADLLCLMPESP-----LPKK-----KIP-----	617
Qy	599	TVOAFTHCASSQHVVTILPQAHVPPPSDPLGSELSPGGSTRDLGQEEETROKAA	658
Db	618	-----ERAKTRKNDKTHRIDTTRQPLDPDV-----SENVTTC	651
Qy	659	KSLPCARWNLAHFARYQFAPLLIQSHAKAIVLVLFGALLGLSYGATLVODGLALTDVVP	718
Db	652	LSVSLTKW-----AKQYAPFIMRPVAKVTSMLALIAVILTSVWGATKVKDGLDITIVP	706
Qy	719	RGTEHAFISAQURYSLYEVALVTQGGFYAHSQRALFDLHORFSSLKAVLPPATQAP	778
Db	707	ENTDEHEFLSRQKTFGFVNMVAVTOGNFEYPTNOKLLYEHQFVRIPNIIKNDNGGLT	766
Qy	779	RTWLHYRYRWLQIOAAFDQDWSAGRTIRHSY--RNGSEDCALAYKLLIOTGDAQEPDLS	837
Db	767	KFWLSFRDWLLDLQVAFDKEVASGCITQBYWCKNADSEGLIAYKLMVQIGHVDNPDKS	826
Qy	838	QLTT--RKLVDREGILPELFYMGITVMVSSDPLGLAASQANFYPPPEWLHXYDTTGEN	896
Db	827	LITAGHVLVDKGLIINPKAFYVLSAWATNDALAYGASQGNLKPQOPQORWIHSPEDV--H	883
Qy	897	LRIPPAQLEFAQFPFLIRGLQKTADVEAIEGARAAACAGQAGVHAYPSGSPFLFEWQ	956
Db	884	LEIKSSPLTYITQLPFFYLSGLSDTSIKTLIRSDTCLYEAKEGLENFSPGIPFLFEWQ	943
Qy	957	YLGRRCLFAVCLILVCTFLVACALLILNPNWAGLIVLVLAMMTVELFGIMGFIKLSA	1016
Db	944	YLRLTSLALACALAAVFIANVLLNNAVAVLVTLATVILQLLGVNALLGVKLSA	1003
Qy	1017	IPVVLVAVSGIGVEFTHVALGELTTQGSRNLRRAHLEHTFAPVTDGAISTLLGLML	1076
Db	1004	MPAVLLVLAIGRVHFTVHLCGLGVTISIGCKRRRASLALESVLAPVVGALAAALASML	1063
Qy	1077	AGSHFDIVRYFFAALVTLLGLLHGLVLLPVLLSILGPPPEVIQMKSPETLSPAP	1136
Db	1064	AASECGFVARLFLRLLDIVFLGLLDGLLFFPIVLISILGPAAEVRPT--EHPERLSTESP	1121
Qy	1137	Q-----GGGLRWGASSLSLQSFARVTTSMT	1161
Db	1122	KSPIHPRKSSSSGGGDKSRTSKSAPRPCAPSLTIT	1160
RESULT 15			
US-09-898-533-3			
; Sequence 3, Application US/09898533			
; Patent No. US20020106656A1			
; GENERAL INFORMATION:			
; APPLICANT: Gemmill, Robert M.			
; APPLICANT: Drabkin, Harry A.			
; TITLE OF INVENTION: TRC8. A GENE RELATED TO THE HEDGEHOG RECEPTOR,			
; TITLE OF INVENTION: PATCHED			
; FILE REFERENCE: 93445-00004			
; CURRENT APPLICATION NUMBER: US/09/898,533			
; CURRENT FILING DATE: 2001-07-02			
; PRIOR APPLICATION NUMBER: US/09/268,140			
; PRIOR FILING DATE: 2000-03-12			
; NUMBER OF SEQ ID NOS: 46			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 1286			
; TYPE: PRT			
; ORGANISM: Drosophila melanogaster			
US-09-898-533-3			

Query Match	31.8%	Score 1992;	DB 9;	Length 1286;
Best Local Similarity	37.4%	Pred. No. 8e-155;		
Matches 429;	Conservative 226;	Mismatches 411;	Indels 80;	Gaps 19;
Qy	18	ARTAAPQILAGSU---KAPLWLRAYFQGLLFSIGCGIQRHCGKVLFLGLAFGALLGLR	74	
Db	34	AQVALDQIDKGARGSRRTAIIYLSRFQSHLETLLGSSVQKHAGKVLFAVILVSTFCVGLK	93	
Qy	75	MAIETNLQWLVEGSRVSQELHYHTEKELGEEAATSQMLIOTARQEGENILTPALGL	134	
Db	94	SAQIHSKVHQLMIQEGRLAEALAYTKTIGEDESATHQLLTQTTTHDPNASVHLHPQALLA	153	
Qy	135	HLQAAALTASKVQVSLYKSKWDLNKKICYKSGVPLIEN-GMIEWIEKLPFCVILTPLDCFW	193	
Db	154	HUEVLVKAIVAKVHLYDYDTWGLRDMCMNPSTPSFEGIYYIEQILRHILIPCSITPLDCFW	213	
Qy	194	EKAQLOG--GSAYLPG-RPDIQWTNLDP-----EQLLEELGPFASLEGFRELIDKAQ	242	
Db	214	EGSOLLGPESAVVPIGLNQRLTLTTLNPASVMQYMKQKSEEEKISF-DFETVEQYMKRAA	272	
Qy	243	VGQAYVGRPCLLHPDDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFHWQBELLLGGM	302	
Db	273	IGSGYMEKPCNPLNCPNCPDTAPNKNSTQPPDVGAILSGGCGYGAAKHMHWPBELIVGGR	332	
Qy	303	ARDPQCELLRAEALQSTFLILMSPROLYEHPRGDYQTHDICWSBEOASTVLAQWRRFVQL	362	
Db	333	KNRSGHLRKAQALQSVVQVLMTEKEMVDQMDNKKVHHLGWTQEKAEVLNMQWNRFSRE	392	
Qy	363	AQALPENNA----SQOIHAFSSTLDDILHAFSEVSAARVVGGYLLMLAYCVTMLRW-D	417	
Db	393	VEQLLRKQSRITATNYDIYVSSAALDDILAKFSPSALSIVIGVAVTVLAFCTLLWRD	452	
Qy	418	CAOSQSVGLAVLLVALVAVSGILGICALLIGITFNAAATTOVLPALAGIGVDDVFLAHA	477	
Db	453	PVRGQSSVGVAGVLLMCFSTAAGLIGLSALLIGIVFNAASTOVVPLAUGLVHDFMLTAA	512	
Qy	478	FTALPPTQERMGECLORTGTSVLTISINNAAFMAALVPIPALRAFSLQAAIIVGVC	537	
Db	513	YAE-----SNREQTLLIKVGSILPSACSTAGSFFAAAFIPVPALKVCLQAAIIVCS	568	
Qy	538	TFVAVMLVFPAILSLDLRRHQRDLVLCFSSPCSAQ---VTQILPQELGDGTVPVGVIA	594	
Db	569	NLAALVFPAMISLDLRRRTAGRADIFCCCFPWKEQPKVAPVPLPNNNG-----	621	
Qy	595	HLTATVQAFTHCEASSQHVVTILPQAHVPPPSDPLGSELSPGGSTRDLGQEEETRQ	654	
Db	622	-----RGARHPKSCNNRVPL-----PAQNPLEQRADIPGSSHSI-----	657	
Qy	655	KAACKSLPCARWNLAHFARYQFAPLLIQSHAKAIVLVLFGALLGLSYGATLVODGLALT	714	
Db	658	-----ASFSLATFAFOHYTFFLMRSVWVKFTVMGFLAALLISSLYASTRLQOGLDII	708	
Qy	715	DVPRGTKEHAFISAQURYSLYEVALVTQGGFYAHSQRALFDLHORFSSLKAVLPPPA	774	
Db	709	DLVPKDSNEHKFLDAQTRLFGFYSMAVATQGNFEYPTQQQLLRDRYHDSFVRVPHVKNDN	768	
Qy	775	TOAPRTWLHYRYRWLQIOAAFDQDWSAGRTIRHS--YRNGSEDCALAYKLLIOTGDAQEP	833	
Db	769	GGLPDFWLLLFSEWLGNLQKIFDEYDRGRUTKECWFFNASSDAILAYKLLIOTGHDVNP	828	
Qy	834	LDFSQLTTRKLVDRREGILPELFYMGITVMVSSDPLGLAASQANFYPPPEWLH--DKYD	891	
Db	829	VDELVLNLRVNSDGIINQAFYNLSAWATNDVFAYGASQGLYEPQRYFHPQNEYD	888	
Qy	892	TTGENLRIPPAQLEFAQFPFLIRGLQKTADVEAIEGARAAACAGQAGVHAYPSGSPF	951	
Db	889	-----LKIPKSLPLVYAQMPPFYLHGLTDTSQIKTLIGHIRDSLVKYEGFGLPNTFSGI	943	
Qy	952	LFWEQYLGRLRCF--LLAVCILLVCTFLVACALLILNPNWAGLIVLVLAMMTVELFGIMGFL	1010	
Db	944	IFWQSYMTLRSSLAMILACVLLAALVLV-SLLLLSVNAAVLVLSVLASLAQIFGAWTIL	1002	

Qy 1011 GIKLSAIPWILVASVGIGVEFTVHVALGFLTTGSRNLRRAHALEHTFAPVTDGAISTL 1070
Db 1003 GIKLSAIPAVILILSVGNMCLCFNVLISLGFMTSVGNRRVQLSMQMSLGLPETHGMLTSG 1062
Qy 1071 LGLMLAGSHPDFIVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEI 1130
Db 1063 VAVFMLSTSPPEFVIRHFCWLLLVLCVGACNSLLVFPILLSMVGPEAEVPL--EHPDR 1120
Qy 1131 LSPEAP 1136
Db 1121 ISTPSP 1126

Search completed: November 22, 2004, 08:08:02
Job time : 335 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 07:45:05 ; Search time 24 Seconds

(without alignments)
3324.190 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPLRELPPSYTPPART.....SPATSSGNLSRGPGPATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6272	100.0	1203	3	US-09-293-505-2
2	6272	100.0	1203	4	US-09-060-939A-2
3	6248	99.6	1203	3	US-09-207-857-2
4	6248	99.6	1203	4	US-09-207-857-2
5	5599	89.3	1182	3	US-09-309-280A-2
6	5599	89.3	1182	4	US-09-309-280A-2
7	3348	53.4	1447	2	US-09-060-939A-7
8	3348	53.4	1447	2	US-08-540-406-19
9	3348	53.4	1447	3	US-08-656-055-19
10	3348	53.4	1447	3	US-08-954-668-19
11	3348	53.4	1447	3	US-09-268-140-5
12	3348	53.4	1447	4	US-09-918-658-19
13	3348	53.4	1447	4	US-09-724-631-19
14	3348	53.4	1447	4	US-08-954-701A-19
15	3337	53.2	1434	5	PCT-US95-13233-19
16	3337	53.2	1434	3	US-08-540-406-10
17	3337	53.2	1434	3	US-08-656-055-10
18	3337	53.2	1434	3	US-08-954-668-10
19	3337	53.2	1434	4	US-08-918-658-10
20	3337	53.2	1434	4	US-09-724-631-10
21	3337	53.2	1434	5	US-08-954-701A-10
22	3048	48.6	1296	4	PCT-US95-13233-10
23	2627	41.9	529	3	US-08-857-636-60
24	2235	35.6	1311	2	US-09-500-063-2
25	2235	35.6	1311	3	US-08-540-406-4
26	2235	35.6	1311	3	US-08-656-055-4
27	2235	35.6	1311	4	US-08-954-668-4

28	2235	35.6	1311	4	US-09-724-631-4	Sequence 4, Appli
29	2235	35.6	1311	4	US-08-954-701A-4	Sequence 4, Appli
30	2235	35.6	1311	5	PCT-US95-13233-4	Sequence 4, Appli
31	1992	31.8	1286	3	US-09-268-140-3	Sequence 3, Appli
32	1961.5	31.3	1299	3	US-08-460-900C-62	Sequence 62, Appli
33	1961.5	31.3	1299	3	US-08-674-509B-48	Sequence 48, Appli
34	1961.5	31.3	1299	3	US-08-954-698-48	Sequence 48, Appli
35	1961.5	31.3	1299	4	US-09-639-695-62	Sequence 62, Appli
36	1961.5	31.3	1299	4	US-09-448-188-48	Sequence 48, Appli
37	1961.5	31.3	1299	4	US-08-954-128-48	Sequence 48, Appli
38	1961.5	31.3	1299	4	US-08-954-740-48	Sequence 48, Appli
39	1936.5	30.9	1285	2	US-08-540-406-6	Sequence 6, Appli
40	1936.5	30.9	1285	3	US-08-954-668-6	Sequence 6, Appli
41	1936.5	30.9	1285	3	US-08-918-658-6	Sequence 6, Appli
42	1936.5	30.9	1285	4	US-09-724-631-6	Sequence 6, Appli
43	1936.5	30.9	1285	4	US-08-954-701A-6	Sequence 6, Appli
44	1936.5	30.9	1285	4	US-08-954-701A-6	Sequence 6, Appli
45	1936.5	30.9	1285	5	PCT-US95-13233-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-293-505-2
; Sequence 2, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE OF INVENTION: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-505-2

Query Match 100.0%; Score 6272; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTRSPPLRELPPSYTPPARTAQTILAGSLKAPLMRAYFOGLFSLGCGIQHCGKVL	60
DB	1	MTRSPPLRELPPSYTPPARTAQTILAGSLKAPLMRAYFOGLFSLGCGIQHCGKVL	60
QY	61	LGLLAFGALALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSOMLIQTAR	120
DB	61	LGLLAFGALALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSOMLIQTAR	120
QY	121	QGENILTPDALGLHQAALTAASKVQVSLYKGSWDINKTCYKSGVPLIENGMIENIEKL	180
DB	121	QGENILTPDALGLHQAALTAASKVQVSLYKGSWDINKTCYKSGVPLIENGMIENIEKL	180
QY	181	PFVILTPDLCFMEGAKQGGSAVLPGRPDITQNTLDPOLLEELGPPASLEGFRELDDK	240
DB	181	PFVILTPDLCFMEGAKQGGSAVLPGRPDITQNTLDPOLLEELGPPASLEGFRELDDK	240
QY	241	AQVGQAYVGRPCHLHPDDLLHCPSPAPNHHSRQAPNVAHELSGGCHGFSHKFMHQBELLLG	300
DB	241	AQVGQAYVGRPCHLHPDDLLHCPSPAPNHHSRQAPNVAHELSGGCHGFSHKFMHQBELLLG	300
QY	301	GMARDPQGLLRARAEALQSTFLMSPRQYEHFRGDYQTHDIGWSEEQASTVLQAWQRFFV	360
DB	301	GMARDPQGLLRARAEALQSTFLMSPRQYEHFRGDYQTHDIGWSEEQASTVLQAWQRFFV	360
QY	361	QLAQALPENASQTHAFSSITLDDILHAFSEVSARVVGVLMLAYACTVTLRWDCAQ	420

361 QLAQALPENASQOIHAFSTTLLDDILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLAIGTVDVDFLLAHAFTE 480
421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLAIGTVDVDFLLAHAFTE 480
481 ALPGTFLQRMGECLOQTGTSVLTINNMAAFMAALVPIPALRAFSQAALVVGCTFV 540
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541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVITQILPQELGDTVPVGHIAHLTATV 600
541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVITQILPQELGDTVPVGHIAHLTATV 600
601 QAFTHCEASSQHVVTILPQAHVLPVPPSPDLGSELSPGSGSTRDILGQEBETROKAAKS 660
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661 LPCARWNLAFHAFYQFAPILLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVRG 720
661 LPCARWNLAFHAFYQFAPILLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVRG 720
721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHSQRALEFHLHQRFSKAVLPFPATQAPRT 780
721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHSQRALEFHLHQRFSKAVLPFPATQAPRT 780
781 WLHYRNWLGQIQAAFPQDQWASGRITRHSYRNSEDCALAYKLLIQTGDAQEPLDPSOLT 840
781 WLHYRNWLGQIQAAFPQDQWASGRITRHSYRNSEDCALAYKLLIQTGDAQEPLDPSOLT 840
841 TRKLVDRGLIPPELFYMGITVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
841 TRKLVDRGLIPPELFYMGITVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
901 PAQPLEFAQPFLLRGILQKTADFVEALEGARAACAEAGQVHAYPSGSPFLFWEQYGLG 960
901 PAQPLEFAQPFLLRGILQKTADFVEALEGARAACAEAGQVHAYPSGSPFLFWEQYGLG 960
961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLAMTVELFNGFGLIKLSAIPV 1020
961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLAMTVELFNGFGLIKLSAIPV 1020
1021 ILVASVIGVEFTHVAGLFTTQGSNRLRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1021 ILVASVIGVEFTHVAGLFTTQGSNRLRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
1141 LRWGASSLPQSFAFVTTMTVAIHPPPLPGAYIHAPDEPPSPATSSGNLSSRGPGP 1200
1141 LRWGASSLPQSFAFVTTMTVAIHPPPLPGAYIHAPDEPPSPATSSGNLSSRGPGP 1200
1201 ATG 1203
1201 ATG 1203

RESULT 2

US-09-060-939A-2

; Sequence 2, Application US/09060939A

; Patent No. 6709838

; GENERAL INFORMATION:

; APPLICANT: Frederic de Sauvage, David A. Carpenter

; TITLE OF INVENTION: Patched-2

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1203 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-060-939A-2

Query Match 100.0%; Score 6272; DB 4; Length 1203;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRSPLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGCGIQRHCKVLF 60
Db 1 MTRSPLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGCGIQRHCKVLF 60
Qy 61 LGLIAGCALGALGMAIETNLEOLAVEGSRVSOELHYTKELGEEAATTSQMLIGTAR 120
Db 61 LGLIAGCALGALGMAIETNLEOLAVEGSRVSOELHYTKELGEEAATTSQMLIGTAR 120
Qy 121 QEGENTILTEALGLHLQAALTASKVQVSLYKGSWDLNKKICYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENTILTEALGLHLQAALTASKVQVSLYKGSWDLNKKICYKSGVPLIENGMIEMIEKL 180
Qy 181 FPCVILTDLPCFWEKAKLQGSAYLPGRPDIQWNTLDPQLLEELGFPASLEGFRELDDK 240
Db 181 FPCVILTDLPCFWEKAKLQGSAYLPGRPDIQWNTLDPQLLEELGFPASLEGFRELDDK 240
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Db 241 AQVQAYVGPCLHPDOLHCPSPAPNHHSQAPNVAHELSCGCHGSHKFMHWQEBELLG 300
Qy 301 GWARDPOGELLRAELAQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GWARDPOGELLRAELAQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Qy 361 QLAQALPENASQOIHAFSSTTLLDDILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Db 361 QLAQALPENASQOIHAFSSTTLLDDILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Qy 421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLAIGTVDVDFLLAHAFTE 480
Db 421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLAIGTVDVDFLLAHAFTE 480
Qy 481 ALPGTFLQRMGECLOQTGTSVLTINNMAAFMAALVPIPALRAFSQAALVVGCTFV 540
Db 481 ALPGTFLQRMGECLOQTGTSVLTINNMAAFMAALVPIPALRAFSQAALVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVITQILPQELGDTVPVGHIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVITQILPQELGDTVPVGHIAHLTATV 600
Qy 601 QAFTHCEASSQHVVTILPQAHVLPVPPSPDLGSELSPGSGSTRDILGQEBETROKAAKS 660
Db 601 QAFTHCEASSQHVVTILPQAHVLPVPPSPDLGSELSPGSGSTRDILGQEBETROKAAKS 660
Qy 661 LPCARWNLAFHAFYQFAPILLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVRG 720

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Db 661 LPCARNLAHFAHQYQAPLILQSHAKAIVLVFGALLGLSLYGATLVQDGLATDVVPRG 720
Qy 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
Db 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
Qy 781 WLHYRNWLOGIOAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQEPDLSOLT 840
Db 781 WLHYRNWLOGIOAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQEPDLSOLT 840
Qy 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Qy 901 PAQPLEFAQPFLLRGLQKTADFVEAIEGARARACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
Db 901 PAQPLEFAQPFLLRGLQKTADFVEAIEGARARACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
Qy 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
Qy 1021 ILVASVGIGVEFTVHVVALGFLTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
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Db 1081 FDFIVRYFFAALTIVLLGLLHGLVLLPVLLSILGPPPEVIQMYKSPETILSPAPQGG 1140
Qy 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPPWSPAATSSGNLSRSGPG 1200
Db 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPPWSPAATSSGNLSRSGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
US-09-207-857-2
; Sequence 2, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: ONV-05001
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: human
US-09-207-857-2

Query Match 99.6%; Score 6248; DB 3; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MTRSPPLRELPPSYTPPARTAQQIILAGSLKAPLWLRAYFQGLLFSIGCGIQRHCKVLF 60
Db 1 MTRSPPLRELPPSYTPPARTAQQIILAGSLKAPLWLRAYFQGLLFSIGCGIQRHCKVLF 60
Qy 61 LGLLAFGALALGRMAIETNLBQWVEGSRVSRVQELHYTKELGREAAVTSQMLIQAR 120
Db 61 LGLLAFGALALGRMAIETNLBQWVEGSRVSRVQELHYTKELGREAAVTSQMLIQAR 120
Qy 121 QEGENILTPEALGHLQAALTASKVQVSLYKSWDLNKLICKYKSGVPLIENGMIERIEKL 180
Db 121 QEGENILTPEALGHLQAALTASKVQVSLYKSWDLNKLICKYKSGVPLIENGMIERIEKL 180
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Db 181 FPCVILTPDLCFWEKAKLQGGSAIYLPGRPDIOQNTNLDPEQLBELGPFASLEGFRELLDK 240
Qy 241 AOYGOVAVGRPCLLHPDOLHCPSPAPNHHSRQAQANVAHELSGGCHGSHKPMHWOEBELLG 300
Db 241 AOYGOVAVGRPCLLHPDOLHCPSPAPNHHSRQAQANVAHELSGGCHGSHKPMHWOEBELLG 300
Qy 301 GMARDQGEILLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEQAQSVLQAWORRFV 360
Db 301 GMARDQGEILLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEQAQSVLQAWORRFV 360
Qy 361 QLAQEAALPENASQOIIHAFSSTLLDDILHAFSEVSAARVVGYYLLMLIAYACVTMLRWDCAQ 420
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Db 421 SOGSVGLAGVLLVALAVASGLGICALLGITFNAAATTOVLPPALGIGVDDVFLLAHAFTE 480
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Db 481 ALPGTFLQERMGECLOQTGTSVVLTSINNMAAFIAMAALVPIPALRAFSLQAAIIVVGCTFV 540
Qy 541 AVMLVPPAILSLDLRRRHQRDLVLCFSSPCSAQVIQILPQELGDTVPVGAHIAHTATV 600
Db 541 AVMLVPPAIFSLDLRRRHQRDLVLCFSSPCSAQVIQILPQELGDTVPVGAHIAHTATV 600
Qy 601 QAFTHCASQOHVVITLPPQAHVLPSPDPLGSELSFGSGSTEDLLGOEBETKQKACKS 660
Db 601 QAFTHCASQOHVVITLPPQAHVLPSPDPLGSELSFGSGSTEDLLGOEBETKQKACKS 660
Qy 661 LPCARNLAHFAHQYQAPLILQSHAKAIVLVFGALLGLSLYGATLVQDGLATDVVPRG 720
Db 661 LPCARNLAHFAHQYQAPLILQSHAKAIVLVFGALLGLSLYGATLVQDGLATDVVPRG 720
Qy 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
Db 721 TKEHAFSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSLKAVLPPATQAPRT 780
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Qy 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDITTCENLRIP 900
Qy 901 PAQPLEFAQPFLLRGLQKTADFVEAIEGARARACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
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Qy 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
Db 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
Qy 1021 ILVASVGIGVEFTVHVVALGFLTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVGIGVEFTVHVVALGFLTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALTIVLLGLLHGLVLLPVLLSILGPPPEVIQMYKSPETILSPAPQGG 1140
Db 1081 FDFIVRYFFAALTIVLLGLLHGLVLLPVLLSILGPPPEVIQMYKSPETILSPAPQGG 1140
Qy 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPPWSPAATSSGNLSRSGPG 1200
Db 1141 LRWGASSLPOSFARVTTSMVAIHPPPLPGAYIHPADPPWSPAATSSGNLSRSGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203
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RESULT 4
US-09-909-280A-2
; Sequence 2, Application US/0990280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2

Query Match      99.6%; Score 6248; DB 4; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MTRSPPLRELPPSYTTPARTAAQIILAGSLKAPILMLRAYFQGLLFSLGGCIQRHCGKVL 60
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DB 61 LGLAFGALALGRMAIETNLEQWVEVGSRSVQELHYTKELGEBAAVTSQMLIQAT 120
QY 121 QEGENILTPALGLHQAALTASKVQVSLYKSKMDLNKI CYKSGVPLIENGMIETWLEKL 180
DB 121 QEGENILTPALGLHQAALTASKVQVSLYKSKMDLNKI CYKSGVPLIENGMIETWLEKL 180
QY 181 FPCVILTLPDCFWEGAKLQGSAYLPGRPDIQWNTLDPQLLELPGFASLEGFRELLDK 240
DB 181 FPCVILTLPDCFWEGAKLQGSAYLPGRPDIQWNTLDPQLLELPGFASLEGFRELLDK 240
QY 241 AQGVQAYVGRPCLPDDLHCPGAPNHHSRQAPNVAHELSCGCHGFSKFMHWQBEILLG 300
DB 241 AQGVQAYVGRPCLPDDLHCPGAPNHHSRQAPNVAHELSCGCHGFSKFMHWQBEILLG 300
QY 301 GMARDPOGELLRAEALQSTELLMSPROLYEHFRGDYQTHDIGNSEEOASTVLQAWORRFV 360
DB 301 GMARDPOGELLRAEALQSTELLMSPROLYEHFRGDYQTHDIGNSEEOASTVLQAWORRFV 360
QY 361 QLAQALPENASQIILHAFSTTLLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWDCAQ 420
DB 361 QLAQALPENASQIILHAFSTTLLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLIGLCALLGITFNATTOVLPFLAIGIGVDVFLIAHAFTE 480
DB 421 SQGSVGLAGVLLVALAVASGLIGLCALLGITFNATTOVLPFLAIGIGVDVFLIAHAFTE 480
QY 481 ALPGTLPQERMGECLOQTGTSVVLTSINNAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
DB 481 ALPGTLPQERMGECLOQTGTSVVLTSINNAAFLMAALVPIPALRAFSLQAAIVVGCTFV 540
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QY 661 LPCARNLHAHFARYQFAPILLQSHAKAIVLVLFQALLGLSLYGATLVQDGLALTDVVVPRG 720
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QY 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRFSSSKAVLPPPATQAPRT 780
DB 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRFSSSKAVLPPPATQAPRT 780
QY 781 WLHYRNWLOGIOAAFDQDQWASGRITRHSYRNSEDEGALAYKLLIQTGDAQEPLDFSQLT 840
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QY 841 TRKLVDRGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDVTGGENLRIP 900
DB 841 TRKLVDRGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDVTGGENLRIP 900
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QY 961 RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
DB 961 RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPV 1020
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DB 1021 ILVASVIGVEFVHVALGFLTTQGRNLRRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
QY 1081 FDFIVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
DB 1081 FDFIVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
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DB 1141 LRWGASSLSPQSFARVTTSMVAIHPPPLPGAVIHAPDEPPNPSAATSSGNLSSRGPG 1200
QY 1201 ATG 1203
DB 1201 ATG 1203

RESULT 5
US-09-293-505-7
; Sequence 7, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-293-505-7

Query Match      89.3%; Score 5599; DB 3; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPPSYTTPARTAAQIILAGSLKAPILMLRAYFQGLLFSLGGCIQRHCGKVL 60
DB 1 MTRSPPLRELPPSYTTPARTAAQIILAGSLKAPILMLRAYFQGLLFSLGGCIQRHCGKVL 60
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661 LLCAHWTLAHFARYQAPLLOLQSHAKAIVLVLFGALLGLSLYCATLVQDGLATDVVPRG 720
721 TKEHAFSLAQLRYFSLEYVALVTQGGFDYAHSQALFDLHQRFSSSLKAVLPPPATQAPRT 780
721 TKEHAFSLAQLRYFSLEYVALVTQGGFDYAHSQALFDLHQRFSSSLKAVLPPPATQAPRT 780
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781 WLHYRNWLGIOQAADFQDOWASGRITRHSYRNGSEGCALAYKLLIQTGDAQBPDPFSOLT 840
841 TRKLVDRGLIPPELFWGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
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1021 ILVASGIGVEFTVHVVALFLLTQGSNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
1021 ILVASGIGVEFTVHVVALFLLTQGSNLRRAHALEHTFAPVTDGAI STLGLMLAGSH 1080
1081 FDPVIRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
1081 FDPVIRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPELSPAPQGGG 1140
1141 LRWGASSLUPQSFAVTTMTVAIHPPPLPGAYIHPADPEP 1181
1141 LRWDRPPTLPQSFAVTTMTVAIHPPPLPGAYIHPADPEP 1181

RESULT 6

US-09-060-939A-7
; Sequence 7, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Minipac (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-060-939A-7

Query Match 89.3%; Score 5599; DB 4; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPPLRLPSPSYTPPARTAPOILLAGSLKAPLWLRAYFOGLLSLGGIQRHCGKVL 60
Db 1 MVRPLSLGSLPSPSYTPPARTAPOILLAGSLKAPLWLRAYFOGLLSLGGIQRHCGKVL 60
QY 61 LGLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAVTSQMLIQTAH 120
Db 61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSRSVQELHYTKELGEEAAVTSQMLIQTAH 120
QY 121 QEGENILTPALGLHLQAALTASKVQVSLYKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENVLTPEALDLHLQAALTASKVQVSLYKSWDLNKKIYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
Db 181 FPCVILTPDLCFWEKAGLQGSAYLPGRDPIQWNTLDPQLLEELGPFASLEGFRELDDK 240
QY 241 AQVGQAYVGRPCPLHPDCLHCPSPAPNHRHQAPNVAHELGGCHGSHKFMHMQEELLG 300
Db 241 AQVGQAYVGRPCPLHPDCLHCPSPAPNHRHQAPNVAHELGGCHGSHKFMHMQEELLG 300
QY 301 GWARDPQGLLRALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRRFV 360
Db 301 GTARDLQGLLRALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRRFV 360
QY 361 QLAQEAALPENASQOIHAFFSTLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQEAALPENASQOIHAFFSTLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWDCAQ 420
QY 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAATQVLPFLALGIGVDDIFLLAHAFTE 480
Db 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAATQVLPFLALGIGVDDIFLLAHAFTE 480

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QY 481 ALPGTFLQRMGECLOQTCTSVVLTSINMAAFIPALRAFSLOAAIVVGCTFV 540
Db 481 APDPTLPERMGCLRTSTGTSVLTSSNNVAFMAALVPIPALRAFSLOAAIVVGCTFV 540
QY 541 AVMLVPAIISLDLRRHRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVPGIAHITATV 600
Db 541 AVMLVPAIISLDLRRHRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVPGIAHITATV 600
QY 601 QATHECASSQHVVTILPPOAHILVPPSDPLGSELPSPGGSTRDLGQEBETKQKAACKS 660
Db 601 QATHECASSQHVVTILPPOAHILVPPSDPLGSELPSPGGSTRDLGQEBETKQKAACKS 660
QY 661 LPCARNLAFHAFYQAPLILQSHAKAIVLFCALLGLSLYCATIVODGLATDVVPRG 720
Db 661 LLCAHMTLAFHAFYQAPLILQSHAKAIVLFCALLGLSLYCATIVODGLATDVVPRG 720
QY 721 TKEHAFLSAQRYFSLYEVALVTQGGPDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
Db 721 TKEHAFLSAQRYFSLYEVALVTQGGPDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
QY 781 WLHYRNWLOGIOAAFDQDQWASGRITHTSYRNGSEDCALAYKLLIQTGDAQEBLDFSOLT 840
Db 781 WLHYRNWLOGIOAAFDQDQWASGRITHTSYRNGSEDCALAYKLLIQTGDAQEBLDFSOLT 840
QY 841 TRKLVDREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQPFLLRGLQKTADFVEALEGARAACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
Db 901 AAQPLEFAQPFLLRGLQKTADFVEALEGARAACAEAGQAGVHAYPSGSPFLFWEQYVGL 960
QY 961 RRCPFLAVCTLLVCTFLVCAALLLNPNWTAGLIVLVLAMTVELFGMGFGLIKLSAIPV 1020
Db 961 RRCPFLAVCTLLVCTFLVCAALLLNPNWTAGLIVLVLAMTVELFGMGFGLIKLSAIPV 1020
QY 1021 ILVASGIGVEFTVHVALGTLTQGSNLRRAAHLEHTFAPVTDGALSTLGLMLAGSH 1080
Db 1021 ILVASGIGVEFTVHVALGTLTQGSNLRRAAHLEHTFAPVTDGALSTLGLMLAGSH 1080
QY 1081 FDIIVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQYKESPEILSPAPQGG 1140
Db 1081 FDIIVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQYKESPEILSPAPQGG 1140
QY 1141 LRWGASSLPQSARVTTSTMTAIIHPPPLPGAVIHPADPEP 1181
Db 1141 LRWDREPTLPQSARVTTSTMTAIIHPPPLPGAVIHPADPEP 1181

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RESULT 7

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US-08-540-406-19
; Sequence 19, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-540-406-19

```

Query Match 53.4%; Score 3348; DB 2; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.7e-314; Indels 186; Gaps 18;

Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

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QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFLSLCGCIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAFALQISKGKATGRKAPLWLRKAFQRLFLKLCYIQKNGKELVWGLLIFGA 111
QY 69 LAIGLRLMAIETWELQIWEVGRVSRVQELHYTKEKLGEEAAYTSQMLIQARQENILT 128
Db 112 FAVGLKAANLETVVEELWVEVGRVSRVRELNYTRQKIGEEAMPNQLMIQTPKEEGANVLT 171
QY 129 FEALGHLOALATASKVQVSLYCKSKDLNKKICVKSVPVLENGMIEMWIKLPCPVLTLP 188
Db 172 TEALLQHLDSALQASRVHVYVYNNRQWKLEHLCKVKSGLITETGYNQOIIBYLPCLITP 231
QY 189 LDCFWEGAKIQGGSAYLPGRPDIQWNLDPQELLEELGPF-ASLEGFRELLDKAQVQAY 247
Db 232 LDCFWEGAKIQSGTAVLLGKPLRWTFDPLFLEELKKNYQVDSWEEMLNKAEVGHY 291
QY 248 VGRPCLHPDDLCPGPAPNHSRQAPNVAAHELGGCHGSHKFMHWQEBELLGLGMARDPQ 307
Db 292 MDRPCLNPADPCPAPNKNSTKPLDMALVLVNGGCHGLSRKFMHWQEBELLGLGMARDPQ 351
QY 308 GELLRAEALQSTELLMSPROLYEHFRG-DYCTHDIGMSBEOASTVLQAWORRFLQAOEA 366
Db 352 GKLVSAHALQTMQLMTPKQMYEHFKGYEVSH-INWEDKAAALEAWORTYVEVYHQS 410
QY 367 LPENASQOIHAFTSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTTLLDILKSFSDSVIRVASGYLLMLAYACLIMLRWDCSKSQAVG 470
QY 427 LAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVDELLAHAFTEALPG-- 484
Db 471 LAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVDELLAHAFTEALPG-- 530
QY 485 TPLQERMGECLQRTGTSVVLTSINMAAFIPALRAFSLOAAIVVGCTFVAVML 544
Db 531 IPEDRTGCKRTIGASVALTSINVTAFPMALIFIPALRAFSLOAAIVVFNFAVLL 590
QY 545 VFPAILSLDLRRRRCORLDVLCFSSPCSAQVITQILPQELGDCGTPVPGIAHITATV 595
Db 591 IFFAILSMDLRYRREDRLDIFCCFTSPCVSRVQVPEQAYTDTHTNTRYSPPPYSSHSF 650
QY 596 -----LTAIVQAFTHCEASSQHVVTILPPOAHILVPPP-----SDPLGSELPSPGGSTRD 644
Db 651 AHETQITMQSTVQLRTEYDPTHTVYTTABPREISVQPVVTVTQDLSQSPSTSTSTRD 710
QY 645 LIGQEBETKQKAACKSLPCARNLAFHAFYQAPLILQSHAKAIVLFCALLGLSLYCA 704
Db 711 LLSQFSDS--SLHCLPPTCKWTLSFAEKHYAPFLKPKAKVVVIFLGLLGLSVLYGT 768
QY 705 TLVQDGLALTDVVPRGTKEHAFLSAQRYFSLYEVALVTQGGPDYAHSQRALFDLHQRFF 764

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Db 769 TVRDLGLDLDIVPRETREYDFIAAQKFYFYNMVIYVTKA-DYPNIQHLLYDLHRFS 827
QY 765 SLKAVLPPATQAPRTWLYHYNWLMGIIQAADFQDQWASGRITRHSYRNSEDEGALAYKLL 824
Db 828 NVKYVMLEENKQLPKWMLHYFRDLWGLQGLQDQFSDWETKIMPNYKNGSDGGLAYKLL 887
QY 825 IOTGDAQEPLDLSOLTRKLVOREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPE 884
Db 888 VQTGSRKPDIDISQLTKQRLVDAGDGIINSPAFIYLTAWVNSDPAAYASQANIRPHRE 947
QY 885 WLHDKYDTTGE-NLRIPPAQLEFAQFPFLRLGLOKTDVFAIEGARAACARAGQGVH 943
Db 948 WYHDKADYMPETELRIPAAEPIEYAFYFYLNGLRUTSDVEAIEKVRTICSNYTSLGLS 1007
QY 944 AYPGSGPFLFWEOYLGLRCLFLAVCILVCTPLVCAILLNPNWTAGLIVLVMAMTVEL 1003
Db 1008 SYNGYFPLFWEOYLGLRCLFLAVCILVCTPLVCAILLNPNWTAGLIVLVMAMTVEL 1067
QY 1004 FGIMGFLGKLSAIPVILVASVIGVETVHVVALGFLTTQGSRLRAAAHLEHTEAPVT 1063
Db 1068 FGMGUGIGKLSAVPVILIASVIGVETVHVVALGFLTTQGSRLRAAAHLEHTEAPVT 1127
QY 1064 DGAISTLLGLMLAGSHFDFIVRYFFAALTPLLLGLHGLVLLPLVLLSLTGPPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSEDFIVRYFFAALTPLLLGLHGLVLLPLVLLSLTGPPPEVSPA 1187
QY 1122 ----QMYKSPE-----ILSP-----APQG 1139
Db 1188 NGLNRLPTSPPEPPSVRFAMPFGHTSGSDSDSEYSSQTTVSGLSBELRHYEAQQA 1247
QY 1140 G-----LRWG-----ASSLPSOFAR 1155
Db 1248 GGAHQVIVEATENPVFAHSTVVHPSRHHPSPNPRQQPHLSDGSLPPGRGQQQPRDDPP 1307
QY 1141 -----LRWG-----ASSLPSOFAR 1155
Db 1308 REGMLPYLRPRDAFEISTEGHSGPSNRARWGRGARGSHNPNRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTVTASVTVVAHPPVPGGRNP 1393

RESULT 8

US-08-656-055-19
; Sequence 19, Application US/08656055
; Patent No. 6027882
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hombach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/540,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-055-19

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAARQIILAGSL---KAPLWIRPAYQGLLFSLCGCIQRHCGKVLFLGLAFLGA 68
Db 53 PSYC-DAAPALEQISKGKATGRKAPLWIRAKTQRLFLKLGCIYQKNCGRFLVVGLLIFGA 111
QY 69 LALGRMAIETNLEQLWVEGSRVSOELHYTKKELGEEAAVTSOMLIOTARQEGENILT 128
Db 112 FAVGLKAANLETNVELWVEGSRVRELYNTRQKIGEEAMFNQPMIQTKEEGANVLT 171
QY 129 PEALGHLQAALTASKVQVSLYKGSMDLNKIYKSGVPLIENGMIEMMIKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHYVMYNRQMKLEHLCYKSGELITETGYMBQIIEYLPCLIIIP 231
QY 189 LDCFWEKAGLQGSAYLPCRPDIOWNTNLPQLELELPGF-ASLEFRELLEDKAQQVQAY 247
Db 232 LDCFWEKAGLQGSAYLPCRPDIOWNTNLPQLELELPGF-ASLEFRELLEDKAQQVQAY 291
QY 248 VGRCPHPDLDLCPSPAPNHHSRQAPNVAHELSGGCHGF-SHKFMHWOEBELLICGMARDPQ 307
Db 292 MDRPCLNLPADPCPATAPNKNSTKPLDMALVINGCHGLSRKYMHWQEBELIVGGETVKNST 351
QY 308 GELLRAELAQSTFLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRFRVQLAQBA 366
Db 352 GKLVSAHALQTMFQMLTPKQMYEHFKGYEVSH-INWNEDKAAAILLEAQRTYVEVHQS 410
QY 367 LPENASQIHTAFSSTLDDILHAFSEVSARVVGVGVLMLAYACVATMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSPFTTTTDDILKSPFSDSVIRVASGVLLMAYACVATMLRWDCAQSGSVG 470
QY 427 LAGVLVALAVASGLGLCALIGITENAAATTVLPALGIGVDDVFLLAHAFTALPG-- 484
Db 471 LAGVLVALSVAGLGLCSLIGISFNAATTVLPALGIGVDDVFLLAHAFTALPG-- 530
QY 485 TPLQERMGECLQRTGTSVVLTSTINNAAFMLAALVPIPALRAFSLQAAIVGCTFVAVML 544
Db 531 IPPEDRTGECLRTGASVALTSISNVTAFPMALIPALRAFSLQAAIVVFNFAVLL 590
QY 545 VFPAILSLDLRRHCOGLDVLCCFSPSCSAQVILQBELD-----GTVPVGAH-- 595
Db 591 IPPAILSMOLYRRDRRLDFCCFTSPCVSRVIOEQPAYTDTHTNTRYSPPPYSSHSF 650
QY 596 -----LTATVQAFTHCEASSQHVVTILPPOAHVPPP-----SDPLGSELSPGGSTRD 644
Db 651 AHETQITMOSQVLRTEYDPHTHYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710
QY 645 LLGQEEETRQKAACKSLPCARNWLAHFARYQAPLQLQSHAKAIVLVLFGALLGLSLYGA 704
Db 711 LLSQSFDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVPGTKKEHAFLSAQLRYFSYIEVALVTQGGFDVAHSORALFDLHQRFS 764
Db 769 TRVRDGLDLDIVPRETREYDFIAAQKFYFYNMVIYVTKA-DYPNIQHLLYDLHRFS 827
QY 765 SLKAVLPPATQAPRTWLYHYNWLMGIIQAADFQDQWASGRITRHSYRNSEDEGALAYKLL 824

Db 828 NVKVMLEENKQLPKWMLHYFRDLWLOGLQDAFDSWETKIMPNYKNGSDGVLAYKLL 887
QY 825 IQGDAQEPDLSGLTRTKLVDRGLPPELFYMGTLVWVSSDPLGLAASQANFYPPPE 884
Db 888 VQIGSRDKPIDISQTKQRLVDAGIINPSAFIYLTAWVSNDDPVAASQANIRPHPE 947
QY 885 WLHDKYDTTGE-NLRIPPAQLEFAQPPFFLLRGLQKTADFVEAIEGARAACAAGQAGVH 943
Db 948 WVKDKADYMETRLRIPAAEPIEVAQPPFYNGRLDTSDFEALKEKVTICSNYTSGLS 1007
QY 944 AYSGSPFLFWQVGLRCLFLLAVCILVCTFLVCAALLINPWTAGLIVLVAMMTVEL 1003
Db 1008 SYNGPYPLFWQVGLRCLFLLAVCILVCTFLVCAALLINPWTAGLIVLVAMMTVEL 1067
QY 1004 FGMWFGIGIKLSAIPVIVLASVIGVGFVTHVALGFLTTQGSRLRAAALHETFAVPT 1063
Db 1068 FGMWFGIGIKLSAIPVIVLASVIGVGFVTHVALGFLTTQGSRLRAAALHETFAVPT 1127
QY 1064 DGAISTLLGLLAGSHFDIVRYFFAALTTLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db 1128 DGAISTLLGLLAGSHFDIVRYFFAALTTLGLLHGLVLLPVLLSILGPPPEVI-- 1187
QY 1122 ----QMYKESPE-----ILSP-----APQG 1139
Db 1188 NGLNRLFTPSPEPPPSVVRPAMPFGHTHSGSDSDSEYSSQTTVSGISELHRHYEAQGA 1247
QY 1140 G-----LRWG-----ASSILPQSFA 1155
Db 1248 GGAHQVIVATENPVFAHSTVVPVHPSRHHPNPROQPHLDGSLPPGQGGQRRDPP 1307
QY 1141 -----LRWG-----ASSILPQSFA 1155
Db 1308 REGMLPPLXPRDAREFISTEGHSGPSNRARWGRGRASHNPNRNPASTAMGSSVPGVCOP 1367
QY 1156 VTT-----SMTVAIHPPPLDGAIVHP 1176
Db 1368 ITTVTASVTVAVHPPVPGGRNP 1393

RESULT 9

US-08-954-668-19
; Sequence 19, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-668-19

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPARTAAPQILAGSL---KAPLWLRAYFOGLFLSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAPALEQISGKATGRKAPLWLRKAFORLFLKLCYIQKCGKFLVGLLIFGA 111
QY 69 LALGLRWAIETNLEQWVEVGRVSRVQELHYTKKIGEEAAYTSQMLIQIARQEGENILT 128
Db 112 FAVGLKAAANLETNVEELWVEVGRVSRVRELNYTRQKIGEEAMFNPQLMIQTPKEGANVLT 171
QY 129 PEALGLHLQAAALASQVQVSLYCKSWDLNKICYKSGVPLIENGMIEMWIEKLPFCVILTP 188
Db 172 TEALLOHLSALQASRVHVYMYNRQMKLEHLCKYSGELITETGYMDQIIEYLPCLLIITP 231
QY 189 LDCFWGAKLQGSAYLPGRPDIQWNTNLDPEOLLEELGPF-ASLEGPRELLDKAQQOAY 247
Db 232 LDCFWGAKLQGSAYLPGRPDIQWNTNLDPEOLLEELGPF-ASLEGPRELLDKAQQOAY 291
QY 248 VGRPCLHPDDLHCPSPAPNHHSQAPNVAHELGGCHGFSHKPMHMQEELLGLGMDPQ 307
Db 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVLNGGCHGSLSKYMHMQEELLIGTVKNST 351
QY 308 GELLRAEALQSTFLMLSPQLYEHPFG-DYQTHDIGWSEQASTVLAQQRVFLQAQEA 366
Db 352 GKLVSAHALQTMFQMLTPKQMYEHFGYEVSH-INNEDKAAAILAEWQRTVEVHQH 410
QY 367 LPENASQQLHAFSTTLDLILHAFSVSAARVGVGYLLMLAYACTVLMRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTLDLILKSFSDSVIRVASGYLLMLAYACTVLMRWDCAQSGSVG 470
QY 427 LAGVLLVALAVASGLGCLCALLGTTFNAATTQVLPFLALGIGVDDVFLAHAFTEALPG-- 484
Db 471 LAGVLLVALAVASGLGCLCALLGTTFNAATTQVLPFLALGIGVDDVFLAHAFTEALPG-- 530
QY 485 TPLQERMGELQRTGTSVLTISINNAEFLMAALVPIPALRAFSLQAAIVVGTFFVAVML 544
Db 531 IPFEDTGBCLKRTGASVALTISINVTAFPMALIIPIPALRAFSLQAAIVVGTFFVAVML 590
QY 545 VFPAILSLDLRRRHQCORLVLCCFSPSCSAQVQIQLPOELGD-----GTVPVGIH-- 595
Db 591 IFPAILSMDLRRHRELDLIFCCFTSPCVSRVLOVEPQATYDTHDNTRSPFPYSHSF 650
QY 596 -----LTATVQAFTHCEASSQHVVTILPPQAHVPPP-----SDPLGSELSPGSGSTRD 644
Db 651 AHETQITMQSTVQLRTEYDPHTHYVYTTAEPRSEISVQPVVTQDTLSCQSPSTSTRD 710
QY 645 LLGOEEETQKAAKSLPCARWNLAFARYQAPLILLOSHAKAIVLVLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHLEPPCTKMTLSSFAEKHYAPFLKPKAKVIVFLFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVPRGTKEHAFSLAQRYFSLYEVALVTQGGFDYAHSGRALFDLHQRF 764
Db 769 TRVRDGLDLTDIVPRETREVDFIAAQFYFSFNWYIVTQKA-DYFNIQHLLYDLHRSFS 827
QY 765 SLKAVLPPPATQAPRTWLHYRNWLOGIOAAFDQDQWASGRITRHSYRNSESGDALAYKLL 824
Db 828 NVKVMLEENKQLPKWMLHYFRDLWLOGLQDAFDSWETKIMPNYKNGSDGVLAYKLL 887
QY 825 IQGDAQEPDLSGLTRTKLVDRGLPPELFYMGTLVWVSSDPLGLAASQANFYPPPE 884
Db 888 VQIGSRDKPIDISQTKQRLVDAGIINPSAFIYLTAWVSNDDPVAASQANIRPHPE 947
QY 885 WLHDKYDTTGE-NLRIPPAQLEFAQPPFFLLRGLQKTADFVEAIEGARAACAAGQAGVH 943

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Db 948 WVDKADYMPETRLRIPAEPIEYAOFPFVINGLROTDSEVEAIEKVRTICSNYTSLSGLS 1007
QY 944 AYPGSPFLFMEQYGLRRCFLAIVACTELVCALLLNPNWTAAGLIVLVLAMTVEL 1003
Db 1008 SYNGYPFLFMEQYIGLRHLLFISVWLACTELVCVAVFLNPNWTAAGIIVMVLAMTVEL 1067
QY 1004 FGIMFGLIKLSAIPVILVASVIGIEFTVHVVALGFLITQGSNRLRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAVPVILVASVIGIEFTVHVVALGFLITQGSNRLRAHALEHTFAPVT 1127
QY 1064 DGAISTLLGLLMLAGSHDFIVRYFAALTVLTLGLLHGLVLLPVLSTILGPPPEVI-- 1121
Db 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVLAILIILGVINGLVLLPVLSTILGPPPEVSPA 1187
QY 1122 ----QMYKESPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRVAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHYEAQOGA 1247
QY 1140 G-----LRWG----- 1140
Db 1248 GGPAHQVIVEATENPVFAHSTVVHPSRHHPPSNPRQPHLDGSLPPGSGQOQPRDPP 1307
QY 1141 -----LRWG-----ASSLSPOSFAR 1155
Db 1308 REGMLPPLYPRRDAFEISTEGHSGPSNRARWGPARGARSHNPRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTWTASVTVAVHPPVPVPGGRNP 1393

RESULT 10
US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-140-5

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFLSGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAPALEQISKGATGRKAPLWLRKAFQRLFLKLCYIQKNGCKFLVVGLLIFGA 111
QY 69 LALGLRMAIETNLEQLWVEGSRVSOELHYTKEKGEEAAYTSOMLIQTARQEGENILT 128
Db 112 FAVGLKAANLETVNEELWVGSRVSRRELNYTRQKIGEEAMFNQPMIQTPKSEGANVLT 171
QY 129 PEALGLHLOAALTASKVOVSLYKGSWDLNKKICVYGVPLIENGMIEMIEKLPVCLTLP 188
Db 172 TEALLQHLDSALQASRVHVTVYRWQKLEHLCVYSGELITETGVMQDIIIEYLPCLITP 231
QY 189 LDCFWEGAKLQGSAYLPGRPDIOQWNLDPQLLEELGPF-ASLEGPRELLDKAQVQAY 247
Db 232 LDCFWEGAKLQSGTAYLLGKPLRWTFNDFPLEFLEELKKNYQVDSWEEMLNKAEGVGHY 291

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QY 248 VGRPCPLHDDLHCPSPAPNHHSRQAPNVAHELSCGCGHGFESHKFMHQBELLGLGMARDPQ 307
Db 292 MDRPCLNADPDPCPATAPNKNSTKPLDMLVNLGGCHGJSRKYHMHQBELLVIGGTVKNST 351
QY 308 GELLRAEALQSTPFLMSPRQLYEHFRG-DYQTHDIDGSEBQASTVLQAMORRERVQLAQEA 366
Db 352 GKLVSAHALQTFEQLMTPKQMYEHFKGYEVSH-INWNEKAAALAEAMQRTVVEVHQS 410
QY 367 LPNASSQTHAFSSSTLDDILHAFSEVSARVVGGLMLLAYACVYMLRWDCAQSQSVG 426
Db 411 VAQNSTQKVLSTFTTTTDDILKSFSDSVIRVASGVLLMLLAYACLTMLRWDCKSKQAGV 470
QY 427 LAGVLLAVAVASGLGICALLGITENAAATVLPALGIGVDDVFLLAHAFTALPG-- 484
Db 471 LAGVLLAVAVASGLGICALLGITENAAATVLPALGIGVDDVFLLAHAFTALPG-- 530
QY 485 TPLQERMGELQRTGTSTSVVLTSTNNMAAFMLAALVPIPALRAFSLQAAIIVGCTFVAVML 544
Db 531 IPEEDRTGELCKRTGASVALTSISNVTAFMAALIPALRAFSLQAAVAVVVFANFVLL 590
QY 545 VFPAILSLDLRRHRCORLQVLCFSSPCSAQVLIQPLQELGD-----GTVPVGAH-- 595
Db 591 IFPAILSLMDLYRREDRLDIFCFTSPCVSRVQVPEQAYTDTHTDNTRYSPPPYSHSF 650
QY 596 -----LTATVQAFTHCEASSQHVVTILPPQAHVPPP-----SDPLGSELFSPGSTRD 644
Db 651 AHETQITMSTVQLRTYDPTHVYTTAPRSEISVQPVTVTQDTLSCSPSESTSTRD 710
QY 645 LLGQEBETRQKAAKSLPCARMNLAHFARYQFAPLLIQSHAKAIVLFLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKWLTLSSFAEKHYAPFLKPKAKVVVFLFLGLLGVSLYGT 768
QY 705 TLVQDGLALTVDVPRGTKEHAFLSAOLRYFSLYEVALVTQGGEDYAHSGRALLFDLHQRF 764
Db 769 TRVRDGLDLTDIVPRETREYDFIAQKFYFSFYNYIVTQKA-DYENIQHLLYDLHRSFS 827
QY 765 SLKAVLPPPATQAPRTWLYHYNWLOGIOAAFDQDWSAGRI TRHSYRNGSEDCALAYKLL 824
Db 828 NVKYVMLEENKOLPKWMLHYFRDMLQGLQDAFDSQWETGKIMNNYKNGSDGGLAYKLL 887
QY 825 IQGTDAQEPLDFSQLTTRKLVDRGLIPPELFYMLGTVMVSSDPLGLAASQANFYPPPE 884
Db 888 VQTGRDQKPIDISQLTQKRLVDADGIINPSAFIYLTAWVNDPVAVASQANIRHPPE 947
QY 885 WHDKYDVTGB-NLRIPPAQPLEFAFPFLRLGKQKTADFEVAIEGARAACAGAGQGVH 943
Db 948 WVDKADYMPETRLRIPAEPIEYAOFPFVINGLROTDSEVEAIEKVRTICSNYTSLSGLS 1007
QY 944 AYPGSPFLFMEQYGLRRCFLAIVACTELVCALLLNPNWTAAGLIVLVLAMTVEL 1003
Db 1008 SYNGYPFLFMEQYIGLRHLLFISVWLACTELVCVAVFLNPNWTAAGIIVMVLAMTVEL 1067
QY 1004 FGIMFGLIKLSAIPVILVASVIGIEFTVHVVALGFLITQGSNRLRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAVPVILVASVIGIEFTVHVVALGFLITQGSNRLRAHALEHTFAPVT 1127
QY 1064 DGAISTLLGLLMLAGSHDFIVRYFAALTVLTLGLLHGLVLLPVLSTILGPPPEVI-- 1121
Db 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVLAILIILGVINGLVLLPVLSTILGPPPEVSPA 1187
QY 1122 ----QMYKESPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRVAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHYEAQOGA 1247
QY 1140 G-----LRWG----- 1140
Db 1248 GGPAHQVIVEATENPVFAHSTVVHPSRHHPPSNPRQPHLDGSLPPGSGQOQPRDPP 1307
QY 1141 -----LRWG-----ASSLSPOSFAR 1155
Db 1308 REGMLPPLYPRRDAFEISTEGHSGPSNRARWGPARGARSHNPRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176

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Db 1368 ITTITASASVTVAHPHPPVPGCRNP 1393

RESULT 12
US-09-724-631-19
; Sequence 19, Application US/09724631
; Patent No. 6551782
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. 6551782-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-724-631-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1,7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPARTAPQILAGSL---KAPLWRAFYQGLLFLSLGCGTQRHCKGLFLGLLAFGA 68
Db 53 PSYC-DAAFALQISGKATGRKAPLWRAKFORLLFKGCTQKNCCKFLWGLLIFGA 111
QY 69 LALGLRMATITNLEQLWVEGVSQELHYTKELGEEAAYTSOMLIQTAROEENILT 128
Db 112 FAVGLKAAINTVEELWVEGVSRELNYTRQKIGEEAMFNQMLIQTPKEGANVLT 171
QY 129 PEALGLHQAALTASKQVSLYKGSNDLNKICYKSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYMYNQRQWKLHCLCYKSGELITETGYMDQIIEYLXPLIITP 231
QY 189 LDCFWEGAKLQGSAYLPGRPDIOQWTLNDEQLLEELGPF-ASLEGPRELLDKAQVQAY 247
Db 232 LDCFWEGAKLQSGTAYLLGKPLPLTNFDFLEFLEELKKINYQVDSWEEMLNKAEVGHGY 291
QY 248 VGRPCLPDDLHCPPSAPNHSRQAPNVAAHSELGSGCHGFSHKFMHQBELLGLGWARDPQ 307

292 MDPRCLNPADPCPATAPNKNSTKPLDMALVINGGCHLSRKYMHQEEILVGGTVKNST 351
308 GELLRAEALQSTFLMLSPQLYEHFRG-DYQTHDIQWSEBQASTVLOAWORRFFVQLAQBA 366
352 GKLVSALHQLTQMTFQPMQYEHFKGYEVSH-INWNEDKAAAILAEAWORTVEVHHQS 410
367 LPENASQOIHAFFSSTLDDILHAFSVAARVVGYYLLMLAYACVMTLWRDCAOSQSVG 426
411 VAQNSTQKVLSTFTTLLDDILKFSFVSIVRASGYLLMLAYACLTMLRWDCKSQGAVG 470
427 LAGVLLVALAVASGLGICALLGITFNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
471 LAGVLLVALSVAAGLGLSLIGISFNAATQVLPFLALGVDDVFLLAHAFSETGQNK 530
485 TPIQERMGECLQRTGTSVLTSSINNMAAFUMLAIPALRAFSLQAAIIVGCTFTVAVML 544
531 IPFEDRTGECLKRTGASVALTSISNTVAFPMALIPALRAFSLQAAVVVVFNFAMVLL 590
545 VFPAILSLDLRRRCORLDVLCFSSPCSAQVLIQLPOELGD-----CTVPVGIH-- 595
591 IFFAILSMDDYRRDRRLDIFCCFTSPCVSRVQVEPQAYTDTHDNTRYSPPPYSHSF 650
596 -----LTATVOAFTHCEASSQHVVTILPPQAHVPPP----SDPLGSELFSPGSTRD 644
651 AHETOITMQSTVQLRTEYDPHTHVYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710
645 LLQGEETROKAAACKSLPCARWNLAHFARYQFAPLLLOSHAKAIVLVFQALLGLSLYGA 704
711 LLSQFSDS--SLHCLPEPCTKWTLSFPAEKHYAPFLKPKAKVVIFFLGLLGSUYGT 768
705 TLVQDGLALTDVVPRGTKEHAFLSAQLRYSLSYVALVTOGGPDYHAHQRAFLDHFORS 764
769 TRVRDGLDLDIVPRETREYDFIAAQKYPSTFNTYITVOKA-DYPMIQLHLLDHLRSFS 827
765 SLKAVLPPPPATQAPRTWLHYRNWLOGIQAAFDQDMASGRITRHSYENGSEDEGALAYKL 824
828 NVKYVMLEENKQLPKMWLHYFRDMLQGLQDAFDSMETGKIMPNYKNGSDGVLAYAKLL 887
825 IQGDAQEPLDPSQLTRKLVLDREGLIPPELFWGLTVVWSSDPLGLAASQANPYPPPE 884
888 VOTGSRDKPIDISQLTKQRLVDADGIINPSAFYIYLTAWYSDNDFVAYASAQANIRHPE 947
885 WLHDKYDTTGE-NLRIPPAQPLEFAOPFFLLRGLGOKTADFEALEGARAAACAGQAGVH 943
948 WVDHKADYMPETRLRIPAAEPIEYAOFPFYNGRLRTDSEFEALEKVRTICSNYTSUGLS 1007
944 AYPGSPFLFWEQYGLRRCFLLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMMTVEL 1003
1008 SYNGYFPLFWEQYIGLRHWWLLFISVLACTFLVCAVFLNPNWTAGIIVMLALMTVEL 1067
1004 FGIMGFLGKLSAIPVVLVASVIGVEFTVHVVALGFLTTQGSRNLRRAHALEHTFAPVT 1063
1068 FGMMGLIGKLSAVPVVILLIASVIGVEFTVHVVALAFLTAIGDKNRRAVLALEHMFAPVL 1127
1064 DGAISTLGLMLAGSHFDFIVRYFAALVTLVTLGLLHGLVLLPVLSSLILGPPPEVI-- 1121
1128 DGAVSTLGLVMLAGSEDFIVRYFAVLAAILITLGLVINGLVLLPVLSPFGPYVPSPA 1187
1122 ----QMYKESPE-----ILSP-----APQGG 1139
1188 NGLNRLPTSPPEPPSVVRFAMPFGTHSGSDSDSEYSSQTTVSGLSBELRHYEQGA 1247
1140 G-----G-----LRWG-----ASSLSQSPAR 1155
1248 GGPAAHVIVEATENPVFAHSTVVHPSRHPPSNRQPHLDGSLPPGRRDPP 1307
1141 -----LRWG-----ASSLSQSPAR 1155
1308 REGVLPVLRPRDAFEISTEGHSGPSNRARWGRGARSHNPRNPASTAMGSSVPGYQCP 1367
1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
1368 ITTITASASVTVAHPHPPVPGCRNP 1393

RESULT 13

US-08-954-701A-19

; Sequence 19, Application US/08954701A

; Patent No. 6610507

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; APPLICANT: GOODRICH, LISA V

; APPLICANT: JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,701A

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36709

; REFERENCE/DOCKET NUMBER: SUV-003.08

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1447 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;
 Best Local Similarity 49.9%; Pred. No. 1.7e-314;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY	12	PSYTPPARTAAPQILAGSL---	KAPLWLRAYFQGLLFSGLGCIQRHCGKVLFLGLAFA	68
DB	53	PSYC-DAAFALQISKGKATGRAPLWRAKFORLLFKLCYIQKCGKFLVGLLIFGA	111	
QY	69	LALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLEGEAAYSQMLIQARQEGENILT	128	
DB	112	FAYGLKAANLETNVEELWVEGSRVRELNYTRQKIGEEAMFNPLMIQTPKEGANVLT	171	
QY	129	PEALGHLOALTASKVOVSLYKSGMDLNKICVKSGVPLENGIEMWIEKLEPCVLTLP	198	
DB	172	TEALLQHLDSALQASRVHVHTYRNRQWKLHCLYKSGELITETGYMDQIIEYLYPCLITP	231	
QY	189	LDCFWEKALQGSAYLPGRPDIQWTNLDPEQLLEELGPF-ASLEGFRELDDKAQVQAY	247	
DB	232	LDCFWEKALQSGTAYLLGKPLPLRWTFNFDPLEFLEELKKNYQVDSWEEMLNKAEVGHY	291	
QY	248	VGRPCLHPPDLHCPGAPNHSQAQPNVAHELGGCHGFSGKHWQEBELLGLGMARDPQ	307	
DB	292	MDRPLCLNPADPCAPAPNKNSTKPLDMALVNLGGCHGLSRKYNHWQEEILVIGSTVKNST	351	
QY	308	GELLRAEALQSTFLLMSPROLYEHRFG-DYOTHDIGWSEQAQSTVLQAWORRRFVOLAQA	366	
DB	352	GKLVSANLQTMQLQMTPKQMYEHFKGYEVSH-INNWEDKAAILEAWORTVEVWHQS	410	
QY	367	LPENASQIHAFSSTLDDIILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCAQSGSVG	426	

DB	411	VAQNSTQKVLSTFTTTLLDDILKSFDSVSVIRVASGYLLMLAYACLTMLRWDSCSQGAVG	470
QY	427	LAGVLLVALAVASGLGICALLGIFTNAAATQVLFFLAGIGVDVDFLLAHAFTEALPG--	484
DB	471	LAGVLLVALSVAGLGLCSLIGISFNAATQVLFFLAGIGVDVDFLLAHAFSETGQNKR	530
QY	485	TPLOERMGECLORTGTSVWLTSTNNMAAFMAALVPIPALRAFSLQAAIVVGCTFVAVML	544
DB	531	IPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPALRAFSLQAAVVVVFAMVLL	590
QY	545	VEPAIISLDLRRHRCORLDVLCFSSPCSAQVLIQLPOELGD-----GTPVPGIAH--	595
DB	591	IPFALLSMDLYRRDRLDIFCCFTSPCVSRVQVEPQAYTTHDNTRYSPPPYSSHSF	650
QY	596	-----LTATVQAFTHEASSQHVVTILPFOAHLVPPP-----SDPLGSELFSPGGSTRD	644
DB	651	AHETQITMQSTVQLRTEYDPHTHYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD	710
QY	645	LLGOEETROKAAACKSLPCARWNLAHFARYQFAPLLLOSHAKAIVLVLFGLLGLSLYGA	704
DB	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLLPKPAKVWVIFLFLGLLGLSVLYGT	768
QY	705	TLVODGLALTVDVVRGTKEHAFLSAQLRYESLYEVALVTOGGEDYAHQSORALFDLHORFS	764
DB	769	TRVEDGLDLTDIVPRETREYDFTAAPKQFYSFVNYMIVTQKA-DYPNIQHLLYDLHRSFS	827
QY	765	SLKAVLPPPTAQPTWMLHYRNWLGIOAQPQDQWASGRITRHSYRNGSESDGALAYKLL	824
DB	828	NVKYVMLEENKQLPKMWLHYFRDLWGLQDAFSDMETGKIMPNYNNKNGSDDGVLAYKLL	887
QY	825	IQTGDAQEPLDFSQITRKLVDREGLIPPELFYWGTLTWVSSDPLGLAASQAQFPPPE	884
DB	888	VQTGSRDKPIDISQLTKQRLVDADGIINPSAFIYLTAWVSNDPFAVYAAQAIRPPE	947
QY	885	WLHDKYDITGE-NLRIPPAQPLEFAQPPFLRLGLQKTADFEALTEGARAACAAGQAGVH	943
DB	948	WVHDKADYMPETRLRIPAAEPFIEYAQPPFYVINGLRTSDFEALIEKVTTICSNYTSGLS	1007
QY	944	AYPSGSPFLFWEOYGLRRCFLLAVALCILLVCTFLVLCALLLNPTWAGLIIVLVLAMMTVEL	1003
DB	1008	SYPNGYPLFWEOYIGLRHWLLLFISVVLACTFLVCAVFLNPWTAGIIVMLALMTVEL	1067
QY	1004	FGWGLGELIKLSAIPVVLVAVSGIGVEFTVHVALGFLTTQGSNRLRAAHAEHTPAVPT	1063
DB	1068	FGWGLGELIKLSAIPVVLVAVSGIGVEFTVHVALGFLTTQGSNRLRAAHAEHTPAVPT	1127
QY	1064	DGAISTLLGLLGLAGSHFDIVRYFAALTTLGLLGLHGLVLLPVLLSLTILGPPPEVI--	1121
DB	1128	DGAVSTLLGLVLMAGSEFFDIVRYFAVLAAILTILGVINGLVLFPVLLSFFGYPPEVSPA	1187
QY	1122	-----QWYKESPE-----ILSPP-----APQG 1139	
DB	1188	NGLNRLPTSPPEPPSVVRFPAMPGGHTHSGSDSDSEYSSQTTVSGLSSELRYEAQQA	1247
QY	1140	G-----	1140
DB	1248	GGPAHQVITEATNPVFAHSTVHVHPSRHHPNPQPHLDGSLPPGQGGQPPRRDPP	1307
QY	1141	-----IRWG-----ASSLSQSFAR 1155	
DB	1308	REGLWPFLYPRDAFEISTEGHSGFSNRARWGPRGASHNPNPNASTAGSSVPGYCQ	1367
QY	1156	VTT-----SMTVAIHPPPLPGAYIHP 1176	
DB	1368	ITTVTASVTVAVHPPFPVPGGRNP 1393	

RESULT 14

PCT-US95-13233-19

; Sequence 19, Application PC/TUS9513233

; GENERAL INFORMATION:

; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY

; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13233
 ; FILING DATE: 06-OCT-1990
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1447 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-13233-19

Query Match 53.4%; Score 3348; DB 5; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.7e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSTPTPARTAQAQLAGSL---KAPLMRAYFQGLFLSLCGGIGRHCCKVFLFGLLAFGA 68
 DB 53 PSYC-DAAPALEQISKGATGRKAPLMRAKFORLLFLKGYIQKNGKFLVWGLLIFGA 111
 QY 69 LALGLRMAIETLEQLWVEVGRVSOELHYTEKLGEEAAYSOMLIQTARAGEENILT 128
 DB 112 FAVGLKAANLETVBEELWVEVGRVSRKELNYTKTGEEAMFNPQMIOPTKEEGANVLT 171
 QY 129 PEALGLHQAALTASKVQVSLYKSGMDLNKICYKSGVPLIENGMIEMIEKLPFCVILT 188
 DB 172 TEALLQHLDSALQASRVHVVMYRNQWKLHLCYKSGELITETGYMDQIIEYLPCLIITP 231
 QY 189 LDCFWEAGAKLQGSAYLPGRPDQIQTWNLDPEQLLEELGPF-ASLEGFRELLDKAQVQYAY 247
 DB 232 LDCFWEAGAKLQGSAYLPGRPDQIQTWNLDPEQLLEELGPF-ASLEGFRELLDKAQVQYAY 291
 QY 248 VGRPCLHPDHLCPSPANHNSRQAPNVAHELSSGCHGFSGHKEHMOEELLGLGMARDPQ 307
 DB 292 MDRPCLNADPDPCATAPNKNSTKPLDMALVNLGGCHGLSRKYNHMOBELIVGGTVKNST 351
 QY 308 GELLRAELQSTFLLSPRLQYEHFRG-DYQTHDIGWSEEQASTVLQAWQRRFVQLAQEA 366
 DB 352 GKLVSAHALQTMFQMTKQMYEHFKGYEVSH-INWNEKAAALILEAQRTYVEVHQS 410
 QY 367 LPENASQOIHAFSTLDDILHAFSEVSAARVVGYYLLMAYACVTMLRWDCQSQSGV 426
 DB 411 VAQNSTQKVLFSFTTTTLLDILKSFSDVSVTRVSAVGLLMLAYACLTMLRWDCSKSQGAV 470
 QY 427 LAGVLLVALAVASIGL-CALLGITENAAATQVLPALGIGVDDVFLAHAFTEALPG-- 484
 DB 471 LAGVLLVALAVASIGL-CALLGITENAAATQVLPALGIGVDDVFLAHAFSETQONKR 530
 QY 485 TPLQRMGECLQRTGTSVLTSTNNMAAFMLAALVPIPALRAFSLQAAIIVVGTTFVAVML 544
 DB 531 IPEDRTGECLRTGASVALTSISNVTAFMAALIPIPALRAFSLQAAVAVVVFNAVLL 590

QY 545 VFPAILSLDLRRRHCORLDVLCFSFSPCSAQVITQILPOELGD-----GTVPVGAIAH-- 595
 DB 591 IFPAILSMDLYRRDRRLDIFCCFTSPCVSRVITQVEFQAYTDTHTDNTRYSPPPPYSHSF 650
 QY 596 -----LTATVCAFTHCRASSQHVVTILPPOAHLVPPP-----SDPLGSLFSPGSGSTRD 644
 DB 651 AHETQITMQSTVQURTEYDHTHTVYTAPRSEISVQPVTVTQDTLSCSPSESTSTRD 710
 QY 645 LLQGEETRQKAAKSLPCARMNLAHFARYQFAPLLIQSHAKAIVLIFGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLPKPKAVVVFIFLGLGLVSLYGT 768
 QY 705 TLVQDGLALTDVVRGTKEHAFLSAQRYFSLYEVALVTQGGFDYAHQSRALEDLHORFS 764
 DB 769 TRVRDGLDLTDIVPRETREYDFIAAQKFYSFFNMVITQKA-DYPNIQHLLDLHRSFS 827
 QY 765 SLKAVLPPPPATQAPRTMLHYRNWLOGIOAAFDODWASGRITRHSYRNGSEDCALAYKLL 824
 DB 828 NVKYVMLEENKQLPKWMLHYFRDMLQGLQDAFSDMETGKIMPNYKNGSDGGLVAYKLL 887
 QY 825 IOTGDAQEPLDFSQLTRKLVDRGLIPPELFFYMGLTVMVSSDPLGLAASQANFYPPPE 884
 DB 888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFYILTAWVSNPDVAVAAQANIRPURPE 947
 QY 885 WLHDKYDTTGE-NLRTPPAQPLEFAQPPFLLRLGLOKTADFEVAIEGARAACAAGQGVH 943
 DB 948 WWHDKADYMPETRLRIIPAAEPIEYQAQFPFYNLGRLDTSDFEAEIKVRTICSNYTSLSLS 1007
 QY 944 AYPGSGPFLFWEQYGLRRCFLILAVCTLCVLCALLLNPTWAGLIVLVLAMTVEL 1003
 DB 1008 SYENGYPFLFWEQYIGLRWLLLPISVULACTELVCVAVFLNPNWTAGIIVVVLAMTVEL 1067
 QY 1004 FGIMGFLGKLSAIPVIVLVAASVIGVETVHVVALGELTTQGSRNLRRAHALEHTFAPVT 1063
 DB 1068 FGMWGLIGIKLSAVPVILLIASVIGVETVHVVALAFLTAIGDKNRRRAVLALEHMFAPVL 1127
 QY 1064 DGAISTLLGLLMLAGSHDFIVRYFFAALTTLTLLGLLHGLVLLPVLVLSILGPPPEVI-- 1121
 DB 1128 DGAISTLLGLVLMAGSEDFIVRYFFAVALAILTLGLVNLGLVLLPVLVLSILGPPPEVSPA 1187
 QY 1122 ----QMKESPE-----ILSP-----APOGG 1139
 DB 1188 NGLNRLFTSPPEPPSVVRFAFPMPGHTHSGSDSDSEYSSQTTVSGLSBELRHYEAQQA 1247
 QY 1140 G-----LRWG----- 1140
 DB 1248 GGPAAQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDGSLPPGFGQQPRDPP 1307
 QY 1141 -----LRWG-----ASSLSPOSFAR 1155
 DB 1308 REGMLPPLXPRRDAFEISTEGHSGPSNRARWGPARGSHNPRNPASTAMGSSVPGYCOP 1367
 QY 1156 VTT-----SMTVAIHPPLPGAVIHP 1176
 DB 1368 ITTVTASAVTVAVHPPPPVPGGRNP 1393

RESULT 15

US-08-540-406-10
 ; Sequence 10, Application US/08540406
 ; Patent No. 5837538
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA

; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,406
 ; FILING DATE: 06-OCT-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: 860190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1434 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-540-406-10

Query Match 53.2%; Score 3337; DB 2; Length 1434;

Best Local Similarity 53.1%; Pred. No. 1.9e-313;

Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;

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DB	28	RAPDRYLHRPSYC--DAAFALQISKGKATGRKAPLWLRAKFORLLKLGCIYQKNCXGK	86
QY	58	VLFGLAFALAGLALGRMAIETNLEQLWVEVSGRSQELHYTKEKLGEBAAYTSQMLIQ	117
DB	87	FLVVGILLIFGAFVAGLKAANLETNVELWVEVSGRSRELNYTRQKIGEEAMFNQMLIQ	146
QY	118	TARQEGENIITPEALGHQLQALTASKVQVSLYKSKDNLNKICYKSGVPLIENGMIEMWI	177
DB	147	TPKEEGANVLITTEALLQHLSDLAQASRVHYMYNRQWKLEHLCYKSGELITETGYMDQII	206
QY	178	EKLFPVCVILTPDCFWEKALQGGSAYLPGRPDIQWNLDPQELLEELGPF--ASLEGFRE	236
DB	207	EYLYPCLIIITPDCFWEKALQGGSAYLPGRPDIQWNLDPQELLEELGPF--ASLEGFRE	266
QY	237	LLDKAQVQAYGRPCILHPDDLCPSPAPNHSGRQAPNVAHELGGCHGFSHKPMHWQEE	296
DB	267	MLNKAIEVGHGMDRCPCLNPADPCPATAPNKNSTKPLDVALVINGGCGQLSRKYMHWQEE	326
QY	297	LLGGWARDPQGLLRALQSTFLMSPRQLYEHFEG--DYQTHDTCWSEQASTVLQAW	355
DB	327	LIVGGTVKNATGKLVSALHALQTMFQMLTPKQMYEHFEGDYVSH--INWNEEDRAAILEAW	385
QY	356	QRFRVLOALAPENASQIIFATSSITDILHAFSEVSAARVVGVGYLLMLAYACTMLR	415
DB	386	QRTYVEVHQSVAPNSTQKVLPTTTITDILKSFSDSVIRVASGYLLMLAYACTMLR	445
QY	416	WDCAQSGSVGLAGVLLVALAVASGLGALLGITFNAATQVLPFIALGIGVDDVFELLA	475
DB	446	WDCSKSQAGVLAGVLLVALVAAGLGLCSLIGISFNAATQVLPFIALGIGVDDVFELLA	505
QY	476	HAFTEALPG--TPIQERMGECLORTGTSVVLTSINMAAFMLMAALVIPALRAFSLQAAI	533
DB	506	HAFSETQNKRIEFTQRTGECLORTGTSVVLTSINMAAFMLMAALVIPALRAFSLQAAI	565
QY	534	VVGCTFVAVMLVFALISLDRRRHQRDLVCCFSSPCSAQVITQILPQELGD-----	586
DB	566	VVFNFAVMLLIPALISLMDLYRREDRLDI FCCFTSPCVSRVIOVEPQAYTEPHSNTRY	625
QY	587	GTVPVGTIAH-----LTATVQAFTHCEASSQHVVTILPQAHLVPPP-----SDPLGS	633

Search completed: November 22, 2004, 07:58:45

Job time : 34 secs

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DB	686	QSPSTSSSTRDILLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVYVILF	743
QY	694	GALLGLSLYGATLVQDGLALTDVVPRGTKEHAFSLAQLRVFSLYEVALVTQGGFDYAHSQ	753
DB	744	LGLLGVSLYGTTRVROGLDITDIPRETRYEDFIAAQFKFSPFNMVIVITQKA--DYENIQ	802
QY	754	RALFDLHQRFSSLKAVLPPPATQAPRTWLYHYRNWLOGIOAADFQDQWASGRITRHSYRNG	813
DB	803	HLLYDLHKSPSNVYVMLEENKQLPQWLHYFRDLQLODAFDSWETGRIMPNNYKNG	862
QY	814	SESGALAYKLLIQTGDAQEPDLFSQLTTRKLVOREGLIPPELPMGLITVWVSSDPLGLAA	873
DB	863	SDDGVLAYKLLVQTSGRDKPIDISQLTQKQLVDADGIINFSAFYIYLTAWVSNPDVAYAA	922
QY	874	SQANFYPPPPPEWLHDKYDITGE--NLRIPPAQPLEFAQFPFLRLGLOKTADEFVEAIEGARA	932
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QY	933	ACAEAGQAGVHAYPSGSPFLFWEQYLGRLRCFLAVCILVCTFLVCAILLINPWTAGLI	992
DB	983	ICNNYTSGLSSYPNGYPPFLFWEQYISLRHLLLSISVWLACTFLVCAVLLNPWTAGII	1042
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DB	1043	VVVALMTVELFGMGLIGIKLSAIPVVIIVASVGIGVEFTHVALGFLTQGSRLRAA	1102
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DB	1103	LALHMFAPVLDGAVSTLLGVLMAGSEDFIVRYRFAVAILTLVGLVGLVLLPVLLS	1162
QY	1113	ILGPPPEVI-----QMYKESPEILSPP-----APQGGGLRWGASSLSPOSFARVTTSS--	1159
DB	1163	FFGCPCEVSPANGLNRLPTSPB--PPSVVRFVAVPFGHTNNGSDSDSDSEVSSQTTVSGI	1220
QY	1160	-----MTVALHPPPLPGAYIHP--APDEPPKSPAA---TSSGNLS	1194
DB	1221	SEELRQYEAQOAGGAGPAHQVIVEATENPVPFARSTVVHPDSRHPPLTPROQPHLDGSL	1280
QY	1195	SRGPG 1199	
DB	1281	---PG 1282	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 08:02:26 ; Search time 155 Seconds

(without alignments)
5516.639 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPRLRLPSYTPPART.....SPATSSGNLSRGPGPATG 1203

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US0990046/runat_21112004_130920_18563/app.query.fasta_1.1351
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0990046.cgn2_1.62/runat_21112004_130920_18563 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/6C COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	6272	100.0	4030	US-09-293-505-1	Sequence 1, Appli
2	6272	100.0	4030	US-09-060-939A-1	Sequence 1, Appli
3	6248	99.6	4391	US-09-207-857-1	Sequence 1, Appli
4	6248	99.6	4391	US-09-909-280A-1	Sequence 1, Appli
5	3955	63.1	4004	US-09-293-505-8	Sequence 8, Appli
6	3955	63.1	4004	US-09-060-939A-8	Sequence 8, Appli
7	3387	54.0	2082	US-09-293-505-9	Sequence 9, Appli
8	3387	54.0	2082	US-09-060-939A-9	Sequence 9, Appli
9	3349	53.4	5288	US-08-540-406-18	Sequence 18, Appl
10	3349	53.4	5288	US-08-656-055-18	Sequence 18, Appl
11	3349	53.4	5288	US-08-954-668-18	Sequence 18, Appl
12	3349	53.4	5288	US-08-918-658-18	Sequence 18, Appl

13	3349	53.4	5288	4	US-09-724-631-18	Sequence 18, Appl
14	3349	53.4	5288	4	US-08-954-701A-18	Sequence 18, Appl
15	3349	53.4	5288	5	PCT-US95-13233-18	Sequence 3, Appli
16	3337	53.2	5187	2	US-08-540-406-3	Sequence 3, Appli
17	3337	53.2	5187	2	US-08-540-406-3	Sequence 9, Appli
18	3337	53.2	5187	3	US-08-656-055-3	Sequence 3, Appli
19	3337	53.2	5187	3	US-08-656-055-9	Sequence 9, Appli
20	3337	53.2	5187	3	US-08-954-668-3	Sequence 3, Appli
21	3337	53.2	5187	3	US-08-954-668-9	Sequence 9, Appli
22	3337	53.2	5187	4	US-08-918-658-3	Sequence 3, Appli
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25	3337	53.2	5187	4	US-09-724-631-3	Sequence 9, Appli
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27	3337	53.2	5187	4	US-08-954-701A-9	Sequence 9, Appli
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29	3337	53.2	5187	5	PCT-US95-13233-9	Sequence 9, Appli
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31	2797.5	44.6	2032	3	US-09-500-063-1	Sequence 1, Appli
32	1972.5	31.4	3900	2	US-08-356-060A-42	Sequence 42, Appl
33	1972.5	31.4	3900	3	US-08-460-900C-42	Sequence 42, Appl
34	1972.5	31.4	3900	3	US-08-674-509B-42	Sequence 42, Appl
35	1972.5	31.4	3900	3	US-08-954-698-42	Sequence 42, Appl
36	1972.5	31.4	3900	3	US-08-957-874-42	Sequence 42, Appl
37	1972.5	31.4	3900	4	US-09-639-695-42	Sequence 42, Appl
38	1972.5	31.4	3900	4	US-09-448-188-42	Sequence 42, Appl
39	1972.5	31.4	3900	4	US-08-954-128-42	Sequence 42, Appl
40	1972.5	31.4	3900	4	US-08-954-740-42	Sequence 42, Appl
41	1972.5	31.4	3900	4	US-09-736-476-42	Sequence 42, Appl
42	1956	31.2	4434	2	US-08-540-406-5	Sequence 5, Appli
43	1956	31.2	4434	3	US-08-656-055-5	Sequence 5, Appli
44	1956	31.2	4434	3	US-08-954-668-5	Sequence 5, Appli
45	1956	31.2	4434	4	US-08-918-658-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-293-505-1
; Sequence 1, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 4030
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-293-505-1

Alignment Scores:
Pred. No.: 0
Score: 6272.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 4030
Matches: 1203
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-990-046-2 (1-1203) x US-09-293-505-1 (1-4030)

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Db 233 ATGACTCGATCGCCGCCCTCAGAGAGTGCCTCCGAGTTACACACCCCGACCTCGACC 292
QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuIysAlaProLeuTrpLeuArgAlaTyrPhe 40

Db 293 GCAGCACCAGATCCTAGCTGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 352
QY
41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe 60
Db 353 CAGGGCTGCTCTCTCTGGATCGGGATCCAGAGACATGTGGCAAGTGTCTTT 412
QY
61 LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr 80
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QY 521 IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
Db 1793 ATCCCTCGGCTGGAGCCTTCTCCCTACAGGCGGCGCATAGTGGTTGGCTGCACCTTGT 1852
QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
Db 1853 GCCGTGATGCTTCTTCCAGCCATCTCCAGCTGGACCTACGCGGCGGCGCACCTGCAG 1912
QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
Db 1913 CGCTTTGATGTCTGCTCTTCTCCAGTCCCTGCTGCTCAGGTGATTCAGATCCTG 1972
QY 581 ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
Db 1973 CCCACAGAGCTGGGAGCGGACAGTACAGTGGGCAATGGCCACCTCACTGCCACAGTT 2032
QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
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QY 661 LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu 680
Db 2213 CTGCCCTGTGCCGCTGGAACTTTGCCCATTTGCCCGCTATCAGTTGCGCGCTTGTG 2272
QY 681 LeuGlnSerHisAlaIysAlaIleValLeuValLeuPheGlyAlaLeuGlyLeuSer 700
Db 2273 CTCAGTCACTGCCAAGGCCATCGTGTGCTTCTTGGTGTCTTCTTGGGCTTGTAGC 2332
QY 701 LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly 720
Db 2333 CTCTACGGAGCCACTTGGTGCAAGCGGCTGGCCCTGCATGCGATGTGGTGCCTCGGGC 2392
QY 721 ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla 740
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QY 741 LeuValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis 760
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 DB 3653 CTTAGTGGGGGATCT 3712
 QY 1161 ThrValAlaIleHisPheProProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
 DB 3713 ACCGTGGCCATCCACCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3772
 QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
 DB 3773 CCCCCCTGGTCT 3832
 QY 1201 AlaThrGly 1203
 DB 3833 GCCACTGGG 3841
 RESULT 2
 US-09-060-939A-1
 ; Sequence 1, Application US/09060939A
 ; Patent No. 6709838
 ; GENERAL INFORMATION:
 ; APPLICANT: Frederic de Sauvage, David A. Carpenter
 ; TITLE OF INVENTION: Patched-2
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,939A
 ; FILING DATE: 15-Apr-1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39,044
 ; REFERENCE/DOCKET NUMBER: P1405
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4030 base pairs
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; US-09-060-939A-1
 Alignment Scores:
 Pred. No.: 0 Length: 4030
 Score: 6272.00 Matches: 1203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-990-046-2 (1-1203) x US-09-060-939A-1 (1-4030)
 QY 1 MetThrArgSerProProLeuArgGluLeuProSerTyrThrProAlaArgThr 20
 DB 233 ATGACTCGATCGCGCCCTCAGAGAGCTGCCCCGAGTTACACACCCCGAGCTCGAAC 292
 QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40

Db	293	GCAGCACCCACGATCCTAGCTGGAGCCTGAAGGCTCCACTCTGGCTTCGCTTACTTC	352	Db	1373	ACCACCTGGATACATCCTGCATCGCTTCTCTGAAGTCAGTGTGCCCGTGTGGTGGGA	1432
QY	41	GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyIysValLeuPhe	60	QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGln	420
Db	353	CAGGGCCCTGCTCTCTCTCTGGATGCGGGATCCAGAGACATTTGTGGCAAGTGTCTTTT	412	Db	1433	GGCTATCTGCTCATCTGGCCTATGCTGTGTGACCATGCTCGGTGGGACTGCGGCCAG	1492
QY	61	LeuGlyLeuLeuAlaPheGlyAlaLeuAlaLeuGlyLeuArgMetAlaIleIleGluThr	80	QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440
Db	413	CTGGGACTGTGGCCCTTTGGGCCCCCTGGCATTAGGTCCTCGCATGGCCATTATTGAGACA	472	Db	1493	TCCAGAGGTTCGCTGGGCTTTCGGGGTACTGCTGTGTGGCCCTGGCGGTGGCCTCAGGC	1552
QY	81	AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr	100	QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460
Db	473	AACTTGGACAGCTCTGGGTAGAGTGGCAGCCGGGTGAGCCAGAGCTGCATTACACC	532	Db	1553	CTTGGGCTCTGTGCCCTGTCTGGCATCACCTTCAATGTGCCACTACCCAGGTGTCTGCT	1612
QY	101	LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg	120	QY	461	PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu	480
Db	533	AAAGGAAGCTGGGGAGAGGCTGCATACACCTCTCAGATGCTGATACAGACCGCAGCG	592	Db	1613	TTCTTGGCTCTGGGAATCGGCGTGATGACGTATTCTCTCTGGCGCATCCCTTTCACAGAG	1672
QY	121	GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu	140	QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500
Db	593	CAGGAGGAGAGACATCTCTCACCCGAGAGCACTTGGGCTCCACCTCCAGGAGGCCCTC	652	Db	1673	GTCTGCTGGCAGCCCTCTCCAGGAGCGCATGGCGAGTGTCTGCAGCGCAGCGGCACC	1732
QY	141	ThrAlaSerIysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnIysIleCys	160	QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520
Db	653	ACTGCCAGTAAGTCCCAAGTATCACTCTATGGGAAGTCTCGGATTTGAACAAATCTGC	712	Db	1733	AGTGTCTACTCACATCCATCAACAACATGGCGGCTTCTCTCATGGCTGCCCTCGTCC	1792
QY	161	TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu	180	QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540
Db	713	TACAAAGTCAGGAGTTCCCTTATTGAAATGGAATGATTTGAGTGGATGATTGAGAAAGCTG	772	Db	1793	ATCCCTGGCCTCGAGGCTTCTCCCTACAGGGGCGCATAGTGGTGGCTGGACCTTTGTA	1852
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly	200	QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgArgHisCysGln	560
Db	773	TTTTCGTGGTGTATCTACCCCTCTCGACTGTCTTCTGGAGGGAGCCCAACTCCAAAGG	832	Db	1853	GGCGTGTGTGTCTTCCAGCCATCTCAGCCTGGACTACGGGCGGCCACTGCCAG	1912
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220	QY	561	ArgLeuAspValLeuCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db	833	GGCTCGCTACTCTGCCCGCGCGCGGATATCCAGTGGACCACTGGATCCAGAGCAG	892	Db	1913	CGCTTGATGTCTCTGTCTCTCCAGTCCCTGTCTGTCTCAGGTGATTGAGATCCTG	1972
QY	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240	QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
Db	893	CTGTGGAGGAGTGGGTCCCTTTGCTTCCCTTTAGGGCTTCCGGGAGCTGTAGACAAG	952	Db	1973	CCCCAGGAGCTGGGGAGCGGACATTACAGTGGGCAATGGCCCACTCTACTGCCAGATT	2032
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCys	260	QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	953	GCACAGTGGCGAGCCCTACGTGGGGCGGCCCTGTCTGCACCTGATCACTCCACTGC	1012	Db	2033	CAGGCTTTACCACTGTGAAGCCAGCAGCATGTGTTCACCATCTCTGCCCTCCCAA	2092
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db	1013	CCACCTAGTGTCCCCAACCATCACAGCAGCGAGGCTCCCAATGTGGCTCAGAGCTGAGT	1072	Db	2093	GCCCACTGGTGTGCCCTTCTGACCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGGG	2152
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuGly	300	QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660
Db	1073	GGGGGTGCGCATGGCTTCTCCACAAATTCATGCATGGCAGGAGAAATGTCTGTGGGA	1132	Db	2153	TCCACAGGGACCTCTAGGCCAGGAGGAGAGACAAGGCAAGGACACCTGCCAAGTCC	2212
QY	301	GlyMetAlaArgAspProGlnGlyLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320	QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
Db	1133	GGCATGGCCAGAGACCCCAAGAGAGCTGTGTAGGGGCGAGAGCCCTGCAGACCACTTC	1192	Db	2213	CTGGCTGTGCCGTGGAACTTGTCCCATTTGCCCCGTATCAGTTTCCCCCGTTGCTG	2272
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340	QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
Db	1193	TTGCTGATGAGTCCCCCGCAGCTGTACGAGCATTTCCGGGTGACTATCAGACACATGAC	1252	Db	2273	CTCCAGTCACATGCCAAGGCCATCTGTGTGTGTCTTTTGGTGTCTTCTGGGCCCTGAGC	2332
QY	341	IleGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgPheVal	360	QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGly	720
Db	1253	ATTGGCTGGAGTGAGAGCAGGCCACGACAGTGTCTAAAGCCTGGCGAGCGGGCTTTGTG	1312	Db	2333	CTCTACGGAGCCACCTTGTGTGAGAGCGCCCTGGCCCTGACGGATGTGTGTCTCGGGC	2392
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380	QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
Db	1313	CAGCTGGCCCCAGAGGCCCTGCTGAGACGCTTCCAGCAGATCCATGCCTTCTCTCTC	1372	Db	2393	ACCAAGGAGCATGCCTTCTCGAGCGCCAGCTCAGGTACTTCTCTCCCTGTACGAGGTGCC	2452
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400	QY	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760
Db				Db	2453	CTGGTGACCCAGGGTGGCTTTGACTACGCCCATTCACAAACGCGCCCTCTTTGATCTGCAC	2512

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QY 761 GluArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr 780
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RESULT 3
US-09-207-857-1
; Sequence 1, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-207-857-1

Alignment Scores:
Pred. No.: 0 Length: 4391
Score: 6248.00 Matches: 1200
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 3 Gaps: 0

US-09-990-046-2 (1-1203) x US-09-207-857-1 (1-4391)

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Db 357 GCAGCACCCAGATCCTAGCTGGGAGCCTGAAGGCTCCACTCTGGCTTCGTGCTTACTTC 416
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 417 CAGGCGCTGCTCTTCTCTCTGGGATGGCGATCCAGAGACATTTGTGCAAAAGTCTCTTT 476
QY 61 LeuGlyLeuLeuAlaPheGlyValAlaLeuAlaLeuGlyLeuArgMetAlaIleGluThr 80
Db 477 CTGGAGCTTTGGCTTTGGGCGCTTGGCGCTTGGCATTAGCTTCCCGATGGCCATTATTAGACA 536
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 537 AACITGGAACAGCTCTGGGTAGAGTGGGACCGCGGTGAGCCAGGAGCTGCATTACACC 596
QY 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
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Db 2997 CCAGCTCAGCCCTGGAGTTGGCCAGTTCCCTTCTCTGCGTGGCCCTCCAGAAAGCT 3056
QY 921 AlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAla 940
Db 3057 GCAGACTTTGTGGAGGCCATCGAGGGGCCCGGGCAGCATGCCGAGAGCGCGCCAGGCT 3116
QY 941 GlyValHisAlaTyrProSerGlySerProPheLeuPheThrProGluGlnTyrLeuGlyLeu 960
Db 3117 GGGGTGCACCCCTACCCAGCGCTCCCCCTTCTCTCTGGGAACAGTATCTGGGCGCTG 3176
QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
Db 3177 CGCGCTGCTCTCTGCTGGCCGTCTGCATCTCTGTGTGCACTTTCTCTGTGTGCT 3236
QY 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetThr 1000
Db 3237 CTGCTGCTCTCAACCCCTGGATGGTGGCTCATAGTGTGCTGCTGGCGATGATGACA 3296
QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
Db 3297 GTGGAACTCTTTGGTATCATGGGTTCCTGGGGCATCAAGCTGAGTGCATCCCGCGTGGT 3356
QY 1021 IleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPhe 1040
Db 3357 ATCCTTTGGCCCTCTAGGCATTTGGCTTGGTTCACAGTCCAGTGTGCTTGGGCTTC 3416
QY 1041 LeuThrThrGlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAla 1060
Db 3417 CTGACCACCCAGGCGAGCGGAACCTGCGGGCGCCCATGCCCTTGAGCACACATTTGCC 3476
QY 1061 ProValThrAspGlyAlaIleSerThrLeuLeuGlyLeuMetLeuAlaGlySerHis 1080
Db 3477 CCCGTGACCATGGGGCCATCTCCACATTTGCTGGGTCTGCTCATGCTTGTGTTCCAC 3536
QY 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeu 1100
Db 3537 TTTGACTTCATTGTAAAGTACTTCTTTGGGGCTGTGACAGTCTACGCTCTCTGGGCCCTC 3596
QY 1101 LeuHisGlyLeuValLeuLeuProValLeuLeuSerIleLeuGlyProProGluVal 1120
Db 3597 CTCCATGGACTCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 3656
QY 1121 IleGlnMetTyrLysGluSerProGluIleLeuSerProProAlaProGlnGlyGly 1140
Db 3657 ATACAGATGTACAAGAAAGCCAGAGATCTCTGAGTCCACAGCTCCACAGGGAGCGGG 3716
QY 1141 LeuArgTGTpGlyAlaSerSerLeuProGlnSerPheAlaArgValThrThrSerMet 1160
Db 3717 CTTAGGTGGGGGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3776
QY 1161 ThrValAlaIleHisProProLeuProGlyAlaTyrIleHisProAlaProAspGlu 1180
Db 3777 ACCGTGGGCATCAACCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3836
QY 1181 ProProTrpSerProAlaAlaThrSerSerGlyAsnLeuSerSerArgGlyProGlyPro 1200
Db 3837 CCCCTTGGTCCCTGCTGCACTAGCTCTGGCAACCTCAGTTCCAGGGGACCAAGTCCA 3896
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QY 1201 AlaThrGly 1203
Db 3897 GCCACTGGG 3905
RESULT 4
US-09-909-280A-1
; Sequence 1, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(3905)
US-09-909-280A-1
Alignment Scores:
Pred. No.: 0 Length: 4391
Score: 6248.00 Matches: 1200
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 3
Query Match: 99.62% Indels: 0
DB: 4 Gaps: 0
US-09-990-046-2 (1-1203) x US-09-909-280A-1 (1-4391)
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QY 21 AlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProLeuTrpLeuArgAlaTyrPhe 40
Db 357 GCAGCACCCACAGATCTAGCTGGGAGCTGAGGGCTCCACTCTGGCTTCTGCTTACTTC 416
QY 41 GlnGlyLeuLeuPheSerLeuGlyCysGlyIleGlnArgHisCysGlyLysValLeuPhe 60
Db 417 CAGGGCCTGCTCTCTCTCTGGGATCGGGATCCAGAGACATTGTGGCAAGTGCTCTTT 476
QY 61 LeuGlyLeuLeuAlaPheGlyValAlaLeuAlaLeuGlyLeuArgMetAlaIleLeuThr 80
Db 477 CTGGAGACTGTGTGGCTTTGGGGCCCTTGGCATTTAGTCTCCGATCGCCATTATTAGACA 536
QY 81 AsnLeuGluGlnLeuTrpValGluValGlySerArgValSerGlnGluLeuHisTyrThr 100
Db 537 AACTTGGAAACAGCTCTGGGTAGAGTGGGACCGGGGTGAGCCAGAGAGCTGTATTACACC 596
QY 101 LysGluLysLeuGlyGluGluAlaTyrThrSerGlnMetLeuIleGlnThrAlaArg 120
Db 597 AAGGAGAAAGCTGGGGAGAGAGCTGCATACACCTCTCAGATGCTGATACAGACCCGACGC 656
QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
Db 657 CAGAGGAGAGAGACATCTCACACCCGAGACATTTGGCCCTCCACCTCCAGGAGCCCTC 716
QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 717 ACTGCCAGTAAGTCCAAGTATCACTCTATGGGAGAGTCTCTGGGATTTGAACAAATCTGC 776
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
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Db	777	TACAAAGTCAGGAGTTCCTCCCTTATGAAATGAATGATTTGACGGAGTGTGAGAGCTG	836	Db	1857	ATCCCTCGCGCTCGGAGCTTCTCCCTACAGGGGGCCATAGTGGTGGCTGCACCTTTGTA	1916
QY	181	PheProCysValIleLeuThrProLeuAspCysPheTIPGluGluAlaLysLeuGlnGly	200	QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560
Db	837	TTTCCGTGGTGATCTCTACCCCTCGCTGCTCTGGAGGGAGCCAAACTCCAAAGG	896	Db	1917	GCGTGTGATGTCTTCCAGCCATCTTCAGCTTGAGCTTACGGGGGGCCACTGCCAG	1976
QY	201	GlySerAlaTyrLeuProGlyArgProAspIleGlnTIPTrpAsnLeuAspProGluGln	220	QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
Db	897	GGCTCCGCTACCTGCCCGCGCCCGGATATCCAGTGAGCAACCTGGATCCAGAGCAG	956	Db	1977	CGCCTTGATGTCTCTGCTGCTTCTCCAGTCCCTGCTGCTCAGGTGATTCAGATCCTG	2036
QY	221	LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240	QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
Db	957	CTGCTGGAGAGCTGGGTCTCTTTGCTCTCTGAGGGCTTCGGAGGTCTGTAGACAAG	1016	Db	2037	CCCCAGGAGCTGGGGACCGGACAGTACACAGTGGGCANTGCCACCTCACTGCCAGATT	2096
QY	241	AlaGlnValGlyGlnAlaTyrValGlyArgProCysLeuHisProAspAspLeuHisCys	260	QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln	620
Db	1017	GCACAGGTGGCCAGGCTAGTGGGGGCGCCCTGTCTGCACCCTGATGACCTCCACTGC	1076	Db	2097	CAAGCCTTTACCCACTGTGAGGCCAGCAGCATGTGTCACCATCTGCTCTCCCAA	2156
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	QY	621	AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly	640
Db	1077	CCACCTAGTGCCTCCCAACCATACAGCAGCAGGCTCCCAATGTGCTCACGAGCTGAGT	1136	Db	2157	GCCCACTGTGTGCCCCCACTTCTGACCCACTGGGCTCTGAGCTCTTCAGCCCTGGAGG	2216
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMetHisTIPGlnGluLeuLeuLeuGly	300	QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaLysLysSer	660
Db	1137	GGGGGCTGCCATGGCTTCTCCCAAAATTCATGCATCGCAGAGGAAATTGCTGTGGGA	1196	Db	2217	TCCACACGGGACCTTCTAGGCCAGGAGGAGACAAAGCAGAGCAGCCTCAAGTCC	2276
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPhe	320	QY	661	LeuProCysAlaArgTIPAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeu	680
Db	1197	GGCATGGCCAGACACCCCAAGGAGAGCTGCTGAGGGCAGAGGCCCTGCAGACACCTTC	1256	Db	2277	CTGCCCTGTGCCCGCTGGAACTTTCGCCATTTCCCGCGCTATCAGTTTCCCCGTTGCTG	2336
QY	321	LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp	340	QY	681	LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer	700
Db	1257	TTCTCTGATGATCCCGCCAGCTGTACGACATTTCCGGGGTGACTATCAGACACATGAC	1316	Db	2337	CTCCAGTCAATGCCAAGGCCATCTGCTGTGTCTCTTGGTGTCTCTTCTGGGCTGAGC	2396
QY	341	IleGlyTIPSerGluGluGlnAlaSerThrValLeuGlnAlaTIPGlnArgPheVal	360	QY	701	LeuTyrGlyAlaThrLeuValGlnAspGlyLeuAlaIleuThrAspValValProAspGly	720
Db	1317	ATTGGCTGGAGTGAGGAGCGCCAGCACAGTGTCTACAAGCTGGCAGCGCGCTTGTG	1376	Db	2397	CTCTACGGAGCCACTTGTGTGAAGCGGCTGGCCCTGACGATGTGGTGCTCGGGC	2456
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380	QY	721	ThrLysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAla	740
Db	1377	CAGCTGCCCCAGGAGGCCCTGCCTGAGAACGCTTCCAGCAGATCCATGCTTCTCTCC	1436	Db	2457	ACCAAGAGCATGCTTCTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGCC	2516
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400	QY	741	LeuValThrGlnGlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHis	760
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QY	401	GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTIPAspCysAlaGln	420	QY	761	GlnArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThr	780
Db	1497	GGCTATCTGCTCATGCTGGCTATGCTGTGACCATGTGCGGTGGACTGCGCCAG	1556	Db	2577	CAGCGCTTCAGTTCCCTCAAGCGCGTGTGCCCCCACCGGCCACCCAGGACCCCGCACC	2636
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaSerGly	440	QY	781	TIPLeuHisTyrTyrArgAsnTIPLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTIP	800
Db	1557	TCCAGGAGTTCCGAGGGGCTTGGCGGGGTACTGTGTGGGCTTGGCGGTGGCTCAGGC	1616	Db	2637	TGGCTGGCATTATACCGCAACTGGCTACAGGGAATCCAGGCTGCTTGTGACAGACTGG	2696
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460	QY	801	AlaSerGlyArgIleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAla	820
Db	1617	CTTGGGCTGTGTGCTGCTCGGATCACCTTCAATGTGCTGCTACCCAGGCTGCTGCC	1676	Db	2697	GCCTTCTGGCGCATCACCCGCACTCGTACCGCAATGGCTCTGAAGATGGGCGCTGGCC	2756
QY	461	PheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHisAlaPheThrGlu	480	QY	821	TyrLysLeuLeuIleGlnThrGlyAspAlaGlnLIPLeuProLeuAspPheSerGlnLeuThr	840
Db	1677	TTCTTGGCTCTGGAAATCGGGCTGGATGACGTATTCCTGTGCTGGCGCATGCTTCCAGAG	1736	Db	2757	TACAAGCTGTCTATCCAGACTGGAGCGCCAGAGGCTCTGGAATTTACGCCAGCTGACC	2816
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QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520	QY	861	ThrValTIPValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrPro	880
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QY 838 ---GlnLeuThrThrArgLysLeuValAspArgGluGlyLeuIleProProGluLeuPhe 856
Db 2750 CTGAGCTGACCAAGAAGAGCTGGTGACAGAGAGGAGCTGATCCACCGAGCTCTTC 2809
QY 857 TyrMetGlyLeuThrValTTPValSerSerAspProLeuGlyLeuAlaSerGlnAla 876
Db 2810 TACATGGGCTGACCGTGGTGAGCAGTGACCCCTGGGTCTGGGAGCTTCACAGGCC 2869
QY 877 AsnPheTyrProProProGluThrLeuHisAspLysTyrAspThrThrGlyGluAsn 896
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QY 897 LeuArg----- 898
Db 2930 CTTGCAGTGAGTCTTGGGGGAGCTCGGCAAGAGCCTCAGCCTCGCCCCACACAGCCCT 2989
QY 898 ----- 898
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QY 899 -----lleProAlaGlnProLeuGluPheAlaGlnPheProPh 912
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QY 912 eLeuLeuArgGlyLeuGlnLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAl 932
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QY 932 aAlaCysAlaGluAlaGlyGlnAlaGlyValHisAlaTyrProSerGlySerProPheLe 952
Db 3170 AGCATGGCAGAGCGCGCAGCTGGGGTGCACGGCTACCCCGAGGGCTCCCTCTCTCT 3229
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QY 992 e----- 992
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QY 1019 alValIleLeuValAlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuG 1039
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RESULT 6

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US-09-060-939A-8
; Sequence 8, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

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; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060, 939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4004 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; US-09-060-939A-8

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Alignment Scores:
Pred. No.: 0 Length: 4004
Score: 3955.00 Matches: 847
Percent Similarity: 65.81% Conservative: 2
Best Local Similarity: 65.66% Mismatches: 10
Query Match: 63.06% Indels: 434
DB: 4 Gaps: 10

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US-09-990-046-2 (1-1203) x US-09-060-939A-8 (1-4004)

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QY 121 GlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyLeuHisLeuGlnAlaLeu 140
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QY 141 ThrAlaSerLysValGlnValSerLeuTyrGlyLysSerTrpAspLeuAsnLysIleCys 160
Db 131 ACTGCCAGTAAAGTCCAGTATCACTATATGGAGTCTCTGGAGTCTGGAATAATCTGC 190
QY 161 TyrLysSerGlyValProLeuIleGluAsnGlyMetIleGluTrpMetIleGluLysLeu 180
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QY 181 PheProCysValIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGly 200
Db 251 TTTCCGTGCGTATCTCTCACCCCTCTGACTCTCTTGGAGGGAGCCAACTCCAGGG 310
QY 201 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln 220
Db 311 GGCTCCGCTACCTGCCCT----- 330
QY 221 LeuLeuGluGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys 240
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QY 301 GlyMetAlaArgAspProGlnGlyLeuLeuLeuArgAlaGluAlaLeuGlnSerThrPhe 320
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QY 321 LeuLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAsp 340
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QY 341 IleGlyTyrSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArgPheVal 360
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QY 360 ----- 360
Db 595 CAGGTCGGTATGGAAGAGACAGGGGGTCCCTGAGGCCATTCCTCTCTCCGCCCT 654
QY 361 -----GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnI 374
Db 655 CCTATCCACCTGTTCTCAGCTGGCCAGAGGCCCTGCTGAGAACGCTTCCAGCA 714
QY 374 nileHisAlaPheSerSerThrThrLeuAspAspIleLeuHisAlaPheSerGluValse 394
Db 715 GATCCATGCTTCTCTCCACACCCCTGGATGATCATCTGCATGCGTCTCTCTGAAGTCAG 774
QY 394 rAlaAlaArgValValGlyGlyTyrLeuLeuMet----- 405
Db 775 TGTGCCCGGTGTGGAGGCTATCTGCTCATGTGGGTCTTGCACTGGCACCTGGCACCTTGCC 834
QY 405 ----- 405
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QY 406 ----LeuAlaTyrAlaCysValThrMetLeuArgTyrAspCysAlaGlnSerGlnGlyse 424
Db 895 ACAGCTGGCCATATGCTGTGTGACCATGCTGCGGTGGGACTGGGCCCCAGTCCAGGGTTC 954
QY 424 rValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCy 444
Db 955 CGTGGGCTTGGCCGGGTACTGCTGTGTGGCCCTGGCGGTGGCCCTCAGGCTTGGGCTCTG 1014
QY 444 sAlaLeuLeuGlyIleThrPheAsnAlaAlaThr----- 456
Db 1015 TGCCTGCTCGGCATCACCTTCAATGTGCGCACTTACCAGGTACGCCAGGACTGCAGGGC 1074
QY 457 -----G 457
Db 1075 AGACTCAGTGCCAGTCACACAGGCTTCACGGGTCTCAGCTGCCCGCTCCTTGCCCTCC 1134
QY 457 lnValLeuProPheLeuAlaGlyIleGlyValAspAspValPheLeuLeuAlaHisA 477
Db 1135 AGGTCGTGCCCTTCTTCACTCTGGAAATCGCGTGGATGACGATTCCTGCTGGCGCATG 1194
QY 477 laPheThrGluAlaLeuProGlyThr----- 485
Db 1195 CCTTCACAGAGGCTCTGCTGGCACCCCTCTCCAGGTGGGCGCTTGTCCCCAGGGGTCA 1254
QY 485 ----- 485
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QY 486 -----ProLeuGlnGluArgMetGlyGlyCysLeuGlnArgThrGlyT 500
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QY 500 hrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValP 520
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QY 520 roileProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheV 540
Db 1674 CCATCCCTGCGCTGCGAGCTTCTCC----- 1699
QY 540 alAlaValMetLeuValPheProAlaIleLeu--SerLeuAspLeuArgArgHisCys 559
Db 1700 -----CTACAGCCTGGACCTACGGCGGCCACTGC 1730
QY 560 GlnArgLeuAspValLeuCysCysPheSer----- 569
Db 1731 CAGCGCTTGTGTGTCTGCTGCTTC--CAGGTACTGCTGGCGCCAGCCCCCTTCCT 1789
QY 569 ----- 569
Db 1790 CCGGTGACCCACGCCAGCCTGCTCCCTCACCAGCATTTCAAGGCACACAGACTGTCTATCCA 1849
QY 570 -----SerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 1850 CTCTCTACCTTCTCCAGTCCCTGCTGTCTCAGTGATTCAGATCTGCCCCAGGAGCTG 1909
QY 585 GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr 604
Db 1910 GGGAGCGGACAGTACAGTGGCANTGCCACCTCCTCAGTCCACAGTTCAGGCTTTACC 1969
QY 605 HisCysGluAlaSerSerGlnHisValValThrIleLeuProGlnAlaHisLeuVal 624
Db 1970 CACTGTGAAGCCAGCAGCAGCATGTGGTCAACATCTCTGCTCCCAAGCCACCTGGTG 2029
QY 625 ProProSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2030 CCCCCACCTTCTCACCACCTGGGCTCTGAGCTCTTACGCCCTGGAGGCTCCACAGGAC 2089
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2090 CTTCTAGCCAGAGGAGGAGACAGGCAGAGGACCTGCAAGTCCCTGCCCTGTGCC 2149
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2150 CGCTGGAATCTTGCCCAATTTGCCCGCTATCAGTTTCCCCGTTGTGCTCCAGTCACT 2209
QY 685 AlalysAlaIleValLeuValPheGlyValAlaLeuGlyLeuSerLeuGlyVala 704
Db 2210 GCCAAGGCCATCGGTGGTGTCTTTGGTGTCTTCTGGGCTTACGCTTCTACGGAGCC 2269
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
Db 2270 ACCTTGTGCAAGAGCGCTTGGCCCTGACGATGTGTGCTCGGGGCACCAAGGAGCAT 2329
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2330 GCCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGTACGAGGTGGCCCTGTGTCACCCAG 2389
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2390 GGTGGCTTGTACTAGGCCCTCTCCAAAGCGGCCCTCTTTGATCTGCACAGCGCTTCAGT 2449

QY	181	PheProCysValIleLeuThrProLeuAspCysPheTrpClnGlyAlaLysLeuGlnGly	200	Db	1600	-----ATCCTCAGCCTGGACCTACGGGGGGCCACTGCCAG	1635
Db	548	TTTCCCTGGGTGATCTCAACCCCTTCGACTGCTTCTGGAGGGAGCCAACTCCAAAGGG	607	QY	561	ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu	580
QY	201	GlySerAlaIleLeuProGlyArgProAspIleGlnTrpThrAsnLeuAspProGluGln	220	Db	1636	CGCCTTGATGTGCTCTGCTGCTTCCAGTCCCTGCTGCTCAGGTGATTCCAGATCCTG	1695
Db	608	GGCTCCGGCTACTGTCGGCGCCGCCGGATATCCAGTGGACCAACCTGGATCCAGAGCAG	667	QY	581	ProGlnGluLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal	600
QY	221	LeuLeuGluGlnLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLys	240	Db	1696	CCCCAGAGCTGGGACCGGACAGTACAGTGGGATTCGCCACCTCACTGCCACAGTT	1755
Db	668	CTGCTGGAGGAGCTGGGTCTCTTTCCTCCCTTGGAGGGCTTCGGGAGCTGTAGACAAG	727	QY	601	GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProProGln	620
QY	241	AlaGlnValGlyGlnAlaIleValGlyArgProCysLeuHisProAspAspLeuHisCys	260	Db	1756	CHAGCCTTTACCCACTGTGAAGCCAGCAGCAGCATGTGTCCACCATCTCTGCTCCCCAA	1815
Db	728	GCACAGTGGCGGCGAGGCTACGTGGGCGGCCCTGTCTGCACCTGATGACCTCCACTGC	787	QY	621	AlaHisLeuValProProProSerAspProLeuGlySerClnLeuPheSerProGlyGly	640
QY	261	ProProSerAlaProAsnHisHisSerArgGlnAlaProAsnValAlaHisGluLeuSer	280	Db	1816	GCCACCTGTGTGCCCCCACTTCTGACCCCACTGGGTCTGAGCTCTTCAGCCCTGGAGGG	1875
Db	788	CCACCTAGTGCCTCCCAACCATCACAGCAGCAGGCTCCCAATGTGGCTCACGAGCTGAGT	847	QY	641	SerThrArgAspLeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSer	660
QY	281	GlyGlyCysHisGlyPheSerHisLysPheMethIleTrpGlnGluGluLeuLeuGly	300	Db	1876	TCCACACGGGACCTTTAGCCAGGAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGTCC	1935
Db	848	GGGGGTGCTGCTTCTCCCAAAATTCATGCTACCTGCGCAGGAGGAAATTCCTGCTGGA	907	QY	661	LeuProCysAlaArgTrpAsnLeuAlaHisPheAlaArgTrpGlnPheAlaProLeuLeu	680
QY	301	GlyMetAlaArgAspProGlnGlyGluLeuArgAlaGluAlaLeuGlnSerThrPhe	320	Db	1936	CTGCCCTGTGCCCTGGAAATCTTGCCCAT-----TTCGGCCCGGAATTC	1980
Db	908	GGCATGCCAGAGACCCCAAGGAGAGCTGCTGAGGGCAGAGGCTTCGACAGCACCTTC	967	QY	681	LeuGln 682	
QY	321	LeuLeuMetSerProArgGlnLeuTrpGluHisPheArgGlyAspTrpGlnThrHisAsp	340	Db	1981	CTGCAG 1986	
Db	968	TTGCTGATGATCCCGCCAGCTGTACGAGCATTTCCGGGTGACTATCAGACACATGAC	1027	RESULT 8			
QY	341	IleGlyTrpSerGluGluGlnAlaSerThrValLeuGlnAlaIleThrGlnArgPheVal	360	US-09-060-939A-9			
Db	1028	ATTGGCTGGAGTAGGAGCAGGCGCAGCACAGTGTCTACAAGCCTGGCAGCGCGCTTTGTG	1087	; Sequence 9, Application US/09060939A			
QY	361	GlnLeuAlaGlnGluAlaLeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSer	380	; Patent No. 6709838			
Db	1088	CAGCTGGCCAGGAGGCGCTCCCTGAGAACCGCTTCCAGCAGATCCATGCTCTCTCTCC	1147	; GENERAL INFORMATION:			
QY	381	ThrThrLeuAspAspIleLeuHisAlaPheSerGluValSerAlaAlaArgValValGly	400	; APPLICANT: Frederic de Sauvage, David A. Carpenter			
Db	1148	ACCACCTGGATACATCTGATCGTCTCTGAGTCACTGTCGCCGCTGGTGGGA 1207	1207	; TITLE OF INVENTION: Patched-2			
QY	401	GlyTrpLeuLeuMetLeuAlaIleAlaCysValThrMetLeuArgTrpAspCysAlaGln	420	; NUMBER OF SEQUENCES: 32			
Db	1208	GGCTATCTGCTCATGCTGGCCTATGCTGTGACCATGCTGCGGTGGGACTGCGGCCAG	1267	; CORRESPONDENCE ADDRESS:			
QY	421	SerGlnGlySerValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGly	440	; ADDRESSEE: Genentech, Inc.			
Db	1268	TCCAGGGTTCCGTGGGCTTTCGGGGGTACTGCTGGTGGCCCTGGCGGTGGCTCAGGC	1327	; STREET: 1 DNA Way			
QY	441	LeuGlyLeuCysAlaLeuLeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuPro	460	; CITY: South San Francisco			
Db	1328	CTTGGGCTCTGCTGCTGCTGCGCATCACTTCAATGCTGCCACTACCCAGGTCTGCC	1387	; STATE: California			
QY	461	PheLeuAlaLeuGlyIleGlyValAspAspValPheLeuLeuAlaHisAlaPheThrGlu	480	; COUNTRY: USA			
Db	1388	TTCTTGGCTCTGGGAATCGCGGTGATGACGTATTCTCTGCTGGGCGCATGCCCTTCACAG	1447	; ZIP: 94080			
QY	481	AlaLeuProGlyThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThr	500	; COMPUTER READABLE FORM:			
Db	1448	GCTCTGCTGGACCCCTCTCCAGGAGCGCATGGCGAGTGTCTGCAGCGCAGCGGCAC	1507	; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
QY	501	SerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValPro	520	; COMPUTER: IBM PC compatible			
Db	1508	AGTGTGCTGACTCATCATCAACACATGGCGGCTTCTCTCATGCTGCTGCTGCTGCT	1567	; OPERATING SYSTEM: PC-DOS/MS-DOS			
QY	521	IleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal	540	; SOFTWARE: WinPatin (Genentech)			
Db	1568	ATCCCTGGCTGCGAGCCTTCTCTTACAGC-----	1599	; CURRENT APPLICATION DATA: US/09/060,939A			
QY	541	AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln	560	; APPLICATION NUMBER: 15-Apr-1998			
				; FILING DATE: 15-Apr-1998			
				; CLASSIFICATION: 435			
				; ATTORNEY/AGENT INFORMATION:			
				; NAME: Svoboda, Craig G.			
				; REGISTRATION NUMBER: 39,044			
				; REFERENCE/DOCKET NUMBER: P1405			
				; TELECOMMUNICATION INFORMATION:			
				; TELEPHONE: 650/225-1489			
				; TELEFAX: 650/952-9881			
				; INFORMATION FOR SEQ ID NO: 9:			
				; SEQUENCE CHARACTERISTICS:			
				; LENGTH: 2082 base pairs			
				; TYPE: Nucleic Acid			
				; STRANDEDNESS: Double			
				; TOPOLOGY: Linear			
				US-09-060-939A-9			
				Alignment Scores:		1.54e-308	
				Pred. No.:		3387.00	
				Score:		Length: 2082	
						Matches: 656	

RESULT 9

US-08-540-406-18
 ; Sequence 18, Application US/08540406
 ; Patent No. 5837538
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,406
 ; FILING DATE: 06-OCT-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-540-406-18

Alignment Scores:
 Pred. No.: 2,75e-304 Length: 5288
 Score: 3349.00 Matches: 662
 Percent Similarity: 70.02% Conservative: 200
 Best Local Similarity: 53.78% Mismatches: 298
 Query Match: 53.40% Indels: 71
 DB: Gaps: 16

US-09-990-046-2 (1-1203) x US-08-540-406-18 (1-5288)

QY	12	ProSerThrProProAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeu---	30
DB	540	CCCGCTACTGCGCTTGGCTCTGGAGCAGATTTCCAAAGGGGAGGCTACT	596
QY	31	-----LysAlaProLeuThrProLeuArgAlaTyrPheGlnGlyLeuLeuPheSerLeuGly	48
DB	597	GGCGGAAAGCGCACTGTGGCTGAGAGCGAAAGTTTCAGAGACTCTTTATTAAACTGGGT	656
QY	49	CysGlyIleGlnArgHisCysGlyLysValLeuPheLeuGlyLeuAlaPheGlyVala	68
DB	657	TGTTACATTCAAAAACCTGGCGCAAGTTCTTGGTTGGGGCTCTCATATTGGGGCC	716
QY	69	LeuAlaLeuGlyLeuArgMetAlaIleIleGlnThrAsnLeuGlnLeuThrProValGlu	88
DB	717	TTCCGCGTGGATTAAAGCAGCGAACCCTGAGACCAACCTGGAGGAGCTGTGGGTGAA	776
QY	89	ValGlySerArgValSerGlnGlnLeuHisTyrThrLysGlnLysLeuGlyGluGluAla	108
DB	777	GTTGGAGGAGGAGTAAGTCGTGAATAAATTATATCTCGCCAGAGATTTGGAGAGAGGCT	836
QY	109	AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr	128
DB	837	ATGTTTAAATCCTCACTCATGATACAGACCCCTAAAGAAGAGGTCTATGTCCTGACC	896
QY	129	ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer	148
DB	897	ACAGAAGCGCTCTCAACACCTGGACTCGGCACTCCAGGCCCGCTGCCATGTATATAC	956
QY	149	LeuTyrGlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValProLeuIle	168
DB	957	ATGTACACAGCGAGTGGAAATTTGGAACATTTGTGTTCAAAATCAGAGAGCTTATACA	1016
QY	169	GluAsnGlyMetIleGlnTrpMetIleGluLysLeuPheProCysValIleLeuThrPro	188
DB	1017	GAAACAGGTTACATGATCAGATAATAGATATCTTTACCTTGTGTTGATTATTACACT	1076
QY	189	LeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTyrLeuProGlyArg	208
DB	1077	TTGGACTGCTTCTGGGAAGGGCGAAATACAGTCTGGGACAGCATACCTCTAGGTAA	1136
QY	209	ProAspIleGlnTrpThrAsnLeuAspProGluGlnLeuLeuGluGlyProPhe	228
DB	1137	CCTCCTTTGCGGTGGACAACTTCGACCCCTTTGGAATCTCTGGAAGATTAAGAAATA	1196
QY	229	--AlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyr	247
DB	1197	AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGGCTGAGTTGTCATGTTAC	1256
QY	248	ValGlyArgProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHis	267
DB	1257	ATGGACCGCCCTGCTCAATCCGCGCATCCAGACTGCCCGCCACAGCCCAACAAA	1316
QY	268	HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyCysHisGlyPheSer	287
DB	1317	AATCAACCAACCTCTGATATGGCCCTTTTGAATGGTGATGTCATGCTTATCC	1376
QY	288	HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln	307
DB	1377	AGAAAGTATATGCACTGGCAGGAGGAGTTGATTGGTGGTGGCACAGTCAAGACGCACT	1436
QY	308	GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln	327
DB	1437	GGAAAACTGTCAGCGCCCATGCTGCGACCATGTTCCAGTTAATGATCTCCCAAGCAA	1496
QY	328	LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu	346
DB	1497	ATGTACGAGCACTTCAGGGGTACAGATATGCTCACAC---ATCACTGGACGAGGAC	1553
QY	347	GlnAlaSerThrValLeuGlnAlaTyrGlnArgPheValGlnLeuAlaGlnGluAla	366
DB	1554	ANAGCGCAGCCATCTGGAGGCTGGCAGAGCAGATATATGGAGGTGGTTTCATCAGAT	1613
QY	367	LeuProGluAsnAlaSerGlnIleHisAlaPheSerSerThrThrLeuAspAspIle	386
DB	1614	GTCCGACAGAACTCCACTCAAAAGGTGCTTCTCCACACCAAGCCCTGGAGCAGATC	1673
QY	387	LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406
DB	1674	CTGAATCTCTCTGACCTGATGTCATCCGGTGGCCAGCGGCTACTTACTCATGCTC	1733
QY	407	AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly	426
DB	1734	GCCTATGCTGTCTAACTGCTGCGCTGGGACTGCTCCAAAGTCCCAAGGTGGCGTGGG	1793
QY	427	LeuAlaGlyValLeuLeuValAlaLeuAlaValaSerGlyLeuGlyLeuGlyAlaLeu	446
DB	1794	CTGGCTGGCTCTCTGCTGTTGCACTGTCAGTGGCTGAGACTGGGCGCTGTGCTCATG	1853
QY	447	LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle	466
DB	1854	ATCGGAATTCCTTTAAACGCTGCACACTCAGGTTTGGCAATTTCTCGCTCTTGGTGT	1913
QY	467	GlyValAspAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----	484

Db 1914 GGTGTGGATGATGTTTCTTCTGGCCACCGCTTCAGTGAACAGGACAGATAAAGA 1973
QY 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGGCAGCAGACCGGGGAGTGCCTGAAGCGCAGGAGCCAGCGTGCCTC 2033
QY 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
Db 2034 ACCTCCATCAGCAATGTCACAGCTTCTTCATGGCGGTATCCCAATCCCGCTCTG 2093
QY 525 ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu 544
Db 2094 CGGGCGTTCCTCCCTCAGCAGCGGTAGTGTAGTGGTTCATTTTGGCCATGGTTCGTCTC 2153
QY 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
Db 2154 ATTTTCTGCTCAATTCCTCAGCATGATTTATCGACCGGAGCAGGAGACTGGATATT 2213
QY 565 LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
Db 2214 TTCTGCTGTTTACAAAGCCCTGCGTCAGCAGAGTGTTCAGGTGGAACCTCAGGCCTAC 2273
QY 595 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
Db 2274 ACCGACACACGACAATACCGCTACAGCCCCCACCCTCCCTACAGCAGCCACAGCTTT 2333
QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
Db 2334 GCCCATGAACGCGAATTACCATCGAGTCCACTCTCCAGCTCCGCGAGTACGAGCC 2393
QY 609 SerSerGlnHisValThrIleLeuProGlnAlaHisLeuValProPro----- 627
Db 2394 CACAGCAGCGTGTACTACACCACCGCTGAGCGCGCTCCGAGATCTCTGTGCACCCGTC 2453
QY 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCCCTCAGCTGCCAGAGCCAGAGCACCAGCTCCACAGGGAC 2513
QY 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
Db 2514 CTGCTCTCCAGTGTCTCCGACTCC-----AGCTCCACTGCTCGAGCCCCCTGTACG 2567
QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2568 AAGTGGACATCTCATCTTTGCTGAGAAGCACTATGCTCTTCTCTTGAACCAAA 2627
QY 685 AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla 704
Db 2628 GCCAAGGTAGTGTGATCTCTTTCTGGGCTTGCTGGGGTACGCTTTATGGCACC 2687
QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValProArgGlyThrLysGluHis 724
Db 2688 ACCGAGTGAAGACGGCTGGACCTTACGGAATGTATCTCGGAAACAGAGAATAT 2747
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATTGCTGCACAAATCAATACTTTCTTCTACAAATGATATAGTACCCAG 2807
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA--GACTACCCGAATATCCAGCACTTACTTTAGACCTACACAGGAGTTTCAGT 2864
QY 765 SerLeuLysAlaValLeuProProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AAGCTGAAGTATGATGTTGGAGAAAAACAAACAGCTTCCCAAAATGTGGTGCATAC 2924
QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGGCTCAGGACTTCAGGATGCAATTTGACAGTACCTGGGAAACCGGAAA 2984
QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824

Db 2985 ATCATGCCAAACAATTACAAGATGGATCAGAGTGGAGTCTTGCCTTACAAACTCTCG 3044
QY 825 IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu 844
Db 3045 GTGCAAAACCGGCAGCGCGATAAGCCATCGACATCAGCCAGTTCACATAAACAGGCTCG 3104
QY 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
Db 3105 GTGGATCAGATGGCATTAATCCACAGCGCTTTTCTACATCTACTCAGCGCTTGGGTC 3164
QY 865 SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu 884
Db 3165 AGCAAGACCCCGTCGCGTATGCTCTCCAGGCCAACATCCGCGCCACACCGACAGAA 3224
QY 885 TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleLeuProAlaGln 903
Db 3225 TGGTCCACGACAAAGCGGACTACATGCTGAAACAGGCTGAGAAATCCCGCAGCAGAG 3284
QY 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe 923
Db 3285 CCCATCAGTATGCCAGTTCCCTTTCTACCTCAACGGGTTGCGGAGCACCTCAGACTTT 3344
QY 924 ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db 3345 GTGAGGCAATTGAAAGTAAGACCATCTGCAGCAACTATACGAGCCTCGGGCTGTCC 3404
QY 944 AlaTyrProSerGlySerProPheLeuPheTyrGluGlnTyrLeuGlyLeuArgArgCys 963
Db 3405 AGTTACCCCAACGCTACCCCTTCTCTTCTGGAGCAGTACATCGCGCTCCGCCACTGG 3464
QY 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu 983
Db 3465 CTGCTGTGTTCATCAGCGTGTGTGGCTGCACATTCCTCGTGTGCGTGTCTCTT 3524
QY 984 LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db 3525 CTGAACCCCTTGACCGCGGGATCAATGTGTCTCTGCGCTGATGAGCGTGCAGCTG 3584
QY 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal 1023
Db 3585 TTCGCATGATGGCTCATCGGAATCAAGCTCAGTCCGCTGCCGCTGGTGCATCTGATC 3644
QY 1024 AlaSerValGlyIleGlyValGluPheThrValHisValAlaLeuGlyPheLeuThrThr 1043
Db 3645 GCTTCTGTGGCATAGAGTGGAGTTCACCGCTTTCACGCTTGTGGCTTTCGACGCGC 3704
QY 1044 GlnGlySerArgAsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThr 1063
Db 3705 ATCGGCGACAAAGAACCGGGCTGTGCTTGGCCCTGGAGCACATGTTTGACCCGCTCTG 3764
QY 1064 AspGlyAlaIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPhe 1083
Db 3765 GATGGCGCTGTCCACTCTGCTGGGAGTGTGATGCTGGCGGATCTGAGTTCGACTTC 3824
QY 1084 IleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuLeuGlyLeuLeuHisGly 1103
Db 3825 ATGTGAGGTATTTCTTCTGTGTGTGGCGATCCTCACCATCCTCGCGGCTTCTCAATGG 3884
QY 1104 LeuValLeuLeuProValLeuLeuSerIleLeuGlyProProProGluVal-IleGlnMe 1123
Db 3885 CTGGTTTCTTCCCGTGTCTTGTCTTCTTGTGGACCATATCTCTGAGGTGTCTCCAGCC 3944
QY 1123 tTyrLys-----GluSerProGluIleLeuSerProProAlaProGlnGlyGln 1139
Db 3945 AACGCTTGAACCGCTGCCACACCTCCCTGAGCCACCCCGCGCG----- 3993
QY 1139 yGlyLeuArgTrpGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrSer 1159
Db 3994 -----TGGTCCGCTTCGCCATGCCGCG-----GCCAC 4022
QY 1159 rMetThrValAlaIleHisProPro----- 1167
Db 4023 ACGCAGCGGCTCTGATTCCTCCGACTCGGAGTATAGTTCCAGACAGACAGTGTGAGC 4082

1734	Db	GCCTATGCCTGTCTTAACCATGCTGCGCTGGGACTGCTCCAAAGTCCCAAGGCTGCCGTGGGG	1793
427	Qy	LeuAlaGlyValLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu	446
1794	Db	CTGGCTGGCGTCTGCTGGTTCACCTGTCAGTGGCTGCAGGACTGGGCGCTGTGCTCATTTG	1853
447	Qy	LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle	466
1854	Db	ATCGGAATTTCTTTAAACGCTGCAACAACACTCAGGTGTTTGGCCATTTCTGCTCTTTGGTGT	1913
467	Qy	GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly	484
1914	Db	GGTGTGGATGATGTTTTCTTCTGGCCACGCCCTCAAGTGAACAGGACAGAAATAAAGA	1973
485	Qy	ThrProLeuGlnArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu	504
1974	Db	ATCCCTTTTGAGGACAGACCGGGAGTGCCTGGAAGCGCACAGAGCCAGCGTGGCCCTC	2033
505	Qy	ThrSerIleAsnMetAlaAlaPheLeuMetAlaLeuValProIleProAlaLeu	524
2034	Db	ACGTCCATCAGCAATGTACAGCCCTTCTTACGTGCGCGGTAAATCCCAATTCGCCGCTCTG	2093
525	Qy	ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu	544
2094	Db	CGGCGTTCCTCCAGGACGCGGTAGTGTGTTCATTTTGGCATGTGTTCTGCTC	2153
545	Qy	ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal	564
2154	Db	ATTTTCTCGAAATTCACGATGGATTTATATCGACGCGAGGACAGGACTGGATATT	2213
565	Qy	LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnLeu	584
2214	Db	TTTCGTGTTTATACAGCCCTCGCTCAGCAGAGTGATTCCAGTTGAACCTCAGGCGCTAC	2273
585	Qy	GlyAsp-----GlyThrValProValGlyIleAlaHis-----	595
2274	Db	ACCGACACACAGCAATACCGCTACAGCCCCCCTCCCTACAGACGCCACAGCTTT	2333
596	Qy	-----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla	608
2334	Db	GCCCATGAACGGCAGATTACATGCAGTCCACTGTCCAGCTCCGCAGCGAGTACGACCCC	2393
609	Qy	SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProPro---	627
2394	Db	CACACGCAGCTGTACTACACCGCTGAGCGCGCTCCGAGATCTCTGTGCAGCCGCTC	2453
628	Qy	-----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644
2454	Db	ACCGTGACACAGACACCCCTCAGCTGCAGCGCCACAGAGACCCAGCTCCACAGGGAC	2513
645	Qy	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664
2514	Db	CTGCTCTCCAGTCTCCGACTCC-----AGCCTCCAGTCCCTCAGGCCCCCTGTACG	2567
665	Qy	ArgTirpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684
2568	Db	AAGTGGACACTCTCATCTTTGTGGAAGCACTATGCTCTCTTCTTGAACCAAAA	2627
685	Qy	AlaAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704
2628	Db	GCCAAGTGTGTGATCTTCCTTTTCTGGGCTTGTGGGGTTCAGCCTTTATGGCAC	2687
705	Qy	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis	724
2688	Db	ACCGAGTGAGACGGGCTGGACCTTACGGACATTTGATCCTCGGGAACCGAGAAATAT	2747
725	Qy	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
2748	Db	GACTTTATTGCTGCACAATTCAAATACTTTCTTCTACAAACATGATATAGTACCCAG	2807
745	Qy	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer	764
2808	Db	AAAGCA---GACTACCCGCAATATCCAGCACTTACTTTACGACCCTACACAGAGTTTCA	2864

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427	Qy	LeuAlaGlyValLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu	446
1794	Db	CTGGCTGGCGTCTGCTGGTTCACCTGTCAGTGGCTGCAGGACTGGGCGCTGTGCTCATTTG	1853
447	Qy	LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle	466
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467	Qy	GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly	484
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525	Qy	ArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheValAlaValMetLeu	544
2094	Db	CGGCGTTCCTCCAGGACGCGGTAGTGTGTTCATTTTGGCATGTGTTCTGCTC	2153
545	Qy	ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal	564
2154	Db	ATTTTCTCGAAATTCACGATGGATTTATATCGACGCGAGGACAGGACTGGATATT	2213
565	Qy	LeuCysCysPheSerProCysSerAlaGlnValIleGlnIleLeuProGlnLeu	584
2214	Db	TTTCGTGTTTATACAGCCCTCGCTCAGCAGAGTGATTCCAGTTGAACCTCAGGCGCTAC	2273
585	Qy	GlyAsp-----GlyThrValProValGlyIleAlaHis-----	595
2274	Db	ACCGACACACAGCAATACCGCTACAGCCCCCCTCCCTACAGACGCCACAGCTTT	2333
596	Qy	-----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla	608
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609	Qy	SerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuValProPro---	627
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628	Qy	-----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644
2454	Db	ACCGTGACACAGACACCCCTCAGCTGCAGCGCCAGAGACCCAGCTCCACAGGGGAC	2513
645	Qy	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664
2514	Db	CTGCTCTCCAGTCTCCGACTCC-----AGCCTCCAGTCCCTCAGGCCCCCTGTACG	2567
665	Qy	ArgTirpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684
2568	Db	AAGTGGACACTCTCATCTTTGTGGAAGCACTATGCTCTCTTCTTGAACCAAAA	2627
685	Qy	AlaAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704
2628	Db	GCCAAGTGTGTGATCTTCCTTTTCTGGGCTTGTGGGGTTCAGCCTTTATGGCAC	2687
705	Qy	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis	724
2688	Db	ACCGAGTGAGACGGGCTGGACCTTACGGACATTTGATCCTCGGGAACCGAGAAATAT	2747
725	Qy	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
2748	Db	GACTTTATTGCTGCACAATTCAAATACTTTTCTTCTACAAACATGATATAGTACCCAG	2807
745	Qy	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer	764
2808	Db	AAAGCA---GACTACCCGCAATATCCAGCACTTACTTTACGACCTACACAGAGTTTCACT	2864

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RESULT 12
US-08-918-658-18
; Sequence 18, Application US/08918658
; Patent No. 6429354
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,658
; FILING DATE: 22-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,055
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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Alignment Scores:
Pred. No.: 2,75e-304 Length: 5288
Score: 3349.00 Matches: 662
Percent Similarity: 70.02% Conservative: 200
Best Local Similarity: 53.78% Mismatches: 298
Query Match: 53.40% Indels: 71
DB: 4 Gaps: 16

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DB	1497	ATGTACGACACTTCAAGGGGTACGAGTAGTGTCTCACAC--ATCAACTGGAACGAGGAC	1553
QY	347	GlnAlaSerThrValLeuGlnAlaTirpGlnArgArgPheValGlnLeuAlaGlnGluAla	366
DB	1554	AAAGCGGACGCCATCTCGAGGCGCTGGCAGAGGCATATGTGGAGGTGTTTCATCAGAGT	1613
QY	367	LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspAspIle	386
DB	1614	GTCGCACGAACCTCCACTCAAAGGTGCTTCCCTTCACCAACGACCCCTGGACGACATC	1673
QY	387	LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406
DB	1674	CTGAATCCTTCTCTGAGCTCAGTGTCTATCCGCGTGGCCACGGCTACTTACTCATCGTCTC	1733
QY	407	AlaTyrAlaCysValThrMetLeuArgTirpAspCysAlaGlnSerGlnGlySerValGly	426
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QY	427	LeuAlaGlyValLeuLeuValAlaLeuAlaValaValaSerGlyLeuGlyLeuCysAlaLeu	446
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QY	447	LeuGlyIleThrPheAsnAlaAlaThrGlnValLeuProPheLeuAlaLeuGlyIle	466
DB	1854	ATCGGAATTCCTTTAAGCTGCAACAACTCAGGTTTTGGCATTTCTCGCTTGTGGTGT	1913
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DB	2214	TTCTGCTGTTTTACAGCCCCCTGGTCAGCAGAGTAGTTCAGGTGAACCTCAGGCGTAC	2273
QY	585	GlyAsp-----GlyThrValProValGlyIleAlaHis-----	595
DB	2274	ACGCACACACAGCAATAACCGCTACAGCCCCCCTCCCTCCACAGCAGCCACAGCTTT	2333
QY	596	-----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla	608
DB	2334	GCCCATGAACGCGAGATTACCATGTCATCTCAGCTCCGCGCAGGAGTACGACCC	2393
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QY	628	-----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644
DB	2454	ACCGTGACACAGGACACCTCAGCTCCAGAGCCCGCAGAGACACAGCTCCACAGGGAC	2513
QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664

Db	2514	CTGCTCTCCAGTTCTTCGGACTCC-----AGCCTCCTACTGCCTCGAGCCCCCTGTACG	2567
Qy	665	ArgTPrAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis	684
Db	2568	AAAGTGGACACTCTCATCTTTTGGCTGAGAAGCACTATGCTCTCTCTCTTGAACCAAAA	2627
Qy	685	AlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeuTyrGlyAla	704
Db	2628	GCCAAAGTAGTGATCTCTCTTTTCTGGGCTGTCTGGGGGTGAGCCTTTATTTGGCACC	2687
Qy	705	ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis	724
Db	2688	ACCCGAGTGAGAGACGGGCTGGACCTTACGGACATTGTACTCTGGGAAACACAGAAATAT	2747
Qy	725	AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln	744
Db	2748	GACTTTATTTGTGTGCACAAATTCAAATACTTTTCTTCTACAACTATATAGTCACCCAG	2807
Qy	745	GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspIleuHisGlnArgPheSer	764
Db	2808	AAAGCA---GACTACCGGAATATCCAGCACTTACTTTACGACCTTACACAGAGTTTCAGT	2864
Qy	765	SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTyrLeuHisTyr	784
Db	2865	AAGGTGAAGTATGTCATGTTGGAGAGAAACAAACAGCTTCCCAAAATGTGGCTGCATC	2924
Qy	785	TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg	804
Db	2925	TTACAGACTCGCTTCAGGCACTTCAGATGTCATTTGACAGTGACTGGGAAACCGGGAAA	2984
Qy	805	IleThrArgHisSerTyrArgAsnGlySerGlnAspGlyAlaLeuAlaTyrLysLeuLeu	824
Db	2985	ATCATGCCAAACAATTACGAATGGATGAGATGGAGTCTCTTGCTTCAAACTCCTG	3044
Qy	825	IleGlnThrGlyAspAlaGlnGluProLeuAspPheSerGlnLeuThrThrArgLysLeu	844
Db	3045	GTGCAAAACCGGACCGCGATAAGCCCATCGACATCAGCCAGTTGACTAAACAGCGTCTG	3104
Qy	845	ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal	864
Db	3105	GTGGATGCAGATGGCATCATTAATCCAGCGCTTTCTACATCTACCTGACGGCTTGGTC	3164
Qy	865	SerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProProProGlu	884
Db	3165	AGCAACGACCCGTCGGGTATGTGCTCTCCAGGCCAACATCCGGCCACACCGACCAGAA	3224
Qy	885	TrpLeuHisAspLysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln	903
Db	3225	TGGTCTCCACACAAAGCCGACTACATCGCTGAAACAAGGCTGAGAATCCCGGCAGCAGAG	3284
Qy	904	ProLeuGlnPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnLysThrAlaAspPhe	923
Db	3285	CCCATCGATGCCCATGTCCTTTCTACCTCAACGGGTTCGGGACACCTCAGACTTT	3344
Qy	924	ValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis	943
Db	3345	GTGGAGCAATTGAAAAGTAAGGACCATTGCGACCACTATACGAGCCTGGGGCTGTCC	3404
Qy	944	AlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLeuGlyLeuArgArgCys	963
Db	3405	AGTTACCCCAACCGGCTACCCCTTCCTTCTGGAGCAGTACATCGGCTCCGCCACTGG	3464
Qy	964	PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeuLeu	983
Db	3465	CTGCTGCTGTTCACAGCGTGGTGTGGCTGCATTCCTCGTGTGGCTGTCTCTTCCTT	3524
Qy	984	LeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu	1003
Db	3525	CTGAAACCCCTGGACGCCCGGATCATTTGATGTGCTCTGGCGCTGATGACGGTCGAGCTG	3584
Qy	1004	PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuVal	1023

Db 1197 AACTATCAAGTGGACAGCTGGGAGGAAATGCTGAATAAGCTGAGGTTGGTCATGTTAC 1256
QY 248 valGlyVArgProCysLeuHisProAspAspLeuHisCysProSerAlaProAsnHis 267
Db 1257 ATGACCGCCCTCGCTCAATCCGGCGGATCCAGACTGCCCCGCCACAGCCCCCAACAA 1316
QY 268 HisSerArgGlnAlaProAsnValAlaHisGluSerGlyGlyCysHisGlyPheSer 287
Db 1317 AATTCAACAAACCTCTTGATATGGCCCTGTTTGAATGGTGGATGTCATGGCTTATCC 1376
QY 288 HisLysPheMethIstPrlGlnGluLeuLeuLeuGlyGlyMetAlaArgAspProGln 307
Db 1377 AGAAATATATGACTCGGAGGAGGAGTTGATTGGGTGGCAGAGTCAAGAACAGCACT 1436
QY 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
Db 1437 GGAATACTCGTCAGCGCCCATCGCCCTGCAGACCATGTTCCAGTTAATGACTCCCAAGCAA 1496
QY 328 LeuThrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTrpSerGluGlu 346
Db 1497 ATCTACGACACTTCAAGGGGTACGAGTATGCTCAC---ATCACTGGAAAGAGGAC 1553
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Db 1554 AAAGCGGACCATCTCGAGGCGCTGGCAGAGGACATATGTGGAGGTGTTTCATCAGACT 1613
QY 367 LeuProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuAspIle 386
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QY 387 LeuHisAlaPheSerGluValSerAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu 406
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QY 407 AlaTyrAlaCysValThrMetLeuArgTrpAspCysAlaGlnSerGlnGlySerValGly 426
Db 1734 GCCTATGCGTGTAAACCTACCATGCTGCGCTGGGACTGCTCCAAAGTCCCGAGGTGCGGGG 1793
QY 427 LeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeu 446
Db 1794 CTGGCTGGCGTCTGCTGGTTCAGTGTGCTGAGTGTGCTGAGGACTGGCGCTGCTCATG 1853
QY 447 LeuGlyIleThrPheAsnAlaAlaThrThrGlnValLeuProPheLeuAlaLeuGlyIle 466
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QY 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
Db 1974 ATCCCTTTTGAGGACAGGACCGGGAGTGCCTGAAAGCGCACAGGACGCGTGGCCCTC 2033
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QY 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
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QY 585 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
Db 2274 ACCGACACACAGCAATACCGCTACAGCCCCCACCCTCCCTACAGCAGCCACAGCTTT 2333

QY 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
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QY 609 SerSerGlnHisValValThrIleLeuProGlnAlaHisIleValProPro--- 627
Db 2394 CACAGCAGTGTACTACACCCGCTGAGCGCGCTCCGAGATCTCTGTGACGCCGTC 2453
QY 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
Db 2454 ACCGTGACACAGGACACCTCAGCTCCAGAGCCGAGAGCAGACAGCTCCACAGGGAC 2513
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QY 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
Db 2568 AAGTGACACTCTCATCTTTTGTGAGAAGCACTATGCTCCTTCTCTTGAACCAAAA 2627
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QY 705 ThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThrLysGluHis 724
Db 2688 ACCCGAGTGAGAGCGGCTGAGACTTACGACATTTGTACCTCGGAAACAGAGAATAT 2747
QY 725 AlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeuValThrGln 744
Db 2748 GACTTTATGTGTGCAATTCAAATACTTTCTTCTCAACATGATATAGTACCCAG 2807
QY 745 GlyGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGlnArgPheSer 764
Db 2808 AAAGCA---GACTACCCGAATATCCAGCACTTACTTTAGCACTACAGGAGTTCACT 2864
QY 765 SerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrpLeuHisTyr 784
Db 2865 AACGTGAATATGTCTATGTTGAAGAAACAAACAGCTTCCCAAAATGTGCTGCACTAC 2924
QY 785 TyrArgAsnTrpLeuGlnGlyIleGlnAlaAlaPheAspGlnAspTrpAlaSerGlyArg 804
Db 2925 TTCAGAGACTGCTCTCAGGAGCTTCAGGATGCATTTGACAGTGGGAAACCCGGAAA 2984
QY 805 IleThrArgHisSerTyrArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeu 824
Db 2985 ATCATGCCAAACAAATTACAAGAAATGATCAGACGATGGAGTCTTGCCTACAACTCTG 3044
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Db 3045 GTGCAAAACCGGAGCGCGGATAAGCCCATCGACATCAGCAGTTCGCTTAACTCTG 3104
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QY 609 SerSerGlnHisValValThrIleLeuProGlnAlaHisLeuValProProPro--- 627
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 QY 984 LeuAsnProTyrThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
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RESULT 15

PCT-US95-13233-18
 ; Sequence 18, Application PC/TUS9513233
 ; GENERAL INFORMATION:
 ; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13233
 ; FILING DATE: 06-OCT-1990
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; PCT-US95-13233-18
 ;
 ; Alignment Scores:
 ; Pred. No.: 2,75e-304 Length: 5288
 ; Score: 3349.00 Matches: 662
 ; Percent Similarity: 70.02% Conservative: 200
 ; Best Local Similarity: 53.78% Mismatches: 298
 ; Query Match: 53.40% Indels: 71
 ; DB: 5 Gaps: 16

US-09-990-046-2 (1-1203) x PCT-US95-13233-18 (1-5288)

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 DB 717 TTCCGCGTGGATTAAGCAGCGCAACCTCGACACCAACCTGGAGGAGCTGTGGGTGAA 776
 QY 89 ValGlySerArgValSerGlnGluLeuHisTyrThrLysGlyLysLeuGlyGluGluAla 108
 DB 777 GTTGGAGGACGAGTAGTGTGAATTAATTACTCGCCAGAGATTGGAGAGAGCT 836
 QY 109 AlaTyrThrSerGlnMetLeuIleGlnThrAlaArgGlnGluGlyGluAsnIleLeuThr 128
 DB 837 ATGTTTAATCCTCAACTCATGATACAGACCCCTTAAAGAGAGAGGTGCTAATGCTGAC 896
 QY 129 ProGluAlaLeuGlyLeuHisLeuGlnAlaAlaLeuThrAlaSerLysValGlnValSer 148
 DB 897 ACAGAGCGCTCTTACACACCTGGAGCTCGGACTCCAGCCAGCCGCTGTCATGTATAC 956
 QY 149 LeuTyrGlyLysSerTyrAspLeuAsnLysIleCysTyrLysSerGlyValProLeuLe 169
 DB 957 ATGTACACAGCAGCAGTGAATTTGGAACATTTGTGTTTACAAATCAGGAGAGCTTATC 1016
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 Db 1257 ATGACCGCCCTCGCTCAATCCGGCCGATCCAGACTGCCCGCCACAGCCCAACAAA 1316
 Qy 268 HisSerArgGlnAlaProAsnValAlaHisGluLeuSerGlyGlyCysHisGlyPheSer 287
 Db 1317 AATTCAACCAAACTCTTGATATGCCCTTGTTTGAATGTGATGTCTATGCCCTTATCC 1376
 Qy 288 HisLysPheMetHisTrpGlnGluGluLeuLeuGlyGlyMetAlaArgAspProGln 307
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 Qy 308 GlyGluLeuLeuArgAlaGluAlaLeuGlnSerThrPheLeuLeuMetSerProArgGln 327
 Db 1437 GGAACACTCTGTACGCGCCATGCCCTGCAGACCATGTTCAGTTAATGACTCCCAAGCAA 1496
 Qy 328 LeuTyrGluHisPheArgGly---AspTyrGlnThrHisAspIleGlyTyrSerGluGlu 346
 Db 1497 ATGTACGAGCACTTCAAGGGTACGAGTATGCTCAC---ATCAACTGGAACGAGGAC 1553
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 Db 1794 CTGGCTGGCGTCTCTGTGTGCTGCTCAGTGGCTGAGTGGCTGAGGACTGGGCTGCTCAT 1853
 Qy 447 LeuGlyIleThrPheAsnAlaAlaThrGlnValLeuProPheLeuAlaLeuGlyIle 466
 Db 1854 ATCGGAATTCCTTAAACGCTGCAACACTCAGTTTTCGCAATTTCTGCTCTGTGTGT 1913
 Qy 467 GlyValAspValPheLeuLeuAlaHisAlaPheThrGluAlaLeuProGly----- 484
 Db 1914 GGTGTGGATGATGTTTCTTCTGGCCACGCTTCAGTGAACAGGACAGCAATAAAGA 1973
 Qy 485 ThrProLeuGlnGluArgMetGlyGluCysLeuGlnArgThrGlyThrSerValValLeu 504
 Db 1974 ATCCCTTTTGGAGCAGACCGGGGAGTGCCTGGAAGCGCACAGGACCGCGTGGCCCTC 2033
 Qy 505 ThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaAlaLeuValProIleProAlaLeu 524
 Db 2034 AGTCCATCAGAAATGTCACGCTTCTTCATGGCGCGGTAAATCCCAATCCCGCTCTG 2093
 Qy 525 ArgAlaPheSerLeuGlnAlaIleValValGlyCysThrPheValAlaValMetLeu 544

Db 2094 CGGCGGTTCCTCCCTCCAGGCGAGCGGTAGTAGTGTGTCAATTTTGCCANGSTTCTGCTC 2153
 Qy 545 ValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGlnArgLeuAspVal 564
 Db 2154 ATTTTCTCTCAATTCCTCAGCATGATTTATATCGCGGAGGACAGGAGCTGGATTT 2213
 Qy 565 LeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeuProGlnGluLeu 584
 Db 2214 TTCTGTGTTTTCAGAGCCCTCGCTCAGCAGAGTGTATCAGGTTGAACCTCAGCCTAC 2273
 Qy 585 GlyAsp-----GlyThrValProValGlyIleAlaHis----- 595
 Db 2274 ACCGACACACAGCAATATCCCGTACAGCCCCCCTCCCTACAGCAGCCACAGCTTT 2333
 Qy 596 -----LeuThrAlaThrValGlnAlaPheThrHisCysGluAla 608
 Db 2334 GCCCATGAAACGAGATTACCATGCTCAGCTCCAGCTCCGACGGAGTAGCAGCC 2393
 Qy 609 SerSerGlnHisValValThrIleLeuProGlnAlaHisLeuValProPro--- 627
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 Qy 628 -----SerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp 644
 Db 2454 ACCGTGACACAGCACCTTCAGTCCGAGCCGACGAGCAGCAGCAGCTCCCAAGGAC 2513
 Qy 645 LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla 664
 Db 2514 CTGCTCTCCAGTCTCCGACTCC-----AGCTCCACTGCTCCGAGCCCTCTGACG 2567
 Qy 665 ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuGlnSerHis 684
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 Qy 845 ValAspArgGluGlyLeuIleProProGluLeuPheTyrMetGlyLeuThrValTrpVal 864
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QY 885 TrpLeuHisAspIysTyrAspThrThrGlyGlu---AsnLeuArgIleProProAlaGln 903
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QY 904 ProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuGlnIysThrAlaAspPhe 923
Db : : : : :
3285 CCATCGAGTATGCCAGATTCCTTTCTACCTCAACGGGTGGGGACACCTCAGACTTT 3344
QY 924 ValGluAlaIleGluGlyAlaAlaAlaCysAlaGluAlaGlyGlnAlaGlyValHis 943
Db : : : : :
3345 GTGAGGCAATTGAAAGATAGAGACCATCTGCAGCAACTATACGAGCCTGGGGCTGTCC 3404
QY 944 AlaTyrProSerGlySerProPheLeuPheThrGluGlnTyrLeuGlyLeuArgCys 963
Db : : : : :
3405 AGTTACCCCAACGGCTACCCCTTCCTCTCTGGGACGATACATCGGCCCTCCGCCACTGG 3464
QY 964 PheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAlaLeuLeu 983
Db : : : : :
3465 CTGCTGCTGTTTCATCAGCGTGGTGGCTGCACATTCCTCGTGTGGCTGTCTTCCTT 3524
QY 984 LeuAsnProThrAlaGlyLeuIleValLeuValLeuAlaMetMetThrValGluLeu 1003
Db : : : : :
3525 CTGAACCCCTGGACGCGCGGATCATTTGATGCTCTGGCGCTGATGACGGTCGAGCTG 3584
QY 1004 PheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValIleLeuVal 1023
Db : : : : :
3585 TTCGGCATGATGGCCCTCATCGGAATCAAGCTCAGTGCCTGGCGGTGTCATCCTGATC 3644
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QY 1139 yGlyLeuArgTyrGlyAlaSerSerSerLeuProGlnSerPheAlaArgValThrThrse 1159
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3994 -----TGGTCCGCTTGGCATCGCCCG-----GCCAC 4022
QY 1159 rMetThrValAlaIleHisProPro----- 1167
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QY 1168 -----ProLeuProGlyValaTyrIleHisProAlaProAspGi 1180
Db : : : : :
4083 CTCACGAGGAGTTCGGCACTACGAGGCCAGCAGGGCGGGAGGCCCTGCCCCACCAA 4142
QY 1180 uProProTrpSerProAlaAlaThrSerSer 1190
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4143 GTGATCGTGGAGCCACAGAAACCCCGTCT 4173

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 22, 2004, 07:58:50 ; Search time 7917 Seconds
(without alignments)

7185.741 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPRLRLPSYTPPART.....SPAATSSGNLSRGPGPATG 1203

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23648489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O=/cgn2.1/USPTO.spool/US09990046/runat_21112004_130919_18532/app_query.fasta_1.1351
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09990046 @CGN 1.1 4879 @runat_21112004_130919_18532 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.hcg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vl.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6272	100.0	3612	9 AF091501	AF091501 Homo sapi
2	6272	100.0	3641	9 AY358555	AY358555 Homo sapi
3	6272	100.0	3765	9 AY359016	AY359016 Homo sapi
4	6272	100.0	4030	6 BD194644	BD194644 Vertebrat

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	6272	100.0	4030	6	AR194379	Sequence
6	6272	100.0	4030	6	AR489133	Sequence
7	6248	99.6	4391	6	AR175919	Sequence
8	6248	99.6	4391	6	AR374936	Sequence
9	6229	99.3	3612	9	AF087651	Sequence
10	5911	94.2	3453	6	BD227641	Homo sapi
11	5911	94.2	3453	9	AF119569	Novel con
12	5599	89.3	3549	10	AB010833	Homo sapi
13	5589.5	89.1	4402	10	BC058397	Mus muscu
14	5490	87.5	3195	6	CO717145	Sequence
15	4682.5	74.7	12886	6	BD227644	Novel con
16	4233.5	67.5	23118	9	AY438664	Homo sapi
17	4119.5	65.7	4762	5	AB037688	Xenopus l
18	4106.5	65.5	4528	5	BC070995	Xenopus l
19	4042.5	64.5	3672	5	DRPATCH	D. rerio mRN
20	3991.5	63.6	170141	2	AL611928	Homo sapi
21	3975	63.4	171656	9	AL136380	Human DNA
22	3955	63.1	4004	6	BD194648	Vertebrat
23	3955	63.1	4004	6	AR194383	Sequence
24	3955	63.1	4004	6	AR489137	Sequence
25	3674.5	58.6	134412	10	AC124037	Mus Muscu
26	3674.5	58.6	230447	10	AL671866	Mouse DNA
27	3387	54.0	2082	6	BD194649	Vertebrat
28	3387	54.0	2082	6	AR194384	Sequence
29	3387	54.0	2082	6	AR489138	Sequence
30	3356	53.5	4305	10	AY357891	Rattus no
31	3349	53.4	4344	6	CQ725013	Sequence
32	3349	53.4	4344	9	HSU59464	Human PATCH
33	3349	53.4	5288	6	AR055796	Sequence
34	3349	53.4	5288	6	AR124819	Sequence
35	3349	53.4	5288	6	AR222516	Sequence
36	3349	53.4	5288	6	AR307508	Sequence
37	3349	53.4	5288	6	AR382414	Sequence
38	3345	53.3	2748	5	AF409095	Gallus ga
39	3340	53.3	4502	5	GGU40074	Sequence
40	3337	53.2	4305	10	MMU46155	U46155 Mus musculu
41	3337	53.2	5187	6	AR055788	Sequence
42	3337	53.2	5187	6	AR055791	Sequence
43	3337	53.2	5187	6	AR124811	Sequence
44	3337	53.2	5187	6	AR124814	Sequence
45	3337	53.2	5187	6	AR222508	Sequence

ALIGNMENTS

RESULT 1	AF091501	3612 bp	mRNA	linear	PRI 30-NOV-1998
LOCUS	AF091501				
DEFINITION	Homo sapiens	receptor protein patched 2 (PTCH2)	mRNA, complete cds.		
ACCESSION	AF091501				
VERSION	AF091501.1	GI:3929234			
KEYWORDS					
SOURCE	Homo sapiens	(human)			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 3612)				
JOURNAL	Characterization of two patched receptors for the vertebrate				
MEDLINE	hedgehog protein family				
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13630-13634 (1998)				
REFERENCE	9811851				
AUTHORS	2 (bases 1 to 3612)				
TITLE	de Sauvage, F.J., and Carpenter, D.				
JOURNAL	Submitted (11-SEP-1998) Molecular Oncology, Genentech Inc, 1 DNA				
FEATURES	Way, So. San Francisco, CA 94080, USA				
source	Location/Qualifiers				
	1..3612				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				

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 QY 521 ILeProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPheVal 540
 Db 1561 ATCCCTCGGTGGAGGCTTCTCCCTACAGCGGCCATAGTGGTGGCTGCACCTTTGTA 1620
 QY 541 AlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCysGln 560
 Db 1621 GCCGTGATGTTGTTTCCAGCCATCTCAGCTTGACCTAGCGCGGCCCATGCCCAG 1680
 QY 561 ArgLeuAspValLeuCysCysPheSerSerProCysSerAlaGlnValIleGlnIleLeu 580
 Db 1681 CGCCTTGATGTCTGCTCTCTCCAGTCCCTGCTCTCTCAGTGATTCAGATCTG 1740
 QY 581 ProGlnLeuLeuGlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrVal 600
 Db 1741 CCCAGAGCTGGGGACGGGACAGTACCAGTGGGCAATTGCCACCTCACTGCACAGTT 1800
 QY 601 GlnAlaPheThrHisCysGluAlaSerSerGlnHisValValThrIleLeuProGln 620
 Db 1801 CRAAGCCTTTACCCACTGTGAGCCAGCAGCCAGCAITGTGTACCATCTCGCCCTCCCCAA 1860
 QY 621 AlaHisLeuValProProSerAspProLeuGlySerGluLeuPheSerProGlyGly 640
 Db 1861 GCCCACTGTGTCGCCCACTTCTGACCACCTGGCTCTGAGCTTTCAGCCCTGGAGGG 1920
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 QY 681 LeuGlnSerHisAlaLysAlaIleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSer 700
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 Db 2641 CCACCTCTCTGAATGGCTGCACGACAAATACGACACACAGCGGGAGAACCTTTCGATCCCCG 2700
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 Db 2821 GGGGTGCACGCTACCCAGCGGCTCCCTCTCTCTCTTTCTGGGAACAGATATCTGGGCGCTG 2880
 QY 961 ArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuValCysAla 980
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 QY 981 LeuLeuLeuLeuAsnProTrpThrAlaGlyLeuIleValLeuValLeuAlaMetMetThr 1000
 Db 2941 CTGTGTCTCTCAACCCCTGGACGGCTGGCTCTCATAGTGTCTGTCTGTGGCGATGATGACA 3000
 QY 1001 ValGluLeuPheGlyIleMetGlyPheLeuGlyIleLysLeuSerAlaIleProValVal 1020
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 QY 1081 PheAspPheIleValArgTyrPhePheAlaAlaLeuThrValLeuThrLeuGlyLeu 1100
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RESULT 2
 AY358555
 LOCUS

AY358555 3641 bp mRNA linear PRI 03-OCT-2003

DEFINITION	Homo sapiens clone DNA35621 Patched 2 (UNQ560) mRNA, complete cds.	DB:	
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VERSION	AY358555.1 GI:37182232		
KEYWORDS	FLI CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	1 (bases 1 to 3641) Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Grimaldi,C., Gu,O., Hass,P.E., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,O., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.		
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)		
PUBMED	12975309		
REFERENCE			
AUTHORS	2 (bases 1 to 3641) Clark,H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
FEATURES	Location/Qualifiers		
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Alignment Scores:			
Pred. No.:	0	Length:	3641
Score:	6272.00	Matches:	1203
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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BD194644
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DEFINITION Vertebrate PATCHED-2 protein.
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VERSION BD194644.1 GI:33004389
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4030)
AUTHORS Soberg, F.J.D. and Carpenter, D.A.

TITLE
JOURNAL
COMMENT
Vertebrate PATCHED-2 protein
Patent: JP 2002511263-A 1 16-APR-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002511263-A/1
PD 16-APR-2002
PF 02-APR-1999 JP 2000543606
PR 15-APR-1998 US 09/060939
PI FREDERICK J DE SOBERGE, DAVID A CARPENTER
PC C12N15/09, C07K14/705, C07K16/00, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12Q1/02, G01N33/15, G01N33/50, G01N33/68// (C12P21/02,
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PC (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), C12N15/00, C12N5/00
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AUTHORS de Sauvage, F. and Carpenter, D.A.
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ACCESSION AR374936
VERSION AR374936.1 GI:40078100
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4391)
AUTHORS Bumcrot,D.A.
TITLE Human patched genes and proteins, and uses related thereto
JOURNAL Patent: US 6605700-A 1 12-AUG-2003;
FEATURES Location/Qualifiers
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Query Match: 99.62% Indels: 0
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US-09-990-046-2 (1-1203) x AR374936 (1-4391)

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AF087651
LOCUS
DEFINITION Homo sapiens patched 2 (PTCH2) mRNA, complete cds.
ACCESSION AF087651
VERSION AF087651.1 GI:4588014
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 3612)

AUTHORS Smyth, I., Narang, M.A., Evans, T., Heimann, C., Nakamura, Y.,
Chenevix-Trench, G., Pletsch, T., Wicking, C. and Wainwright, B.J.
TITLE Isolation and characterization of human patched 2 (PTCH2), a
putative tumour suppressor gene in basal cell carcinoma and
medulloblastoma on chromosome 1p32
JOURNAL Hum. Mol. Genet. 8 (2), 291-297 (1999)
MEDLINE 99135908
PubMed 9931336
REFERENCE 2 (bases 1 to 3612)
AUTHORS Smyth, I., Narang, M.A., Evans, T., Heimann, C., Nakamura, Y.,
Chenevix-Trench, G., Pletsch, T., Wicking, C. and Wainwright, B.J.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-1998) Center for Molecular and Cellular Biology,
University of Queensland, Ritchie Laboratories, Research Rd.,
Brisbane, QLD 4072, Australia
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source

gene
CDS

ORIGIN

Alignment Scores:

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DB: 9 Gaps: 0

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RESULT 10
BD227641
LOCUS
DEFINITION Novel constitutional elements in hedgehog transmission pathway.
ACCESSION BD227641
VERSION BD227641.1 GI:33037411
KEYWORDS JP 2002526050-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3453)
Zaphiropoulos,P.G., Unden,A.B., Toftgard,R., Rahnana,F. and
Hollingsworth,R.E.
Novel constitutional elements in hedgehog transmission pathway
Patent: JP 2002526050-A 1 20-AUG-2002;
KAROLINSKA INNOVATIONS AB, PHARMACIA AND UPJOHN CO
OS Homo sapiens (human)
FN JP 2002526050-A/1
PD 20-AUG-2002
PR 06-OCT-1999 JP 2000573395
PF 06-OCT-1998 SE 9803393-9
PI PETER G ZAPHIROPOULOS, ANNE BIRGITTE UNDEN, RUNE TOFTGARD, PI
FAHMEH RAHNANA,
PI ROBERT E HOLLINGSWORTH
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P25/16,A61P35/00,
PC C07K14/705,
PC C07K16/28,C12N5/10,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
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 AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
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 and up-regulated in basal cell carcinomas
 JOURNAL Cancer Res. 59 (4), 787-792 (1999)
 MEDLINE 99151521
 PUBMED 10029063
 REFERENCE 2 (bases 1 to 3453)
 AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and
 Toftgard,R.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-1999) Bioscience, Karolinska, Huddinge 141 57,
 Sweden

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ACCESSION AB010833.1 GI:2842557
VERSION ptch2.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
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AUTHORS Takabatake,T., Ogawa,M., Takahashi,T.C., Mizuno,M., Okamoto,M. and
Takeshima,K.
TITLE Hedgehog and patched gene expression in adult ocular tissues
JOURNAL FEBS Lett. 410 (2-3), 485-489 (1997)
MEDLINE 97379366
PUBMED 9237688
REFERENCE 2 (sites)
AUTHORS Motoyama,J., Takabatake,T., Takeshima,K. and Hui,C.
TITLE Ptch2, a second mouse Patched gene is co-expressed with Sonic
hedgehog
JOURNAL Nat. Genet. 18 (2), 104-106 (1998)
MEDLINE 98122566
PUBMED 9462734
REFERENCE 3 (bases 1 to 3549)
AUTHORS Takabatake,T.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1998) Takashi Takabatake, Nagoya University,
Radioisotope Research Center, Furo-cho, Chikusa, Nagoya, Aichi
464-8602, Japan (E-mail:j45998@nucc.cc.nagoya-u.ac.jp,
Tel:052-789-2573, Fax:052-789-2567)
COMMENT On Feb 6, 1998 this sequence version replaced gi:2598660.
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ORIGIN

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 Best Local Similarity: 90.94% Mismatches: 64
 Query Match: 89.27% Indels: 0
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 REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Udgin, T.B., Toshiyuki, S., Abramson, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Carninci, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalish, D.E., Gnerich, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Strausberg, R.
 Direct Submission
 Submitted (16-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska, Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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DEFINITION Sequence 3079 from Patent WO02068579.
ACCESSION CQ717145
VERSION CQ717145.1 GI:42278002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3079 06-SEP-2002;
FEATUES PE Corporation (NY) (US)
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KEYWORDS JP 2002526050-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12886)
AUTHORS Zaphiropoulos, P.G., Unden, A.B., Toftgard, R., Rahnama, F. and Hollingsworth, R.E.
TITLE Patent: JP 2002526050-A 4 20-AUG-2002;
JOURNAL KAROLINSKA INNOVATIONS AB, PHARMACIA AND UPJOHN CO
COMMENT OS Homo sapiens (human)
PN JP 2002526050-A/4
PD 20-AUG-2002
PF 06-OCT-1999 JP 2000573395
PR 06-OCT-1998 SE 9803393-9
PI PETER G ZAPHIROPOULOS, ANNE BIRGITTE UNDEN, RUNE TOFTGARD, PI FAHIMEH RAHNAMA,
PI ROBERT E HOLLINGSWORTH

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Db 1887 ACGCCAGGAGGAGAGAAATCCTCACACCGAAGCACTTGGCCCTCCACCTCCAGGCGAGC 1946
QY 139 aLeuThrAlaSerLysValGlnValSerLeuTyrGlyLysSer----- 153
Db 1947 CCTCACTGCCAGTAAGATCAAGTATCACTCTATGGGAAGGT-GAGTCTGGCTGAGCCCC 2005
QY 153 ----- 153
Db 2006 TGAGCAGCTGGGGCGGAGCGTGTCTGGGGGTTCGGAGTGGGAATCCCTTCTCTGC 2065
QY 154 -----TrpAspLeuAsnLysIleCysTyrLysSe 163
Db 2066 TGATCTCTATGCCCCCTGGCTATTGCAGTCTCTGGATTGGAACAAATCTGCTACAAGTC 2125
QY 163 rGlyValProLeuIleGluAsnGlyMetIleGlu----- 174
Db 2126 AGAGTTCCTCTTATTGAAATGGAATGATTGAGCGGTAAAGTGTCTCTGAGAGGAGTAG 2185
QY 174 ----- 174
Db 2186 AGGCAGAACTTTTCTGTAGCTGGGAGGACTCAGAGACCGAGCAAGCCCCCAGCGCTGC 2245
QY 174 ----- 174
Db 2246 AATCTGCCCCCTTAAAACTAAGAGGGGATTGACAGAGGSCATCTACAAAGTTGTGGG 2305
QY 175 -----Trp-----MetIleGluLysLeuPheProCysVa 184
Db 2306 GCAGGACTGACGTGGGCGCGGGTATCCCTGGCAGATGATTGAGAAGCTGTTCCGTGCGT 2365
QY 184 lIleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnGlyGlySerAlaTy 204
Db 2366 GATCTCAACCCCTCGACTGTCTTCTGGAGGGAGCCAACTCCAAGGGGGTCCCGCCTA 2425
QY 204 rLeuProGly----- 207
Db 2426 CCTGCGGTG-AGTGCCACTCTCTGGGSCCTGCTTCATCTCCGCTGGGACTCTCCAGC 2484
QY 207 ----- 207
Db 2485 AGAAAGGAGGGTCTGGGAATGAGGATGATCAAAACCTTACCAAGGTCTTAATTACCTC 2544
QY 207 ----- 207
Db 2545 CCAGGCCAGAACAGAGACATGGGCTTCCCAAGGCTCTCTCCACATCTCTCTCTCTT 2604
QY 207 ----- 207
Db 2605 TCCCTCTCAAGGAAGAGACCTGACTATTATTACACAAACTTAACACAAAGATCTGTAA 2664
QY 207 ----- 207
Db 2665 GATCTGACAAAGGAGAAAAAGATCCCCAACAGAGGCTTTCGTGGGGAAATTACCTAG 2724
QY 207 ----- 207
Db 2725 GTGTTTGCTAACCATTGCCAGGCGCAGAAAGAAACCTGTACAGGATGTGCTGTGTG 2784
QY 207 ----- 207
Db 2785 GTTGATATTAGAACCAAGCACACAGCTTGTGAAGAACTCAGTGGGGCCCTTCTGGGCC 2844
QY 207 ----- 207
Db 2845 CTTTCTATGTATTAGTTAAACCTGCCCTGATATCGTCTCAGCCCTTGTACTCTTCTAC 2904

QY 207 ----- 207
Db 2905 AGCTCACTGTAGCACCCCTGGTGGGCCCATCAGCCTGGCAGTTCTGAGAAGCTGAGGCTT 2964
QY 207 ----- 207
Db 2965 GCACACCCCTCCATATGGAAGGACAAATCGGCAGATAAGAGGAGGGTGGGTACAGCATGG 3024
QY 207 ----- 207
Db 3025 CGCCCCAGCAGCAGTGTGGAGCCCTGGGTTTTTCGTCCTGACCCCTCACCACACTATAGGCTT 3084
QY 208 -----ArgProAspIleGlnIleThrAsnLeuAspProGluGlnLeuLeuGl 223
Db 3085 TTCCCTCAGCGCGCGCCGATATCCAGTGGACCAACTGGATCCAGACAGCAGCTGCTGGA 3144
QY 223 uGluLeuGlyProPheAlaSerLeuGluGlyPheArgGluLeuLeuAspLysAlaGlnVa 243
Db 3145 GGAGCTGGGTCCCTTTGCCCTCCCTGAGGCTTCCGGGAGCTCTAGACAAGCACAGGT 3204
QY 243 lGlyGlnAlaTyrValGlyArgProCysLeuHisProAspLeuHisCysProProSe 263
Db 3205 GGCCAGGCGCTACGTGGGCGGCGCTGTCTGCACCTGTATGACTCCACTGCCACCTAG 3264
QY 263 rAlaProAsnHisHisSerArg----- 270
Db 3265 TGCCCCCAACCATCACAGCAGCGAGTGGGTTCCAACACAGGTCTGCCAGGAAAGGCTGT 3324
QY 270 ----- 270
Db 3325 TTTCCTTCCCTTCCCTTCTCTCACTCTCTGTGTTCTGGGGAGAGTGAAGTCTGTGTC 3384
QY 270 ----- 270
Db 3385 CTGACCCCGCACTTCTGTGCCATTTATACCTGCTCCACAGTGCAGCGCCCCCATGT 3444
QY 270 ----- 270
Db 3445 CCATTCCCATTCAGTTATCTCAGGAGCCCTCAAGTGGTATATATGAATCCCTTTTCT 3504
QY 270 ----- 270
Db 3505 TTTCTAAGCTAGATAAGSCTGGACTTCTTTTCTTTTCTTTTGTAGTCTCACTCTGTC 3564
QY 270 ----- 270
Db 3565 ACCCAGGCTGAGTGCAGTGTTCGATCTTGCTCACTGCAACCTCGGCTCAGCAATTC 3624
QY 270 ----- 270
Db 3625 TCCCTGCTTAGCCTCTCAGTAGCTGGGATTACAGGTGCCACCACCATGCCCCGCTAAT 3684
QY 270 ----- 270
Db 3685 TTTTATTAGCTCCCAAAAGTGTGGGATTACAGGCGTGAAGCACTGCGCTGGCCAAAGC 3744
QY 270 ----- 270
Db 3745 TGGACTTTTATCAAAATAGACTAATACAGGGAAACTAAGBAACACAGCAGGTAAAGCATGA 3804
QY 270 ----- 270
Db 3805 ATATCATACCTGGTTTCCAGGTTTCTTTGTGGCCCTGCAAAATGTGTACTTTTTTCAGA 3864
QY 270 ----- 270
Db 3865 ATCCGCCAGTTACACCAGCTCTCCCAAGACCTACTTCCAGGCTCTGTTCCCTCTGG 3924
QY 270 ----- 270
Db 3925 GGCCTCTGTCTGGGGATAGTGTGTACTCTCTGAGAGAGTCAAGAGGCTCAGAA 3984
QY 270 ----- 270

Db	3985	FRAGTACCTACACTCCAGCCCTACTGAGCTTCATGCGACGGTGGTTCTCTGGAGGTGGAG	4044	Db	5063	CAGGTGCTGCCCTTCTTGCTCTGGGAATCGCGGTGGATGACGTATTCTCTGCTGGCGCAT	5122
QY	270	-----	270	QY	477	AlaPheThrGluAlaLeuProGlyThrProLeu	487
Db	4045	CCAGGGACACTCAGTTATCCACGGCCAGGGCCTTGAGCATTAACCCCTCTCTGTTCCCT	4104	Db	5123	GCTTCACAGAGGCTCTGCTGGCACCCCTCTCCAGGTGGGCCCTTGTCGCCACAGGGCTC	5182
QY	271	-Gln-AlaProAsnVallAlaHisGluLeuSerGlyCysHisGlyPheSerHisLysP	290	QY	487	-----	487
Db	4105	CCAGGGCTCCCAATGTGGCTCAGAGCTGAGTGGGGCTTGCCATGGCTTCTCCCAAAAT	4164	Db	5183	ATCTGAGGAGCTCAGCTTACTGTTTAAGAGCCTCTTGTTCAAGTGACCCCTTGSGCTGC	5242
QY	290	heMetHisTrpGlnGluLeuLeuLeuGlyGlyMetAlaArgAspProGlnGlyGluL	310	QY	487	-----	487
Db	4165	TCATGCACTGGCAGGAGGAATTGCTCTGGAGGCATGCCAGAGACCCCCAGGAGAC	4224	Db	5243	TAATGAACCTCGTGCTCTTGTCGCCATCTCTAAACAGGGGAAATAATAGTGTGTGTC	5302
QY	310	euLeu	311	QY	487	-----	487
Db	4225	TGCTGAGGTAGGCTCTCCTCTGGAGTTGGTGAGGGGACTCTGTTTCATGAGAACCCTAC	4284	Db	5303	CTAAGGTTAATGTTTGGATCAGTGAGGTAACTCAAGTTGAATGCTTAGAACAGCCCATC	5362
QY	311	-----	311	QY	487	-----	487
Db	4285	TGTAATGCCAGGAGCTCTGGCAAAAGGCCCTTCACATCCCTCACAGGTGTTTGGGCCA	4344	Db	5363	ATACGTACATGGTACCCCAATNAATGCTAGCCACTGTGTTATGACTGCCCCACCTCTGCAC	5422
QY	312	-----	312	QY	487	-----	487
Db	4345	GCTCTGACCCCTGGTCTCCACACCCACAGGCAGAGCCCTGAGAGCCTTCT	4404	Db	5423	CCCAAGTTCCTGAGCCTCCCTTCACTCCACTTTGACACGGCCCTCCCTTGACCTGA	5482
QY	321	euLeuMetSerProArgGlnLeuTyrGluHisPheArgGlyAspTyrGlnThrHisAspI	341	QY	488	-----	488
Db	4405	TGCTGATGATGCCCGCAGCTGTACGAGCATTTCCGGGTGACTATCAGACATGACA	4464	Db	5483	GGGAGGTCCCACTCTGCTGGCAGGAGCGCATGGCGAGTGTCTGACGCCACGGGC	5542
QY	341	leGlyTrpSerGluGlnAlaSerThrValLeuGlnAlaTrpGlnArgArg	358	QY	500	ThrSerValValLeuThrSerIleAsnAsnMetAlaAlaPheLeuMetAlaLeuVal	519
Db	4465	TTGGCTGGAGTGAGGAGCAGGCCAGCACAGTGCTACAAGCCTGGCAGCGCGCTTGTGTC	4524	Db	5543	ACCAGTGTGCTACTCACATCCATCAACAACATGGCGCCTTCTCATGTGCTGCCCTGTT	5602
QY	358	-----	358	QY	520	ProIleProAlaLeuArgAlaPheSerLeuGlnAlaAlaIleValValGlyCysThrPhe	539
Db	4525	AGTCTGGTATGGAACAGGACAAGGGGGTGCCTGAGGCCATTCCTCTCTGCCCCCT	4584	Db	5603	CCCATCCCTCGCTGGAGCCTTCTCCCTACAGCGCGCATATGTTGTTGGCTGCACCTTT	5662
QY	359	-----	359	QY	540	ValAlaValMetLeuValPheProAlaIleLeuSerLeuAspLeuArgArgHisCys	559
Db	4585	CCPATCACCCCTGTTCTC-CAGCTGGCCAGAGGCCCTGCTGAGAACGCTTCCGACG	4643	Db	5663	GTAGCGGTGATGCTTCTTCCAGCCATCCTCAGCCTGGACTACGGCGGCCCTCTGC	5722
QY	374	-----	374	QY	560	GlnArgLeuAspValLeuCysCysPheSer	569
Db	4644	AGATCCATGCTTCTCTCCACCACTGGATGACATCTGCAATGCGTCTCTGAAAGTCA	4703	Db	5723	CAGCGCTTGATGCTCTGCTGCTCTC-CAGGTACTGCTGCGGCCACAGCCCTTCT	5781
QY	394	erAlaAlaArgValValGlyGlyTyrLeuLeuMetLeu	406	QY	569	-----	569
Db	4704	GTGCTGCCGTGTGGTGGAGGCTATCTGCTCATGGT-GGGTCTTGACCTGGCACCTTG	4762	Db	5782	CCGTCACCCACGCCAGCCTGTCCCTCACCAGCATTTTCAAGGCACAGACCTGTGATCCA	5841
QY	406	-----	406	QY	570	-----	570
Db	4763	CCCCACCCACCTCCAAACAGTGCCACCCCTGGAGCCCTGAGACTGCGCTTTCCTCC	4822	Db	5842	CTCTACCTCTTCCAGTCCCTGCTCTGCTCAGGTGATTCAGATCTCTGCCAGGAGCTG	5901
QY	407	-----	407	QY	585	GlyAspGlyThrValProValGlyIleAlaHisLeuThrAlaThrValGlnAlaPheThr	604
Db	4823	CACAGCTGGGCTATGCTGTGTACCATGTGCTGGGTGGGACTGCGCCAGTCCAGGGTT	4882	Db	5902	GGGACGGGACACTACAGTGGGCAATGCCACCTCCTCCTCAGTCCAGTTCAGGCTTACC	5961
QY	424	erValGlyLeuAlaGlyValLeuLeuValAlaLeuAlaValAlaSerGlyLeuLeuC	444	QY	605	HisCysGluAlaSerSerGlnHisValValThrIleLeuProProGlnAlaHisLeuVal	624
Db	4883	CCGTGGGCTTGGCGGGTACTGCTGTGGCTGGCGGTGGCTCAGGCTTGGGCTCT	4942	Db	5962	CACGTGAAGCCAGCAGCAGCATGTGGTCAACATCTCTGCCCAAGCCACCTGGTG	6021
QY	444	ysAlaLeuLeuGlyIleThrPheAsnAlaAlaThr	456	QY	625	ProProSerSerAspProLeuGlySerGluLeuPheSerProGlyGlySerThrArgAsp	644
Db	4943	GTGCCCTGCTCGGCATCACCTTCAATGTGCCACTACCCAGGTACGCCAGGACTGCAGGG	5002	Db	6022	CCCCACCTTCTGACCCACTGGGCTCTGAGCTCTTTCAGCCCTGGAGGGTCCACACGGAC	6081
QY	456	-----	456	QY	645	LeuLeuGlyGlnGluGluThrArgGlnLysAlaAlaCysLysSerLeuProCysAla	664
Db	5003	CAGACTCAGTGCCAGTCAACAGGCTTACGGGTCTCAGTGCCTGCTCTGCTCCCTC	5062	Db	6082	CTTCTAGGCCAGGAGGAGAGACAAGGCAGGACGCTTCAAGTCCCTGCTGCTGCTG	6141
QY	457	GlnValLeuProPheLeuAlaLeuGlyIleGlyValAspValPheLeuLeuAlaHis	476	QY	665	ArgTrpAsnLeuAlaHisPheAlaArgTyrGlnPheAlaProLeuLeuLeuSerHis	684
Db		-----		Db	6142	CGCTGGAATCTTCCCATTTTCGCCCGCTATCAGTGTGCCCCGTTGCTGCTCCAGTCAAT	6201

QY 685 AlaLysAla----- 687
DB 6202 GCTAAGGT--AAGACTGGGAGAGCAGGCGAGAGACTTAGCATCTCTGGGCCCCAGAGAGGC 6260
QY 687 ----- 687
DB 6261 AGAGAGGGCTTAGTCCACTGCCTGAGGGGCTGGGGGAGCCCTGGGGTCTCCAGCTTAGT 6320
QY 688 -----lleValLeuValLeuPheGlyAlaLeuLeuGlyLeuSerLeu 701
DB 6321 TCCTACATCCCGAGGCCATCTGCTGGTGGTCTCTTTGGTGGTCTCTTCTGGGCTGAGCCTC 6380
QY 702 TyrGlyAlaThrLeuValGlnAspGlyLeuAlaLeuThrAspValValProArgGlyThr 721
DB 6381 TAGGGAGCCACTTGTGTGAAGACGGCCTGGCCCTCAGCGATGTGGTCTCGGGCACC 6440
QY 722 LysGluHisAlaPheLeuSerAlaGlnLeuArgTyrPheSerLeuTyrGluValAlaLeu 741
DB 6441 AAGGAGCATGCCCTTCTGAGCGCCAGCTCAGGTACTTCTCCCTGACGAGGTGGCCCTG 6500
QY 742 ValThrGlnGlyPheAspTyrAlaHisSerGlnArgAlaLeuPheAspLeuHisGln 761
DB 6501 GTGACCCAGGGTGGCTTTGACTACGCCCACTCCCAACGGCCCTCTTTCATCTGCACACAG 6560
QY 762 ArgPheSerSerLeuLysAlaValLeuProProAlaThrGlnAlaProArgThrTrp 781
DB 6561 CCGTTTCAGTTCCTCAAGCGGTGCTGCCCCCAGCGGCCACCCAGGCACCCCGCACCTGG 6620
QY 782 LeuHisTyrTyrArgAsnTrpLeuGlnGlyIle----- 792
DB 6621 CTGCACATTATCCGCAACTGGCTACAGGGTGA- GAGGCGAGGAGAGCGGCAGGAGGGGT 6679
QY 792 ----- 792
DB 6680 GCTGAGGGAGAAACGCCCTGGGGCCACCCAGCTAATAGAACCCCTATCTGGTCTCCCCCA 6739
QY 793 -----GlnAlaAlaPheAspGlnAspTrpAlaSerGlyArgIleThrArgHisSerTyr 810
DB 6740 GGAATCCAGGCTGGCTTTTGACCAGGACTGGGCTTCTGGGCGCATCACCGCCACCTCGAC- 6798
QY 811 ArgAsnGlySerGluAspGlyAlaLeuAlaTyrLysLeuLeuIleGlnThrGlyAspAla 830
DB 6799 CGCAATGGCTCTGAGAGTGGGCCCTTGCCCTACAGCTGCTCATCCAGACTGGAGACGCC 6858
QY 831 GlnGluProLeuAspPheSer----- 837
DB 6859 CAGGAGCTTCTGGAATTCAGCCAGGTTGGGAGGGCTGGAGGGTCCACTAGTACAGGG 6918
QY 838 -----GlnLeuThrThrArg 842
DB 6919 GCTGACAGGCTCTCTGGGCGCCAGGCTTCAGCCCTCTGCGCTCTGCGAGCTGACCAAGG 6978
QY 843 LysLeuValAspArgGluGlyLeuIleProGluLeuPheTyrMetGlyLeuThrVal 862
DB 6979 AAGCTGGTGGACAGAGAGGACTGATTCCACCCGAGCTCTTCTCATGCGGGCTGACCGTG 7038
QY 863 TrpValSerSerAspProLeuGlyLeuAlaAlaSerGlnAlaAsnPheTyrProPro 882
DB 7039 TGGGTGAGCAGTGACCCCTGGGTCTGGCAGCCTCACAGGCCAACTTCTACCCCCCACT 7098
QY 883 ProGluTrpLeuHisAspLysThrThrGlyGluAsnLeuArg----- 898
DB 7099 CCTGAATGGCTGCACGACAAATACACACCACGGGGGAGAACTTTTCGAGTGAGTCTTGG 7158
QY 898 ----- 898
DB 7159 GGGGAGCTGGCAAGAGCCTCAGCCTCGCCCAACAAGCCCTGAGCCTGAGCCCTGGCC 7218
QY 898 ----- 898
DB 7219 ACTCTGCCCGGTCTACCGGCCCTGTCCCTCTCCCTCTTCTCTCTCTCCCTCCCTCCCTCCAC 7278

QY 899 -lleProProAlaGlnProLeuGluPheAlaGlnPheProPheLeuLeuArgGlyLeuG 918
DB 7279 AGTCCCGCAGCTCAGCCCTTGGAGTTTGCAGTTTCCCTTCTCTCTCTGCTGCTGCCCTCA 7338
QY 918 nLysThrAlaAspPheValGluAlaIleGluGlyAlaArgAlaAlaCysAlaGluAlaG 938
DB 7339 GAAGACTGCAGACTTTGTGGAGCCATCAGAGGGGCCCGGGCAGCAITGGCAGAGCCGG 7398
QY 938 YGlnAlaGlyValHisAlaTyrProSerGlySerProPheLeuPheTrpGluGlnTyrLe 958
DB 7399 CCAGGCTGGGGTGCACGCCCTACCCAGCGGCTCCCCCTTCTCTCTCTGGGAACAGTATCT 7458
QY 958 uGlyLeuArgArgCysPheLeuLeuAlaValCysIleLeuLeuValCysThrPheLeuVa 978
DB 7459 GGGCCTGGGGCTGCTCTCTGCTGGCGCTCTGCATCTCTGCTGGTGGTGCATCTTCTCTCT 7518
QY 978 lCysAlaLeuLeuLeuAsnProTrpThrAlaGlyLeuIle----- 992
DB 7519 CTGTGCTCTGCTGCTCTCTCAACCCCTGGACGGCTGGCCTCATAGTGAGTGTTCAGGAG 7578
QY 992 ----- 992
DB 7579 TGGGACAGAGACACCCACCCCTTCCCTGCCAGCCTGTCTATCCCTCTCTGCGAGAGCCC 7638
QY 993 -----ValLeuValLeuAlaMetMetThrValGluLeuPheG 1005
DB 7639 TCTGTGAGCCCTGTCTCTCCCTCAGGTGCTGCTGCTGGCGATGATGACAGTGGAACTCTTG 7698
QY 1005 lYileMetGlyPheLeuGlyIleLysLeuSerAlaIleProValValIleLeuValAlaAs 1025
DB 7699 GTATCATGGTTCCTTGGGCATCAAGCTGAGTGCATCCCGCTGGTGTATCTCTTGGGCT 7758
QY 1025 erValGlyIleGlyValGluPheThrValHisValAlaLeu----- 1038
DB 7759 CTGTAGGCATTGGCGTTGAGTTTCAGTTCACAGTCCACGTGGCTCT-GGTGAGCACGGCACCCCG 7817
QY 1038 ----- 1038
DB 7818 GGGAGGGACCAATCAGCTGATTTCAGTATTCAACATATTGTTCAAGCCCCCTACTATGTG 7877
QY 1038 ----- 1038
DB 7878 CTAGTACTATTAAAGAAATTTGGGCTGGGTGGACGTGTAGCTCATTCCTGTAATCCCGAG 7937
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DB 7938 CACTTTGGGAGCCCGAGGACGTGGATCACCTGAGGTGAGGAGTTTCGAAACCCAGCCTGGC 7997
QY 1038 ----- 1038
DB 7998 CAACATGTTGAAACCCCTGTCTTTACTAAAAATACAAAAAATTAGCCGCGTGGTGCCAC 8057
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DB 8058 ATGCCAGTAATCCAGCTACTTTTGGAGGCTGAGGAGAAATTTGCTTGAACCTGGGAGGCGA 8117
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QY 1038 ----- 1038
DB 8178 CTCGCTCTCAAAAAAAGAAATTTGGGCTGGGCACAGTGGCTCATGCTGT 8237
QY 1038 ----- 1038
DB 8238 AATTGGGATGATGTGGGCAATTTTGGAGGCCAAGCAGCGGATCCCTCTGAAGTCAAG 8297
QY 1038 ----- 1038
DB 8298 AGTTCAAGACCGCTGGCCAAACATTGCAAAACCCCGTCTCTACTGAAATACAAAAATT 8357
QY 1038 ----- 1038

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Db      8358  ACCTGGGCGTGGTGCCTCATGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCAGAGAA 8417
Qy      1038  -----
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Qy      1038  -----
Db      8478  CTGGGCAAAAGACGAGATTCAATCTTCAAAAAGAAATTTGGAAAATAAAAAG 8537
Qy      1038  -----
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Qy      1038  -----
Db      8598  GAGATAGACATAAGGGCTGGGTGAGGTGGCTTACGCTGTAAATCCAGCACTTTGGGAA 8657
Qy      1038  -----
Db      8659  GCCGAGGTGGGCACATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCGACATGGTGA 8717
Qy      1038  -----
Db      8718  AACCCCATCTCTACTTAAATAATGAAATTTAGCTGGGTGTGGGGTGATGCTGTAAATC 8777
Qy      1038  -----
Db      8778  CCAGCTACTTTGGAAGCTGAGGAGGAGAAATCACTTTGAACCGGGAGGTGGAGTTGCC 8837
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Qy      1038  -----
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Qy      1038  -----
Db      8958  CCCGGGCTTTGTTTAAAGACAGGGTCTCACTCTGTACCCAGGCTGTACCCCTATT 9017
Qy      1038  -----
Db      9018  TTCTACGTGTCTGTGTCTAAGCTCACCAAACCCATCCATACAGTGTACCTAAAGGA 9077
Qy      1038  -----
Db      9078  CTCAGCATGCTCCCTGTACAGTTCCCATTAAGTTAGTTTACCCAGCCTTTGGTGGCCA 9137
Qy      1038  -----
Db      9138  AGGTATCGTTGAGCTCTGAAGACAGATACAGCTCGGGACATGGCTGAGCTGGCCATGACT 9197
Qy      1039  -----
Db      9198  GGCAGAGGACGAGCTCCAGGACCACCTGTGTTTCTTAGGGCTTCTGACACCCAGGGCA 9257
Qy      1046  -----GlyPheLeuThrGlnGlys 1046
Db      1046  eArghsnLeuArgAlaAlaHisAlaLeuGluHisThrPheAlaProValThrAspGlyA 1066
Qy      1046  -----
Db      9258  GCCGGAACCTGGGGCGGCCCATGCTTGGAGCACACATTTGGCCCGGTGACCGATGGGG 9317
Qy      1066  laIleSerThrLeuLeuGlyLeuLeuMetLeuAlaGlySerHisPheAspPheIleVal - 1085
Db      9318  CCATCTCCACATTTGCTGGGTCTGCTCATGCTTGTGTTTCCCATTTTGACTTCAATTGT -A 9376
Qy      1085  -----
Db      9377  AGGTAGGGAGGCTCGGGGAGGAGGAGGAGGCTCAGGAGCCTCAGGAGCCTGGGTGACTCCCC 9436
Qy      1086  -----ArgTyrPhePheAlaAlaLeuThrValLeuLeuLeuGlyLeuL 1101
Qy      1101  -----
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Db      9437  CACACCTACCCCTAGGTACTTCTTTTGGGGCGCTCAGAGTGTCTCAGCTCTCTGGGCGCTCC 9496
Qy      1101  euHisGlyLeuValLeuLeuLeuProValLeuLeuSerIleLeuGlyProProGlu --- 1119
Db      9497  TCCATGGACTCGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 9556
Qy      1119  -----
Db      9557  CCACACCTCGGCACCATCTCTACTCCAGCCCCAAGSGGAGCGGTAGGGAGAGGCAAG 9616
Qy      1119  -----
Db      9617  GGAAGGACAGAGCCCTGTGGCCCAAGAGAGTACTCCCAACAGAGTGCACACAGCTG 9676
Qy      1119  -----
Db      9677  AAGTGGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9736
Qy      1119  -----
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Qy      1119  -----
Db      9797  GCCTCAACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9856
Qy      1119  -----
Db      9857  GCTTCCCAACAGCTATGGTAATCCCCAGCGAGATGCTAAGGGGAGCGGAGGCCACAGGG 9916
Qy      1120  -----ValIleGlnMetTyrLysGluSerP 1128
Db      9917  CCGGTGGGCTTACTGGGGCTGGTGTCTCCCAAGGTGATACAGATGTACAAGGAAGCC 9976
Qy      1128  roGluIleLeuSerProProAlaProGlnGlyGlyLeuArgTrrpGlyAlaSerSerS 1148
Db      9977  CAGAGATCTCTGAGTCCACAGCTCCACAGGAGGGGGCTTAGGTGGGGGCTATCTCTCT 10036
Qy      1148  erLeuProGlnSerPheAlaArgValThrThrSerMetThrValAlaIleHisProProP 1168
Db      10037  CCTTGGCCAGAGCTTTGCCAGAGTACTTCCATGACCGTGGCCATCCACCCACCCC 10096
Qy      1168  roLeuProGlyAlaTyrIleHisProAlaProAspGluProProThrSerProAlaAla 1188
Db      10097  CCTGCTGCTGTGCTACATCCATCCAGCCCTGATGAGCCCTTGGTCCCTGCTGTCTGCTA 10156
Qy      1188  hrSerSerGlyAsnLeuSerSerArgGlyProGlyProAlaThrGly 1203
Db      10157  CTAGCTCTGGCAACCTCAGTTCCAGGGGACAGGTCCAGCCACTGGG 10203
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Search completed: November 22, 2004, 10:37:39
Job time : 8123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 06:48:29 ; Search time 93 Seconds
(without alignments)
7442.749 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPLRLPSPYTPPART.....SPAATSSGNLSSRGPGPATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6272	100.0	1203	2	AaQ89375
2	6272	100.0	1211	2	O6UX14
3	6272	100.0	1211	2	AaQ88919
4	6258	99.8	1203	1	PTC2_HUMAN
5	5599	89.3	1182	1	PTC2_MOUSE
6	5599	89.3	1182	2	CAC88120
7	4119	65.7	1413	2	Q9DEF3
8	4106	65.5	1422	2	O61RA5
9	4106	65.5	1422	2	AaH70395
10	4042.5	64.5	1220	1	PTC1_BRARE
11	3348	53.4	1447	1	PTC1_HUMAN
12	3340	53.3	913	2	Q90XB9
13	3340	53.3	1442	1	PTC1_CHICK
14	3339.5	53.2	1434	2	O6UY90
15	3339.5	53.2	1434	2	AaQ67738
16	3337	53.2	1434	1	PTC1_MOUSE
17	3308	52.7	1239	2	Q9DEF4
18	3308	52.7	1418	2	Q98SW6
19	3253	51.9	1243	2	Q9W6T6
20	2242	35.7	1318	2	Q9XPV5
21	2025.5	32.3	1157	2	Q7Q2Y4
22	1992	31.8	1286	1	PATC_DROME
23	1812	28.9	651	2	Q6TKP9
24	1812	28.9	651	2	AaR21239
25	1776.5	28.3	608	2	Q922A1
26	1708.5	27.2	1405	1	PTC1_CAEEL
27	1625	25.9	1388	2	Q9N4A1
28	1623.5	25.9	1391	2	Q95Y30
29	992	15.8	714	2	Q95540
30	984	15.7	255	1	PTC2_CVNPY
31	866.5	13.8	287	2	Q9DDZ0

RESULT 1

AAQ89375 PRELIMINARY; PRT; 1203 AA.
 ID AAQ89375
 AC AAQ89375;
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Patched 2.
 GN UNQ560.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vasta A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Vi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RA "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment."
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL: AY359016; AAQ89375.1; ..
 SQ SEQUENCE 1203 AA; 130573 MW; FFFA069997EEB6EB CRC64;

Query Match 100.0%; Score 6272; DB 2; Length 1203;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRSPPLRLPSPYTPPARTAAPQILAGSLKAPLMRAYFQGLLPSLOGCIQRHCGKVL 60

DB 1 MTRSPPLRLPSPYTPPARTAAPQILAGSLKAPLMRAYFQGLLPSLOGCIQRHCGKVL 60

QY 61 LGLAFAGLALGLRMAIITETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQ 120

DB 61 LGLAFAGLALGLRMAIITETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQ 120

QY 121 QEGENILTPALGLHQAALTSKQVSVLYGKSWDLNLCYKSGVPLIENGMIENWIEKL 180

DB 121 QEGENILTPALGLHQAALTSKQVSVLYGKSWDLNLCYKSGVPLIENGMIENWIEKL 180

QY 181 FPCVILTLPDLCFWEGAKLQGGSAVLPGRPDICQNTNLDPEQLLELPGFPASLEGFREL 240

DB 181 FPCVILTLPDLCFWEGAKLQGGSAVLPGRPDICQNTNLDPEQLLELPGFPASLEGFREL 240

QY 241 AQVGAAYVGRCLHPDDDLHCPSPAPNHHSRAPVAHLSGCGHGFSGKFWHWBELLG 300

DB 241 AQVGAAYVGRCLHPDDDLHCPSPAPNHHSRAPVAHLSGCGHGFSGKFWHWBELLG 300

Db 241 AQVQAYVGRPCCLHPDLLHCPSPAPNHHSRQAPNVAHELSGGCHFSKFMHWQEBLLAG 300
QY 301 GWARDPQGLLRAELAQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
Db 301 GWARDPQGLLRAELAQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
QY 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSARVVGYYLLMLAYACVTMLRWDCQA 420
Db 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSARVVGYYLLMLAYACVTMLRWDCQA 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLAHAFTE 480
QY 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSIQAAIVVGCTTV 540
Db 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSIQAAIVVGCTTV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGIHAHTATV 600
Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGIHAHTATV 600
QY 601 QAFTHCEASSQHVVTILPQAHLVPPSPDLGSELPSPGSTRDLGQEBEETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPQAHLVPPSPDLGSELPSPGSTRDLGQEBEETRQKAACKS 660
QY 661 LPCARNLAFHARYQAPALLOSHAKAIVLVIFGALLGLSLYGATVQDGLATDVVPRG 720
Db 661 LPCARNLAFHARYQAPALLOSHAKAIVLVIFGALLGLSLYGATVQDGLATDVVPRG 720
QY 721 TREHAFSLAQRLYFSLYEVALVTQGGFDVAHSORALFDLHORFSSLKAVLPPPAQAPRT 780
Db 721 TREHAFSLAQRLYFSLYEVALVTQGGFDVAHSORALFDLHORFSSLKAVLPPPAQAPRT 780
QY 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPDLFSQLT 840
Db 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPDLFSQLT 840
QY 841 TRKLVDRGLIPPELFPYMGITVWSSDPLGLAASQANFYPPPEWHLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFPYMGITVWSSDPLGLAASQANFYPPPEWHLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLRLGLQKTAQFVEAIEGARACACAGAGVHAYPSGSPFLPWEQYGL 960
Db 901 PAQPLEFAQFPFLRLGLQKTAQFVEAIEGARACACAGAGVHAYPSGSPFLPWEQYGL 960
QY 961 RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPVV 1020
Db 961 RRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFLGKLSAIPVV 1020
QY 1021 ILVASVIGVEFTVHVALGFLTQGSRNRAHALEHTAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVIGVEFTVHVALGFLTQGSRNRAHALEHTAPVTDGAISTLLGLMLAGSH 1080
QY 1081 FDFIVRYFAALTVLTLGLLHGLVLLPVLLSLTGPPPEVIQMYKESPELSPAPQGGG 1140
Db 1081 FDFIVRYFAALTVLTLGLLHGLVLLPVLLSLTGPPPEVIQMYKESPELSPAPQGGG 1140
QY 1141 LRWGASSSLPQSFARVTTSMVAIHPPPLPGAYIHPADPEPWPSPAAATSSGNLSSRGPGP 1200
Db 1141 LRWGASSSLPQSFARVTTSMVAIHPPPLPGAYIHPADPEPWPSPAAATSSGNLSSRGPGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203

RESULT 2

Q6UX14 PRELIMINARY; PRT; 1211 AA.
ID Q6UX14
AC Q6UX14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Patched 2.
GN ORFNames=UNQ560;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358555; AAQ88919.1; -.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
SQ SEQUENCE 1211 AA; 131568 MW; 303D4FC55D39FB77 CRC64;

Query Match 100.0%; Score 6272; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRSPRLRLPSYTPPARTAAPQILAGSLKAPLMRAYFOGLLFLSGGIGRHCCKVL 60
Db 1 MTRSPRLRLPSYTPPARTAAPQILAGSLKAPLMRAYFOGLLFLSGGIGRHCCKVL 60
QY 61 LGLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIQAR 120
Db 61 LGLAFGALALGLRMAIETNLEQLWVEVGSRSVQELHYTKELGEEAAYTSQMLIQAR 120
QY 121 QGRENILTPREALGLHQAALTASKVQVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
Db 121 QGRENILTPREALGLHQAALTASKVQVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
QY 181 FFCVILTPLDCEWEGAKLOGGSAYLPGRPDIOWTNLDPEQLLEELGPPASLEGFRELDDK 240
Db 181 FFCVILTPLDCEWEGAKLOGGSAYLPGRPDIOWTNLDPEQLLEELGPPASLEGFRELDDK 240
QY 241 AQVQAYVGRPCCLHPDLLHCPSPAPNHHSRQAPNVAHELSGGCHFSKFMHWQEBLLG 300
Db 241 AQVQAYVGRPCCLHPDLLHCPSPAPNHHSRQAPNVAHELSGGCHFSKFMHWQEBLLG 300
QY 301 GWARDPQGLLRAELAQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
Db 301 GWARDPQGLLRAELAQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWORRV 360
QY 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSARVVGYYLLMLAYACVTMLRWDCQA 420
Db 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSARVVGYYLLMLAYACVTMLRWDCQA 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLAHAFTE 480
QY 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSIQAAIVVGCTTV 540
Db 481 ALPGTLPQRMGECLQRTGTSVVLTSINNMAFLMAALVPIPALRAFSIQAAIVVGCTTV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQILPQELGDTVPVGIHAHTATV 600

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Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTGTVPGIAHLTATV 600
QY 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLOSHAKAIVLVLFGALLGLSLYGATLVODGLALTDVVRG 720
Db 661 LPCARWNLAHFARYQFAPILLOSHAKAIVLVLFGALLGLSLYGATLVODGLALTDVVRG 720
QY 721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTAQAPT 780
Db 721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTAQAPT 780
QY 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPLDFSQT 840
Db 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPLDFSQT 840
QY 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960
Db 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960
QY 961 RRCFLAVACILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFGIKLSAIPVV 1020
Db 961 RRCFLAVACILLVCTFLVCAILLNPNWTAGLIVLVLAMMTVELFGIMFGIKLSAIPVV 1020
QY 1021 ILVASVIGIEFVTHVALGFLTTQGSNRLRAHALESHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVIGIEFVTHVALGFLTTQGSNRLRAHALESHTFAPVTDGAISTLLGLMLAGSH 1080
QY 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
Db 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPQGGG 1140
QY 1141 LRWGASSSLPQSFAVTTSMVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSRSGPGP 1200
Db 1141 LRWGASSSLPQSFAVTTSMVAIHPPPLPGAYIHPADPEPWSPAATSSGNLSRSGPGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203

RESULT 3
AAQ88919 ID AAQ88919 PRELIMINARY; PRT; 1211 AA.
AC AAQ88919;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Patched 2.
GN UNQ560.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1) _
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;

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RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358555; AAQ88919.1; -.
SQ SEQUENCE 1211 AA; 131568 MW; 303D4FC55D39FB77 CRC64;

Query Match 100.0%; Score 6272; DB 2; Length 1211;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRSPRLRELPSYTPPARTAQAQIILAGSLKAPLMLRAYFOGLLPSLGGCIQHQHCKVLF 60
Db 1 MTRSPRLRELPSYTPPARTAQAQIILAGSLKAPLMLRAYFOGLLPSLGGCIQHQHCKVLF 60
QY 61 LGLLAFGALALGLRMAIIEITNLEQLWVEVGSRSVQELHVTKEKLGEEAAYTSQMLQTAR 120
Db 61 LGLLAFGALALGLRMAIIEITNLEQLWVEVGSRSVQELHVTKEKLGEEAAYTSQMLQTAR 120
QY 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTLPDLCFWEKAKLOGGSAYLPRPDIQWNTLDPQLLEELGFPFASLEGFRELLOK 240
Db 181 FPCVILTLPDLCFWEKAKLOGGSAYLPRPDIQWNTLDPQLLEELGFPFASLEGFRELLOK 240
QY 241 AQVGQAYVGRPCILHPDDLHCPSPAPNHHSRQAPNVAHELSSGGCHGFSHKFMHQEELLG 300
Db 241 AQVGQAYVGRPCILHPDDLHCPSPAPNHHSRQAPNVAHELSSGGCHGFSHKFMHQEELLG 300
QY 301 GWARDPQGBELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIQWSEEQASTVLQAWORRFV 360
Db 301 GWARDPQGBELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIQWSEEQASTVLQAWORRFV 360
QY 361 QLAQALPENASQOIHAFSSTTLDLILHAFSVAARVGVGLMLLAYACVMTLWRDCAQ 420
Db 361 QLAQALPENASQOIHAFSSTTLDLILHAFSVAARVGVGLMLLAYACVMTLWRDCAQ 420
QY 421 SQSGVGLAGLVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVLLAHAFTE 480
Db 421 SQSGVGLAGLVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVLLAHAFTE 480
QY 481 ALPGTLPQERMGECLQRTGTSVLTSSINMAAFLMAALVPIIPALRAFSLQAAIIVGCTFV 540
Db 481 ALPGTLPQERMGECLQRTGTSVLTSSINMAAFLMAALVPIIPALRAFSLQAAIIVGCTFV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTGTVPGIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVLIQLPQELGDTGTVPGIAHLTATV 600
QY 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGTRDLGQEBETRQKAACKS 660
QY 661 LPCARWNLAHFARYQFAPILLOSHAKAIVLVLFGALLGLSLYGATLVODGLALTDVVRG 720
Db 661 LPCARWNLAHFARYQFAPILLOSHAKAIVLVLFGALLGLSLYGATLVODGLALTDVVRG 720
QY 721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTAQAPT 780
Db 721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTAQAPT 780
QY 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPLDFSQT 840
Db 781 WLHYRNWLOGIOQAADFQDQWASGRITRHSYRNGSEGDALAYKLLIQTGDAQEPLDFSQT 840
QY 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLRLGLQKTADFEVAIEGARAAAEAGAGVHAYPSGSPFLFWEQYVGL 960

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Db 901 PAQLEFAQFPFLRLGLQKTADEFVAIEGARACAAAGQVHAYPSGPFLEWQYLGL 960
QY 961 RCFFLLAVCILVCTFLVCAALLNPWTAGLVLVLAMVTVELFGIMFLGKLSAIPV 1020
Db 961 RCFFLLAVCILVCTFLVCAALLNPWTAGLVLVLAMVTVELFGIMFLGKLSAIPV 1020
QY 1021 ILVASGVIGVETVHVALGFLTQGSRNRAAHAEHTFAPVTDGAIISLLGLMLAGSH 1080
Db 1021 ILVASGVIGVETVHVALGFLTQGSRNRAAHAEHTFAPVTDGAIISLLGLMLAGSH 1080
QY 1081 FDFIVRYFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQWYKESPEILSPAPQGG 1140
Db 1081 FDFIVRYFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQWYKESPEILSPAPQGG 1140
QY 1141 LRGWASSILPQSFARVTTMTVAIHPPPLPGAYIHPADPEPWPSPATSGNLSRGP 1200
Db 1141 LRGWASSILPQSFARVTTMTVAIHPPPLPGAYIHPADPEPWPSPATSGNLSRGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203

RESULT 4
PTC2_HUMAN
ID PTC2_HUMAN STANDARD; PRT; 1203 AA.
AC Q9Y6C5; O95341; O95856;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 2 (PTC2).
GN Name=PTCH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99030620; PubMed=9811851;
RA Carpenter D., Stone D.M., Brush J., Ryan A., Armanini M., Frantz G.,
Rosenthal A., de Sauvage F.J.;
RT "Characterization of two patched receptors for the vertebrate hedgehog
protein family";
RT Proc. Natl. Acad. Sci. U.S.A. 95:13630-13634 (1998).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND INVOLVEMENT IN MDB AND BCC.
RX MEDLINE=99135908; PubMed=9931336;
RA Smyth I., Narang M.A., Evans T., Heilmann C., Nakamura Y.,
Chenevix-Trench G., Pietsch T., Wicking C., Wainwright B.J.;
RT "Isolation and characterization of human patched 2 (PTCH2), a putative
tumour suppressor gene in basal cell carcinoma and medulloblastoma on
chromosome 1p32.";
RT Hum. Mol. Genet. 8:291-297 (1999).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99151521; PubMed=10029063;
RA Zaphiropoulos F.G., Unden A.B., Rahnama F., Hollingsworth R.E.,
Toftgard R.;
RT "PTCH2, a novel human patched gene, undergoing alternative splicing
and up-regulated in basal cell carcinomas.";
RT Cancer Res. 59:787-792 (1999).
RL [4]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GLN-346; LYS-493;
RP TYR-622; MET-988; MET-1019 AND MET-1121.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
RT "NIHNS-SNPs, environmental genome project, NIHES ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May have a role in epidermal development. May act as a
CC receptor for Sonic hedgehog (SHH).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=Q9Y6C5-1; Sequence=Displayed;
Name=2;
IsoId=Q9Y6C5-2; Sequence=VSP_004542;
-!- DISPASS: Defects in PTC2 are a cause of medulloblastoma (MDB)
(MIM:155255). MDB is a malignant, invasive embryonal tumor of the
cerebellum with a preferential manifestation in children. Although
the majority of medulloblastomas occur sporadically, some manifest
within familial cancer syndromes such as Turcot syndrome and basal
cell nevus syndrome (Gorlin syndrome).
-!- DISPASS: Defects in PTC2 are a cause of sporadic basal cell
carcinoma (BCC) (MIM:605462).
-!- SIMILARITY: Belongs to the patched family.
-!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
EMBL; AF091501; AAC79847.1; -
EMBL; AF087651; AAD25953.1; -
EMBL; AF119569; AAD17260.1; -
EMBL; AY438664; AAR05447.1; -
Genew; HGNC:9586; PTC2.
MIM; 603673; -
MIM; 155255; -
MIM; 605462; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0008544; P:epidermal differentiation; TAS.
GO; GO:0006461; P:protein complex assembly; TAS.
GO; GO:0007283; P:spermatogenesis; TAS.
InterPro; IPR003392; Patched.
InterPro; IPR004786; Patchedtm_recept.
InterPro; IPR000731; SSD_5TM.
Pfam; PF02460; Patched; 1.
TIGRFAMS; TIGR00918; 2A060602; 1.
PROSITE; PS50156; SSD; 1.
Alternative splicing; Glycoprotein; Receptor; Transmembrane.
DOMAIN 1 57 Cytoplasmic (Potential).
TRANSMEM 58 78 Potential.
DOMAIN 79 392 Extracellular (Potential).
TRANSMEM 393 413 Potential.
DOMAIN 414 428 Cytoplasmic (Potential).
TRANSMEM 429 449 Potential.
DOMAIN 450 457 Extracellular (Potential).
TRANSMEM 458 478 Potential.
DOMAIN 479 501 Cytoplasmic (Potential).
TRANSMEM 502 522 Potential.
DOMAIN 523 531 Extracellular (Potential).
TRANSMEM 532 552 Potential.
DOMAIN 553 686 Cytoplasmic (Potential).
TRANSMEM 687 707 Potential.
DOMAIN 708 963 Extracellular (Potential).
TRANSMEM 964 984 Potential.
DOMAIN 985 991 Cytoplasmic (Potential).
TRANSMEM 992 1012 Potential.
DOMAIN 1013 1013 Extracellular (Potential).
TRANSMEM 1014 1034 Potential.
DOMAIN 1035 1064 Cytoplasmic (Potential).
TRANSMEM 1065 1085 Potential.
DOMAIN 1086 1093 Extracellular (Potential).
TRANSMEM 1094 1114 Potential.
DOMAIN 1115 1203 Cytoplasmic (Potential).
DOMAIN 394 552 SSD.
DOMAIN 370 812 N-linked (GLNAC. . .) (Potential).
CARBOHYD 812 N-linked (GLNAC. . .) (Potential).

```

FT	VARSPIC	1143	1203	WGASSLPQSFAVTTMTVAHPPLPGAYIHPADPPW SPATSSGNLSRGPGATG -> PEEI (in isoform 2)..	601	QAFTHCEASSQHVITLPPQAHVLPSPDPLGSELSPGSTRDLLGQEBETRQKAACKS	660
FT				/FTid=vsp_004542.	661	LPCARWNLAFARYQAPAPLLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG	720
FT	VARIANT	346	346	E -> Q.	661	LPCARWNLAFARYQAPAPLLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG	720
FT				/FTid=var_018935.	721	TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSKAVLPPATQAPRT	780
FT	VARIANT	493	493	E -> K.	721	TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHQRSSSKAVLPPATQAPRT	780
FT				/FTid=var_018936.	781	WLHYRNWLQGIQAAPFDQDQWASGRITRHSYRNGSEGDALAYKLLIOTGDAQEPLDFSOLT	840
FT	VARIANT	622	622	H -> Y.	781	WLHYRNWLQGIQAAPFDQDQWASGRITRHSYRNGSEGDALAYKLLIOTGDAQEPLDFSOLT	840
FT				/FTid=var_018937.	841	TRKLVDRGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDITTGENLRIP	900
FT	VARIANT	988	988	T -> M.	841	TRKLVDRGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDITTGENLRIP	900
FT				/FTid=var_018938.	901	PAQPLEFAQFPFLRLRGLQKTADFVEAIEGARAACAGAGVHAYPSGSPFLFWEQYLG	960
FT	VARIANT	1019	1019	V -> M.	901	PAQPLEFAQFPFLRLRGLQKTADFVEAIEGARAACAGAGVHAYPSGSPFLFWEQYLG	960
FT				/FTid=var_018939.	961	RRCFLLAVCILLVCTFLVCALLLNPWTAGLIVLVLMMTVELFGTMGFLGKLSAIPV	1020
FT	VARIANT	1121	1121	I -> M.	961	RRCFLLAVCILLVCTFLVCALLLNPWTAGLIVLVLMMTVELFGTMGFLGKLSAIPV	1020
FT				/FTid=var_018940.	1021	ILVASVGIGVEFTVHVALGFLTQGSRLNRAHALEHTFAPVTDGAISTLLGLMLAGSH	1080
FT	CONFLICT	2	2	T -> N (in Ref. 2).	1021	ILVASVGIGVEFTVHVALGFLTQGSRLNRAHALEHTFAPVTDGAISTLLGLMLAGSH	1080
FT	CONFLICT	120	120	R -> L (in Ref. 2).	1081	FDIVRYRYFAALTTLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG	1140
FT	CONFLICT	175	175	R -> W (in Ref. 1).	1081	FDIVRYRYFAALTTLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG	1140
FT	CONFLICT	753	753	Q -> R (in Ref. 2).	1141	LWGGASSLPQSFAVTTMTVAIHPPLPGAYIHPADPPWSPAAATSSGNLSRGPGP	1200
FT	CONFLICT	787	787	N -> S (in Ref. 2).	1141	LWGGASSLPQSFAVTTMTVAIHPPLPGAYIHPADPPWSPAAATSSGNLSRGPGP	1200
FT	CONFLICT	833	833	P -> L (in Ref. 3).	1201	ATG 1203	
FT	CONFLICT	837	837	S -> G (in Ref. 2).	1201	ATG 1203	
FT	CONFLICT	846	846	D -> E (in Ref. 2).			
FT	CONFLICT	897	897	L -> F (in Ref. 3).			
FT	SEQUENCE	1203 AA;	130543 MW;	4FAB06999782C031 CRC64;			
SQ							
Query Match					99.8%; Score 6258; DB 1; Length 1203;		
Best Local Similarity					99.9%; Pred. No. 0;		
Matches 1202; Conservative					0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	MTRSPPLRELPSYTPPARTAAPQIILAGSLKAPLMURAYFOGLFSLGCGIORHCKVLF	60		QY	1081	FDIVRYRYFAALTTLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG
Db	1	MTRSPPLRELPSYTPPARTAAPQIILAGSLKAPLMURAYFOGLFSLGCGIORHCKVLF	60		Db	1081	FDIVRYRYFAALTTLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG
QY	61	LGLLAFGALGLRMAIIEETNLEQLWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAR	120		QY	1141	LWGGASSLPQSFAVTTMTVAIHPPLPGAYIHPADPPWSPAAATSSGNLSRGPGP
Db	61	LGLLAFGALGLRMAIIEETNLEQLWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAR	120		Db	1141	LWGGASSLPQSFAVTTMTVAIHPPLPGAYIHPADPPWSPAAATSSGNLSRGPGP
QY	121	QGENILTPALGLHLQAAATASKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180		QY	1201	ATG 1203
Db	121	QGENILTPALGLHLQAAATASKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180		Db	1201	ATG 1203
QY	181	FPVILTPDLCFMEGAKOGGSAIYLPGRDIIQWNLDPQILLEELGPPASLEGFRELDDK	240				
Db	181	FPVILTPDLCFMEGAKOGGSAIYLPGRDIIQWNLDPQILLEELGPPASLEGFRELDDK	240				
QY	241	AQVGQAYVGRPCLPDLDLCPSPAPNHHSRQAPNVAHELSSGCHGFSHKFMHQBELLLG	300				
Db	241	AQVGQAYVGRPCLPDLDLCPSPAPNHHSRQAPNVAHELSSGCHGFSHKFMHQBELLLG	300				
QY	301	GMARDPOGELLRAEALQSTFLMSRQLYVEHPRGYQTHDQWSEBQASTVLOAWQRRPV	360				
Db	301	GMARDPOGELLRAEALQSTFLMSRQLYVEHPRGYQTHDQWSEBQASTVLOAWQRRPV	360				
QY	361	QLAQALPENASQOIHAFSSITLDDIILHAFSVSAARVVGYYLLMAYACVTMLRDCAQ	420				
Db	361	QLAQALPENASQOIHAFSSITLDDIILHAFSVSAARVVGYYLLMAYACVTMLRDCAQ	420				
QY	421	SGQSVGLAGVLLVALAVASGLGALLGITFNAAATQVLPFLALGIVGDDVFLLAHAFTE	480				
Db	421	SGQSVGLAGVLLVALAVASGLGALLGITFNAAATQVLPFLALGIVGDDVFLLAHAFTE	480				
QY	481	ALPGTFLQRMGECLQRTGTSVLTSSINMAAFMAALVPIPALRAFSLQAAIVVGCTFV	540				
Db	481	ALPGTFLQRMGECLQRTGTSVLTSSINMAAFMAALVPIPALRAFSLQAAIVVGCTFV	540				
QY	541	AVMLVFPAILSDLRHRCORLDVLCFSSPCSAQVQILPOELGDTVPVGIHATV	600				
Db	541	AVMLVFPAILSDLRHRCORLDVLCFSSPCSAQVQILPOELGDTVPVGIHATV	600				
QY	601	QAFTHCEASSQHVITLPPQAHVLPSPDPLGSELSPGSTRDLLGQEBETRQKAACKS	660				

RESULT 5

PTC2 MOUSE

ID PTC2 MOUSE STANDARD; PRT: 1182 AA.

AC O35595;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Patched protein homolog 2 (PTC2).

GN Name=Ptc2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=98125566; PubMed=9462734;

RA Motoyana J., Takabatake T., Takeshima K., Hui C.-C.;

RT "Ptc2, a second mouse patched gene is co-expressed with Sonic

hedgehog.";

RL Nat. Genet. 18:104-106(1998).

RN [2]

RP SEQUENCE OF 196-446 FROM N.A.

RC STRAIN=BALB/c; TISSUE=Neuroretina;

RX MEDLINE=97379366; PubMed=9237688;

RA Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,

RT Takeshima K.;

RT "Hedgehog and patched gene expression in adult ocular tissues.";

RL FEBS Lett. 410:485-489(1997).

CC !- FUNCTION: May have a role in epidermal development. May act as a

CC receptor for Sonic hedgehog (SHH).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in epithelial cells of the
CC developing hair, tooth and whisker.
CC -!- DEVELOPMENTAL STAGE: Detected in 8.5 to 17.5 dpc embryos.
CC -!- SIMILARITY: Belongs to the patched family.
CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB010833; BAA24691.1; -;
CC FIC; T13952; T13952.
CC MGD; MGI:1095405; Ptc2.
CC InterPro; IPR003392; Patched.
CC InterPro; IPR004766; Patchedtm_recept.
CC InterPro; IPR000731; SSD_5TM.
CC Pfam; PF02460; Patched; 1.
CC TIGRPFAM; TIGR00918; 2A060602; 1.
CC PROSITE; PS0156; SSD; 1.
KW Glycoprotein; Receptor; Transmembrane.
FT DOMAIN 1 57 Cytoplasmic (Potential).
FT TRANSMEM 58 78 Potential.
FT DOMAIN 79 394 Extracellular (Potential).
FT TRANSMEM 395 414 Potential.
FT DOMAIN 415 428 Cytoplasmic (Potential).
FT TRANSMEM 429 449 Potential.
FT DOMAIN 450 457 Extracellular (Potential).
FT TRANSMEM 458 478 Potential.
FT DOMAIN 479 501 Cytoplasmic (Potential).
FT TRANSMEM 502 522 Potential.
FT DOMAIN 523 531 Extracellular (Potential).
FT TRANSMEM 532 552 Potential.
FT DOMAIN 553 686 Cytoplasmic (Potential).
FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 963 Extracellular (Potential).
FT TRANSMEM 964 984 Potential.
FT DOMAIN 985 991 Cytoplasmic (Potential).
FT TRANSMEM 992 1012 Potential.
FT DOMAIN 1013 1033 Extracellular (Potential).
FT TRANSMEM 1034 1034 Potential.
FT DOMAIN 1035 1064 Cytoplasmic (Potential).
FT TRANSMEM 1065 1085 Potential.
FT DOMAIN 1086 1086 Extracellular (Potential).
FT TRANSMEM 1087 1107 Potential.
FT DOMAIN 1108 1182 Cytoplasmic (Potential).
FT TRANSMEM 1182 1182 SSD.
FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 812 812 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1182 AA; 128585 MW; 715233D912C352F2 CRC64;

Query Match 89.3%; Score 5599; DB 1; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPRLPLPSYTPPARTAQAPOILAGSLKAPLWLRAYFQGLFSLGCGIQRHCKGVLF 60
DB 1 MYRPLSLGLPLPSYTPPARTASSAPHILLAGSLQAPLWLRAYFQGLFSLGCGIQKHCKGVLF 60

QY 61 LGLAFGALALGLRMAIETNLEQLWVEVSGRSVQELHYTKEKLGEEAAYTSOMLIQTAR 120
DB 61 LGLVAFGALALGLRVAIVETDLEQLWVEVSGRSVQELHYTKEKLGEEAAYTSOMLIQTAR 120

QY 121 QEGENTLTPEALGLHQAALTASKQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
DB 121 QEGGNVLTPEALDLHQAALTASKQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180

QY 181 FPCVILTPDCEWGAQKQGSAYLPGRPDIQWNLDPQELLEELGFPFASLEGFRELDDK 240

DB 181 FPCVILTPDCEWGAQKQGSAYLPGRPDIQWNLDPQELLEELGFPFASLEGFRELDDK 240
QY 241 AQVQAYVGRPCLDHPDDLHCPSPANHHRSQAPNVAHLSGGCHGFSHKFMWQEBLLIG 300
DB 241 AQVQAYVGRPCLDHPDHPCHPSPANRRHSQAPNVAQELSGGCHGFSHKFMWQEBLLIG 300
QY 301 GVARPQGBELLRAELAQSTFLLMSPROLYEHFPGDYQTHDLCWSEEQASTVLQAMORRV 360
DB 301 GTARDLQGLLRAELAQSTFLLMSPROLYEHFPGDYQTHDLCWSEEQASTVLQAMORRV 360
QY 361 QLAQALPENASQOIHAFSTTDLDDLHAFSEVSAARVVGGLYLLMLAYACVTLMLRWDCAQ 420
DB 361 QLAQALPANASQOIHAFSTTDLDDLILRAFSEVSTRVVGGLYLLMLAYACVTLMLRWDCAQ 420
QY 421 SQGSVGLAGVLIVAVASGLGLCALLGITFNAATQVLPFLALGIGVDVFLAHAFTE 480
DB 421 SQGAVGLAGVLIVAVASGLGLCALLGITFNAATQVLPFLALGIGVDVFLAHAFTE 480
QY 481 ALPGTPLQERMGECLQRTGTSVLTINNMAFLMAALVPIPALRAFSLQAAIVVGCFTV 540
DB 481 APPDTPLERMGECLRSTGTSVALTSVNNWVAFMAALVPIPALRAFSLQAAIVVGCFTV 540
QY 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPSCSAQVIQILPOELSGDGTVPVGIHLTAIV 600
DB 541 AVMLVFPAILSLDLRRHRCQRLDVLCCFSSPSCSAQVIQILPOELSGDGTVPVGIHLTAIV 600
QY 601 QAFTHCEASSQHVVTILPQAHLVPPPDLSEILFSPGSGTRDILLQBEETROKAACKS 660
DB 601 QAFTHCEASSQHVVTILPQAHLLSPASDPLSGSELYSPGSGTRDILLQBEETROKAACP 660
QY 661 LPCAENWLAHFARYOFAPILLQSHAKAIVLVLFGLLGLSLYGATLVQDGLALTVDVVRG 720
DB 661 LICAHTWLAHFARYOFAPILLQTRAKALVLLFFGLLGLSLYGATLVQDGLALTVDVVRG 720
QY 721 TKEHAFSLAQRYFSLYEVALVTQGGFDYAHQORALFDLHQRFSSIKAYLPPFPATQAPT 780
DB 721 TXEHAFSLAQRYFSLYEVALVTQGGFDYAHQORALFDLHQRFSSIKAYLPPFPATQAPT 780
QY 781 WLHYRNWLGIOAAFDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQPLDPSOLT 840
DB 781 WLHYRWSWLGIOAAFDQWASGRITCHSYRNGSEDEGALAYKLLIQTGNAQPLDPSOLT 840
QY 841 TRKLVDRGLIPPELFYMGILTVMVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
DB 841 TRKLVDRGLIPPELFYMGILTVMVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYGL 960
DB 901 PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYGL 960
QY 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLMAMTVELFGIMGLGKLSAIPV 1020
DB 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLMAMTVELFGIMGLGKLSAIPV 1020
QY 1021 ILVASGIGVEFTVHVALGFLTQGSRLRAHALEHTFAPVTDGAIISTLGLLMLAGSH 1080
DB 1021 ILVASGIGVEFTVHVALGFLTSHGSRNLRAHALEHTFAPVTDGAIISTLGLLMLAGSH 1080
QY 1081 FDFIVRYFFAALTTLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
DB 1081 FDFIIRYFFVLTTLTLLGLLHGLLVPVLLSILGPPPVQVQYKESPTLNSAAPQGG 1140
QY 1141 LRWGASSLSQSFARVTTSMVAIHPPPLPGAYIHPADEP 1181
DB 1141 LRWDPRPTLPQSFARVTTSMVAIHPPPLPGAYIHPASEP 1181

RESULT 6
CAC88120
ID CAC88120 PRELIMINARY; PRT; 1182 AA.
AC CAC88120;
DT 02-MAR-2004 (TREMBLrel. 27, Created)

```

DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Patched 2 protein.
GN PTCH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SvJ; TISSUE=Liver;
RA Froehlich L., Zhanquin L., Beier D.R., Lanske B.;
RT "Genomic structure and refined chromosomal localization of the mouse
RT ptch2 gene.";
RL Cytogenet. Genome Res. 97:106-110(2002).
DR EMBL; AJ133482; CAC88120.1; -.
DR EMBL; AJ133483; CAC88120.1; JOINED.
DR EMBL; AJ133484; CAC88120.1; JOINED.
DR EMBL; AJ133485; CAC88120.1; JOINED.
SQ SEQUENCE 1182 AA; 128585 MW; 7152333D912C352F2 CRC64;

Query Match 89.3%; Score 5599; DB 2; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSYTPPTAPTRAPQILAGSLKAPLMIRAYFOGLIFSLGCGIQHCHGVLF 60
Db 1 MYRPLSLGELPSYTPPTAPTRAPQILAGSLKAPLMIRAYFOGLIFSLGCGIQHCHGVLF 60
QY 61 LGLAFGALALGLRMAIETNLEQLWVEVGSVQELHYTKELGEEAAYTSQMLIQTAH 120
Db 61 LGLVAFGALALGLRVAVIETDLEQLWVEVGSVQELHYTKELGEEAAYTSQMLIQTAH 120
QY 121 QGEMNLTPEALGLHLQAALTASKVQVSLYGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
Db 121 QEGGNVLTPEALDLHLQAALTASKVQVSLYGSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPLDCEWEGAKQGGSAIYLPGRDIOWTNLDPEQLLEELGPPASLEGFRELDDK 240
Db 181 FPCVILTPLDCEWEGAKQGGSAIYLPGRDIOWTNLDPEQLLEELGPPASLEGFRELDDK 240
QY 241 AQVGAYVGRPCLDHDLHCPSPAPNHHSRQAPNVAHLSGGCHGFSHKFMHWQELLIG 300
Db 241 AQVGAYVGRPCLDHDLHCPSPAPNHHSRQAPNVAHLSGGCHGFSHKFMHWQELLIG 300
QY 301 GMRAPQBELRAELAQSTFLLMSRQLYEHPRGYQTHDIGWSEBQASTVLQAWQRFRV 360
Db 301 GTARDLQGLLRAELAQSTFLLMSRQLYEHPRGYQTHDIGWSEBQASTVLQAWQRFRV 360
QY 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSAARVVGGLLMLAYACVTMLBWDCAQ 420
Db 361 QLAQALPENASQOIHAFSTTLDLILHAFSEVSAARVVGGLLMLAYACVTMLBWDCAQ 420
QY 421 SQGSVGLAGLVLAVALASGLGCLALLGITFENAAITQVLPFLALGIGVDDVFLLAHAFTE 480
Db 421 SQGAVGLAGLVLAVALASGLGCLALLGITFENAAITQVLPFLALGIGVDDVFLLAHAFTE 480
QY 481 ALPGTPLQRMGECILQRTGTSVLTSTNNMAFLMAVLVPIPALRAFSLQAAIVVGCFTV 540
Db 481 APPDTPLQRMGECILQRTGTSVLTSTNNMAFLMAVLVPIPALRAFSLQAAIVVGCFTV 540
QY 541 AVMLVFPAILSLDLRRRHCRDLVLCFSSPCSAQVQIQLPQELGDTVPVGIHLTATV 600
Db 541 AVMLVFPAILSLDLRRRHCRDLVLCFSSPCSAQVQIQLPQELGDTVPVGIHLTATV 600
QY 601 QAFTHCEASSQHVVTILPPOAHVLPPLPPDPLGSELFPGSGSRDLGQEEETROKAAKCS 660
Db 601 QAFTHCEASSQHVVTILPPOAHVLPPLPPDPLGSELFPGSGSTRDLGQEEETROKAAKCS 660
QY 661 LPCARNLHAHFARYQFAPLLQLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDDVPRG 720
Db 661 LICAHTWLHAHFARYQFAPLLQLQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDDVPRG 720

QY 721 TYEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPATQAPRT 780
Db 721 TYEHAFSLAQRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPATQAPRT 780
QY 781 WLHYRNMLQGIQAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQBELDFSQLT 840
Db 781 WLHYRSMWQGIQAADFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTGDAQBELDFSQLT 840
QY 841 TRKLVDRGLIPPELFYMGSLTVWSSDPLGLAASQANFYPPPEWLHDKYDITTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGSLTVWSSDPLGLAASQANFYPPPEWLHDKYDITTTGENLRIP 900
QY 901 PAQPLEFAQFPFLIRGLQKTADFVAIEGARAACAEAGAGVHAYPSGSPFFLFWEOYIGL 960
Db 901 AAQPLEFAQFPFLIRGLQKTADFVAIEGARAACAEAGAGVHAYPSGSPFFLFWEOYIGL 960
QY 961 RRCFLAVCILLVCTFLVCALLLHPWTAGTLVLVLAAMTVELFGLMGLKLSAIPVV 1020
Db 961 RECFLAVCILLVCTFLVCALLLHPWTAGTLVLVLAAMTVELFGLMGLKLSAIPVV 1020
QY 1021 ILVASVIGVEFTVHVALGFLTQGSRLRAHAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASIGIGVEFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLGLMLAGSN 1080
QY 1081 FDIIVRYFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOYKESPEILSPAPQGG 1140
Db 1081 FDIIRYFVFWLTVTLGLLHGLLVPVLLSILGPPPVQVQYKESPOTLNSAAPQGG 1140
QY 1141 LRWGASSLPQSFAVTTSMTHVHPPLPGAYIHPADPEP 1181
Db 1141 LEWDPPPLPQSFAVTTSMTHVHPPLPGAYIHPADPEP 1181

RESULT 7
Q9DEF3 PRELIMINARY; PRT; 1413 AA.
AC Q9DEF3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Patched-2.
GN Name=Xotch-2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RP SEQUENCE FROM N.A.
RX MEDLINE=20500895; PubMed=11044611;
RA Takabatake T., Takahashi T.C., Takabatake Y., Yamada K., Ogawa M.,
RA Takeshima K.;
RT "Distinct expression of two types of Xenopus Patched genes during
RT early embryogenesis and hindlimb development.";
EL Mech. Dev. 98:99-104(2000).
DR EMBL; AB037688; BAB18575.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; I.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS0156; SSD; 1.
SQ SEQUENCE 1413 AA; 157372 MW; 1215D2D7733E7F17 CRC64;

Query Match 65.7%; Score 4119; DB 2; Length 1413;
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QY 129 PEALGLHQAALTASKVQSVLKGKWDLNKICYKSGVPLIENGMIEMIEKLFPCVILTP 188
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DB 693 LDESKEKRECVLPFLKWSLDFAREKXAPVLLKAKTGIVTLFWALLGLGLYGTVMH 752
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DB 1113 TLGLVLMLAGSBDFILRYFFAVFVTLTLGLLHGLVLPVLLSLILGPPPEVI-----Q 1172

QY 1123 MYKESPEILSPPAOGGLRWGASSSLPOS-----FARVTTMTVAIHPPPL--PGAYIHP 1176
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DB 1231 IPPKPP 1236
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AC Q6IRAS;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Krzyszewski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070995; AAH70995.1; -.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; I.
DR TIGRPFAM; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
KW Hypothetical protein.
SQ SEQUENCE 1422 AA; 158128 MW; 2884B2656E60CE72 CRC64;

Query Match 65.5%; Score 4106; DB 2; Length 1422;
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 DT 24-MAY-2004 (TREMREL. 27, Last sequence update)
 DT 24-MAY-2004 (TREMREL. 27, Last annotation update)
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 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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 RL Dev. Dyn. 225:384-391 (2002).
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 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
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 RA Klein S., Strausberg R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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 KW Hypothetical protein.
 SQ SEQUENCE 1422 AA; 158128 MW; 28842656E60CE72 CRC64;

Query Match 65.5%; Score 4106; DB 2; Length 1422;
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 Matches 787; Conservative 165; Mismatches 215; Indels 39; Gaps 9;
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QY 549 ILSLDLRRHRCORLDVLCFSPSCSAQVIQILPQELGDC-----TVPGVIA 594
Db 574 ILSLDLRRHRCORLDVLCFSPSCSAQVIQILPQELGDC-----TVPGVIA 632
QY 595 HUTATVQATHEAASQHVVTILPQAHVLPVPPS-----DLGSELFPFGSSTRLLCQ 648
Db 633 QITTTVQATQCDPSGHHVITLPTTSQISTSPSVIPTMDPLGVSQVFPSSSTRLLAQ 692
QY 649 BEETROKAAKSLPCARWNLHAFYQAPFLLQSHAKAIVLFCALLGLSLYGATLQV 708
Db 693 LDESKEKRECVLPFLKWSLSPAREKAPVLLKATKGLVVALFALLGLGLYGTWVH 752
QY 709 DGLALTDVVPRTKEHAFSLAQLRYESLYEVALVTQGGFDYAHSQRALFDLHQRFSLKA 768
Db 753 DGLYLTDIIPRETKEYNEFISAQFKYEFYNMFIVTKDGFNYPKAQBSLYDLHEAFGSVRY 812
QY 769 VLPFPATQAPRWLHYRNWLOQIOAAPQDQWASGRITRHSYRNGSGEDGALAYKLLIQTG 828
Db 813 VYREGRDLPKMWLHYFQDMLRGLQAFDKDMEGSGMTQDNVNGTGEDGLAYKLLIQTG 872
QY 829 DAQEPDLRSQLTRKLVADREGILIPPELFYMGVTVVSSDPLGLAASQANFYPPPPWMLHD 888
Db 873 NKKEPFNFQLTSRRVLDEKGLIPQAFYIYLVVWSNDPLGLVAASQANFYPPPPWMLHD 932
QY 889 KYDTGTENLRIPPAQPLEEFAQFPFLRLGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSG 948
Db 933 RYDTGTENLRIPAAEPIEFAQFPFYNGLRQLTSDFIEAIESVRSICEEFVKQGVHPSYG 992
QY 949 SPFLFWEQVGLRRCFLAVCILLVCTFLVCAILLNPNWTAGLIVLVLAMTVELFGIMG 1008
Db 993 YPFLFWEQVIGLRHWFLLAISIVLACTFLVCAILLNPNWTAGLIVLVLAMTVELFGIMG 1052
QY 1009 FLGIKLSAIPVWTLVASGVIGVEFTVHVALGFTLTQGSRLNRAHALEHTFADVTGATIS 1068
Db 1053 LGIKLSAIPVWTLVASGVIGVEFTVHVALGFTLTGDRNQRSVLALEHWFAPVLDGALS 1112
QY 1069 TLGLGLMLAGSHDFIVRYFFAALTVTLTGLGLHGLVLLPVLISILGPPPEVI-----Q 1122

Db 1113 TLLGVLMLAGSEDFILRYFFAVLTILTLGLINGLIVLLVLLSLIGPPAEVTPADNGSR 1172
QY 1123 MYKESPEITLSPAPOGGGLRWGASSLPOS-----FARVTTSMTVAIHPPL--PGAYIHP 1176
Db 1173 LFTPPELPPLPSHAFYMNHKFSDEPSESSEYSETITTSGLLEDDPRLYERSAYI-- 1230
QY 1177 APDEPP 1182
Db 1231 IPPKPP 1236
RESULT 10
PTCL BRARE
ID PTCL BRARE STANDARD; PRT; 1220 AA.
AC Q9864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 1 (Patched 1) (PTC1).
GN Name=ptcl;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1] _TaxID=7955;
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=96379744; PubMed=8787757;
RA Concordet J.-P., Lewis K.E., Moore J.W., Goodrich L.V., Johnson R.L.,
RA Scott M.P., Ingham P.W.;
RT "Spatial regulation of the zebrafish patched homologue reflects the
RT roles of sonic hedgehog and protein kinase A in neural tube and somite
RT patterning.";
RL Development 122:2835-2846(1996).
CC -! FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC smoothened protein (SMO) to transduce the hedgehog's proteins
CC signal (By similarity).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: Detected in embryonic presomitic mesoderm,
CC neuroectoderm, tissue surrounding the notochord, ventral neural
CC tube.
CC -! DEVELOPMENTAL STAGE: At all stages, expression corresponds to the
CC localization of SHH. First detected during gastrulation. By 36
CC hours, PTC1 appears in the first branchial arch and the posterior
CC mesenchyme of the fin bud; by 48 hours, in the hindbrain and
CC foregut.
CC -! INDUCTION: Activated by Sonic hedgehog.
CC -! PTM: Glycosylation is necessary for SHH binding (By similarity).
CC -! SIMILARITY: Belongs to the patched family.
CC -! SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X98883; CAA67386.1; --
CC F01; T18291; T18291.
CC ZFIN; ZDB-GENE-980526-44; ptcl.
CC InterPro; IPR003392; Patched.
CC InterPro; IPR004766; Patchedtm_recept.
CC InterPro; IPR000731; SSD_5TM.
CC Pfam; PF02460; Patched; 1.
CC TIGRfam; TIGR00918; 2A060602; 1.
CC PROSITE; PS50156; SSD; 1.
KW Glycoprotein; Receptor; Transmembrane.
FT DOMAIN 1 84 Cytoplasmic (Potential).
FT TRANSMEM 85 105 Potential.

QY	587	-----GTVPVGIAHLTATQAFTHCBASSOHVVVTILTPQAHLL-VPPPS	628
Db	620	RAPATPYTGSTITTTTVAQFQCDAAGOHVITLIPPSIQISTTPPSMWLSTPTP	679
QY	629	--DPLGSELPSPGSTRDLGQBEETRQAKAACKSLPCARWNLHAFARYQFAPLLQSHAK	686
Db	680	TTDPYGSQVFTSSSTRDLAQVEEPKRGECVPLPFFRNWLSFAREKYPALLKPETK	739
QY	687	AIVLVFGALLGLSLYCATIVQDGLATDVVPGRTKEHAFLSAQRLRFVSFYEVALVTQGG	746
Db	740	TVVVVFEVALLSLXGTTMVDGLYLTIVPRDTQYEFITAQKYFSFYNNMYLVITMDG	799
QY	747	FDVAHSORALFDLHQRFSLLKAVLPPPATCAPRTWLHYNNWLGIOGIAAADQDQWASGRIT	806
Db	800	FDVARSORQLLQHNAPNSVKYVKDGNHKLPRMWLHYFQDWLKGLOATFDADWEAGKIT	859
QY	807	RHSYRNGSDGALAYKLLIQTGDAQEPDLDFSQLTTRKLDVDRGLIPPELFYMGITVWVSS	866
Db	860	YDSYRNGTEDGALAYKPLIQTGSKPEPFNYSQLTSSRLVDGDLIPPEVFYILTVWVSN	919
QY	867	DPLGLAASQANFYPPPEWHLKDYDTGENLRIPPAQPLEFAQPPFLLRGLQKTADFVEA	926
Db	920	DPLGYAASQANFYHPREWTHDKYDTTGENLRIPAAEPLEFAQPPFYINGLRQASDFIEA	979
QY	927	IEGARAACAAGQAGVHAYPSGSPFLFWEOYGLRRCFLAVCLILVCTFLVCAILLNLP	986
Db	980	IESVRTICEBFMQGKINYPNGVYFLEWQYIGLRHWFLLSISVVLACTFLVCAILLNLP	1039
QY	987	WTAGLIVLVAMTVELFGIMFGLIGKLSAIPVIVILVASVIGVGEFTVHVALGFLTQGS	1046
Db	1040	WTAGVIVFLPMWTVELFGIMGLIGKLSAIPVIVILVASVIGVGEFTVHVALGFLTQGS	1099
QY	1047	RNIRAAHALHTAPYTDGAIISTLLGLMLAGSHFDIVRYFPFAALTVLTLGLLHGLVL	1106
Db	1100	RNTRSVAMEHMFAPVIDGAISTLLGLVLAGSEFDFIMRYFPFAVLAITLLGLLHGLVL	1159
QY	1107	LPVLLSLITGPPPPVI-----OMYKESPEILSPAPQGGGLRWGASSLLPQSFAVTTTS	1159
Db	1160	LPVLLSLMGPEAEVFNANNHILQSPSPMPMPMHHGYYAGHIPKASHQAFSETSDS	1218
RESULT 11			
PTC1 HUMAN			
AD	PTC1 HUMAN	STANDARD;	PRT; 1447 AA.
AC	Q13635; Q13463;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Patched protein homolog 1 (PTC1) (PTC).		
GN	Names=PTCH; Synonyms=PTCH1;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A., AND VARIANTS BCC PRO-175 AND PRO-ASN-ILE-815 INS.		
RC	TISSUE=Lung;		
RX	MEDLINE=96247324; PubMed=8658145;		
RA	Johnson R.L., Rothman A.B., Xie J., Goodrich L.V., Bare J.W.,		
RA	Bonifas J.M., Quinn A.G., Myers R.M., Cox D.R., Epstein E.H. Jr.,		
RA	Scott M.P.;		
RT	"Human homolog of patched, a candidate gene for the basal cell nevus		
RT	syndrome."		
RL	Science 272:1668-1671(1996).		
RN	[2]		
RP	SEQUENCE OF 152-1447 FROM N.A.		
RC	TISSUE=Fetal brain;		
RX	MEDLINE=96218118; PubMed=8647801;		
RA	Hahn H., Christiansen J., Wicking C., Zaphiropolous P.G.,		
RA	Chidambaram A., Gerrard B., Vorechovsky I., Bale A.E., Toftgard R.,		
RA	Dean M., Mainwright B.J.;		
RT	"A mammalian patched homolog is expressed in target tissues of sonic		

FT	DOMAIN	106	419	Extracellular (Potential).
FT	TRANSMEM	420	440	Cytoplasmic.
FT	DOMAIN	441	449	Cytoplasmic (Potential).
FT	TRANSMEM	450	470	Potential.
FT	DOMAIN	471	484	Extracellular (Potential).
FT	TRANSMEM	485	505	Potential.
FT	DOMAIN	506	528	Cytoplasmic (Potential).
FT	TRANSMEM	529	549	Potential.
FT	DOMAIN	550	558	Extracellular (Potential).
FT	TRANSMEM	559	579	Potential.
FT	DOMAIN	580	739	Cytoplasmic (Potential).
FT	TRANSMEM	740	760	Potential.
FT	DOMAIN	761	1016	Extracellular (Potential).
FT	TRANSMEM	1017	1037	Potential.
FT	DOMAIN	1038	1044	Cytoplasmic (Potential).
FT	TRANSMEM	1045	1065	Potential.
FT	DOMAIN	1066	1072	Extracellular (Potential).
FT	TRANSMEM	1073	1093	Potential.
FT	DOMAIN	1094	1110	Cytoplasmic (Potential).
FT	TRANSMEM	1111	1131	Potential.
FT	DOMAIN	1132	1143	Extracellular (Potential).
FT	TRANSMEM	1144	1164	Potential.
FT	DOMAIN	1165	1220	Cytoplasmic (Potential).
FT	TRANSMEM	421	579	SSD.
FT	DOMAIN	624	695	Thr-rich.
FT	CARBOHYD	397	397	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	865	865	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	888	888	N-linked (GlcNAc. . .) (Potential).
FT	SEQUENCE	1220 AA;	135544 MW;	D10A9D04115F532D CRC64;

Query Match
Best Local Similarity 64.5%; Score 4042.5; DB 1; Length 1220;
Matches 775; Conservative 156; Mismatches 224; Indels 44; Gaps 8;

QY	2	TRSP	-----LRELPSYTPPARTAPAILAGSL-----KAPLWIRAYPQGLSLGCGIQ	52
Db	23	TRSP	PVNSDLLRR--PSYC-HAAPALKQSKGAVGOKAPLWIRAFQAFPLFSLGCHI	79
QY	53	RHCG	VILFGLAFALGALGRMAIETNLEQLVVEVSGRSVQBLHYTKKELGEEAAYTS	112
Db	80	RHCG	KVILFVGLSVGLRVAAIETDIEKLWVAGSRVSKELRYTKKEQGEESVFTS	139
QY	113	QMLI	QTARQGENILTPAELGLHLOAALTASKVQVSVLYGKSWDLNKKI CYSGVPLIENG	172
Db	140	QMLI	QTQPKQGTNLTQEAALLHLEAALSASKVQVSVLYGKSWDLNKKI CFKSGVPIIEN	199
QY	173	IEMI	EKLPFCVILTPDCFEWAGKLOGGAYLPGRPDIQWTNLDPPQLLEEGLFPFASLE	232
Db	200	IERM	DKLPFCMIVTPDCFEWGLKOGGAYLPGMPDIQWMLNDPLKLMEEELSQFTSLE	259
QY	233	GFRE	LDKAQGVYGRPCILHPDDLHCPPSAPNHHSRQAPNVAHLSGGCHGFSHKFMH	292
Db	260	GFRE	MDKAQVGHAYMNRPCLDPSDTPCHSAPNKPQVQVFNIAEELQGGCHGFSKFMH	319
QY	293	WQBE	LIGCMARDPQGBLLBAELQSTFLMSRQLYHEPRGDIQTHDI GWSBEQASTVL	352
Db	320	WQBE	LIGERVKQSQNALQSAEALQTMFLMSPKQLYHEFKDDYIEIHDINWEDKATAIL	379
QY	353	QAWO	RREVLQAEALPENASQOIHAFSSTLTDLTHAFSFSVSAARVGVGYLLMLAYACVT	412
Db	380	ESWQ	KEVEVHSGIPQNSNNVAFSTTTNDLMGFSQVSVIRVAGGYLLMLAYACVT	439
QY	413	MLRW	DCAQSGSVGLAGVLLVALAVASGLGICALLGHTFNAATTVQLPFLALGIGVDVDF	472
Db	440	MLRW	DCAKSQGAVGLAGVLLVALSVAGLGLCSLLGLSFNAAITQVLP LSLALGIGVDDMF	499
QY	473	LLHA	FTAALPGTLPQRMGECLQRTGTSVVLITSINNMAFLMAALVP IIPALRAFSLOAA	532
Db	500	LLGH	SFTETSRNIPPKERTGDCLRRTGTSVVALTSVNNNIAFFMAALVP IIPALRAFSLOAA	559
QY	533	IVGC	TEVAVMLVPATLSLDLRHRCORLDVLCFSSPSCAQV IQLPDELG-----	586
Db	560	VVVV	FNAMALLIPATLSLDLRHREDKRDILCCFSPSCSRV IQLPDELSDANDNHQ	619

RT hedgehog and maps to a region associated with developmental
 RT abnormalities.";
 RN J. Biol. Chem. 271:12125-12128(1996).
 RN [3]
 RN VARIANTS BCNS ARG-509; VAL-509; GLN-816 DEL AND TYR-1132.
 RX MEDLINE=96438609; PubMed=8840969;
 RA Chidambaram A., Goldstein A.M., Gailani M.R., Gerrard B., Bale S.J.,
 RA DiGiovanna J.J., Bale A.E., Dean M.;
 RA "Mutations in the human homologue of the Drosophila patched gene in
 RT Caucasian and African-American nevoid basal cell carcinoma syndrome
 RT patients.";
 RL Cancer Res. 56:4599-4601(1996).
 RN [4]
 RN VARIANTS BCNS TYR-513 AND ARG-1069.
 RX MEDLINE=97136566; PubMed=8981943;
 RA Wicking C., Shanley S., Smyth I., Gillies S., Negus K., Graham S.,
 RA Suthers G., Hailes N., Edwards M., Wainwright B.J.,
 RA Chenevix-Trench G.;
 RA "Most germ-line mutations in the nevoid basal cell carcinoma syndrome
 RT lead to a premature termination of the PATCHED protein, and no
 RT genotype-phenotype correlations are evident.";
 RL Am. J. Hum. Genet. 60:21-26(1997).
 RN [5]
 RN VARIANT NBCCS ASP-1438.
 RX MEDLINE=98001068; PubMed=9341860;
 RA Lench N.J., Telford E.A.R., High A.S., Markham A.F., Wicking C.,
 RA Wainwright B.J.;
 RA "Characterisation of human patched germ line mutations in naevoid
 RT basal cell carcinoma syndrome.";
 RL Hum. Genet. 100:497-502(1997).
 RN [6]
 RN VARIANT PRO-1315.
 RX MEDLINE=99211211; PubMed=10200051;
 RX DOI=10.1002/(SICI)1098-1004(1998)11:6<480::AID-HUMU9>3.3.CO;2-W;
 RA Hasenpuesch-Thell K., Bataille V., Laehdetie J., Obermayr F.,
 RA Sampson J.R., Frischauf A.-M.;
 RA "Corlin syndrome: identification of 4 novel germ-line mutations of the
 RT human patched (PTCH) gene.";
 RL Hum. Mutat. 11:480-480(1998).
 RN [7]
 RN VARIANTS BCNS SER-376 AND VAL-1083 INS, AND VARIANT BCC TRP-1114.
 RX MEDLINE=98281604; PubMed=9620294;
 RA Aszterbaum M., Rothman A.L., Johnson R.L., Fisher M., Xie J.,
 RA Bonifas J.M., Zhang X., Scott M.P., Epstein E.H.Jr.;
 RA "Identification of mutations in the human PATCHED gene in sporadic
 RT basal cell carcinomas and in patients with the basal cell nevus
 RT syndrome.";
 RL J. Invest. Dermatol. 110:885-888(1998).
 RN [8]
 RN VARIANT PRO-1315.
 RX MEDLINE=20334946; PubMed=10874314;
 RX DOI=10.1002/1098-1004(200007)16:1<89::AID-HUMU18>3.3.CO;2-Z;
 RA Dong J., Gailani M.R., Pomeroy S.L., Reardon D., Bale A.E.;
 RA "Identification of PATCHED mutations in medulloblastomas by direct
 RT sequencing.";
 RL Hum. Mutat. 16:89-90(2000).
 RN [9]
 RN VARIANT BCNS PRO-1132.
 RX MEDLINE=21154106; PubMed=11231326;
 RA Reifemberger J., Arnold N., Kiechle M., Reifemberger G., Hauschild A.;
 RA "Coincident PTCH and BRCA1 germline mutations in a patient with nevoid
 RT basal cell carcinoma syndrome and familial breast cancer.";
 RL J. Invest. Dermatol. 116:472-474(2001).
 RN [10]
 RN VARIANTS SQUAMOUS CELL CARCINOMA MET-829 AND LYS-1242.
 RX MEDLINE=21184537; PubMed=11286632;
 RA Ping X.L., Ratner D., Zhang H., Wu X.L., Zhang M.J., Chen F.F.,
 RA Silvers D.N., Peacocke M., Tsou H.C.;
 RA "PTCH mutations in squamous cell carcinoma of the skin.";
 RT J. Invest. Dermatol. 116:614-616(2001).
 RL -1- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
 CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
 CC smoothened protein (SMO) to transduce the hedgehog's proteins
 CC

CC signal. Seems to have a tumor suppressor function, as inactivation
 CC of this protein is probably a necessary, if not sufficient step
 CC for tumorigenesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: In the adult, expressed in brain, lung, liver,
 CC heart, placenta, skeletal muscle, pancreas and kidney. Expressed
 CC in tumor cells but not in normal skin.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, found in all major target
 CC tissues of sonic hedgehog, such as the ventral neural tube,
 CC somites, and tissues surrounding the zone of polarizing activity
 CC of the limb bud.
 CC -1- PTM: Glycosylation is necessary for SHH binding (By similarity).
 CC -1- DISEASE: Defects in PTCH are probably the cause of basal cell
 CC nevus syndrome (BCNS) [MIM:109400]; also known as Gorlin syndrome
 CC or Gorlin-Goltz syndrome. BCNS is an autosomal dominant disease
 CC characterized by nevoid basal cell carcinomas (NBCCS) and
 CC developmental abnormalities such as rib and craniofacial
 CC alterations, polydactyly, syndactyly, and spina bifida. In
 CC addition, the patients suffer from a multitude of tumors like
 CC basal cell carcinomas (BCC), fibromas of the ovaries and heart,
 CC cysts of the skin, jaws and mesentery, as well as medulloblastomas
 CC and meningiomas. PTCH is also mutated in squamous cell carcinoma
 CC (SCC). Could also be associated with large body size observed in
 CC BCNS patients.
 CC -1- DISEASE: Defects in PTCH are a cause of sporadic basal cell
 CC carcinoma (BCC) [MIM:605462].
 CC -1- SIMILARITY: Belongs to the patched family.
 CC -1- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC -1- DATABASE: NAME=PTCH mutation database;
 CC WWW="http://www.cybergene.se/PTCH/ptchbase.html".
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PTCH100.html".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; U59464; AAC05550.1; -;
 CC DR EMBL; U43148; AAC50496.1; -;
 CC DR Genew; HGNC:9585; PTCH.
 CC DR MIM; 601309; -;
 CC DR MIM; 109400; -;
 CC DR MIM; 605462; -;
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0004872; P:receptor activity; TAS.
 CC DR GO; GO:0008283; P:cell proliferation; TAS.
 CC DR GO; GO:0009653; P:morphogenesis; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR InterPro; IPR004766; Patchedtm_recept.
 CC DR InterPro; IPR000731; SSD 5TM.
 CC DR Pfam; PF02450; Patched; 1.
 CC DR TIGRFAMs; TIGR00918; 2A060602; 1.
 CC DR PROSITE; PS50156; SSD; 1.
 CC DR Anti-oncogene; Disease mutation; Glycoprotein; Polymorphism; Receptor;
 KW Transmembrane.
 FT DOMAIN 1 100 Cytoplasmic (Potential).
 FT TRANSMEM 101 121 Potential.
 FT DOMAIN 122 436 Extracellular (Potential).
 FT TRANSMEM 437 457 Potential.
 FT DOMAIN 458 493 Cytoplasmic (Potential).
 FT TRANSMEM 473 493 Potential.
 FT DOMAIN 494 501 Extracellular (Potential).
 FT TRANSMEM 502 522 Potential.
 FT DOMAIN 523 547 Cytoplasmic (Potential).
 FT TRANSMEM 548 568 Potential.
 FT DOMAIN 569 577 Extracellular (Potential).
 FT TRANSMEM 578 598 Potential.
 FT DOMAIN 599 748 Cytoplasmic (Potential).

FT	TRANSMEM	749	769	Potential.		QY	645	LLGQEEETROKAAKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLFGLLGLSLYGA	704
FT	DOMAIN	770	1027	Extracellular (Potential).		Db	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768
FT	TRANSMEM	1028	1048	Potential.		QY	705	TLVQDGLATDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764
FT	DOMAIN	1049	1055	Cytoplasmic (Potential).		Db	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNIIVTQKA-DYPNIQHLIYDLHRSFS	827
FT	TRANSMEM	1056	1076	Potential.		QY	765	SLKAVLPPPATQAPRTLHYYRNWLGQIAAFDQDQWASGRITHSYRNGSEDCALAYKIL	824
FT	DOMAIN	1077	1083	Extracellular (Potential).		Db	828	NVYVWLEENKQLPKWMLHYPRDMLQGLQDAFSDWETGKIMNNYKNGSDGVLAYKLL	887
FT	TRANSMEM	1084	1104	Potential.		QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMVSSDPLGLAASQANFPPTT	884
FT	DOMAIN	1105	1121	Cytoplasmic (Potential).		Db	888	VOTGRDXPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947
FT	TRANSMEM	1122	1141	Potential.		QY	885	WLHDKVDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943
FT	DOMAIN	1142	1154	Extracellular (Potential).		Db	948	WVHDKADWPETRLRIPAAEPIEYAFPYLNGLRDTSDFVEAIEKVRTICSNYSLSLGS	1007
FT	TRANSMEM	1155	1175	Potential.		QY	944	AYPSGSPFLFWQYLGRLRRCFLLAVCIILVCTFLVCAILLNLPWTAGLIVLVLMVTEL	1003
FT	DOMAIN	1176	1447	Cytoplasmic (Potential).		Db	1008	SYPNGYPLFWQYIGRLHLLFIISVVLACTFLVCAVFLNPNWTAGIIVVLMVTEL	1067
FT	TRANSMEM	1448	1468	Gly-rich.		QY	1004	FGIMFGLIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1063
FT	DOMAIN	1469	1489	N-linked (GlcNAc. . .) (Potential).		Db	1068	FGMGLIGIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1127
FT	TRANSMEM	1490	1510	N-linked (GlcNAc. . .) (Potential).		QY	1064	DCAISTLLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121
FT	DOMAIN	1511	1531	N-linked (GlcNAc. . .) (Potential).		Db	1128	DCAVSTLLGLMLAGSEDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1187
FT	TRANSMEM	1532	1552	N-linked (GlcNAc. . .) (Potential).		QY	1122	---QMYKESP---ILSP---APQG	1139
FT	DOMAIN	1553	1573	N-linked (GlcNAc. . .) (Potential).		Db	1188	NGLNLPSPRPVPPVVRFPFPGHSGSDSSDYSSQTTVSGLSSELRHYEAQQA	1247
FT	TRANSMEM	1574	1594	N-linked (GlcNAc. . .) (Potential).		QY	1140	G---G---	1140
FT	DOMAIN	1595	1615	N-linked (GlcNAc. . .) (Potential).		Db	1248	GGPAHQVIVATEPVFAHSTVHPHPSNRQOPHLDGSLPFGRCQQRRDPP	1307
FT	TRANSMEM	1616	1636	N-linked (GlcNAc. . .) (Potential).		QY	1141	---LRWG---	1155
FT	DOMAIN	1637	1657	N-linked (GlcNAc. . .) (Potential).		Db	1308	REGLMPLVPRPRDAFEISTEGHSGPSNRMPGRGKSHNPNPASTAMGSSVPGYCP	1367
FT	TRANSMEM	1658	1678	N-linked (GlcNAc. . .) (Potential).		QY	1156	VTT-----SMTVAIHPPPLPGYIHP	1176
FT	DOMAIN	1679	1699	N-linked (GlcNAc. . .) (Potential).		Db	1368	ITVTASASVTVAVHPPPVPGGRNP	1393
FT	TRANSMEM	1700	1720	N-linked (GlcNAc. . .) (Potential).		QY	645	LLGQEEETROKAAKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLFGLLGLSLYGA	704
FT	DOMAIN	1721	1741	Extracellular (Potential).		Db	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768
FT	TRANSMEM	1742	1762	Potential.		QY	705	TLVQDGLATDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764
FT	DOMAIN	1763	1783	Cytoplasmic (Potential).		Db	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNIIVTQKA-DYPNIQHLIYDLHRSFS	827
FT	TRANSMEM	1784	1804	Potential.		QY	765	SLKAVLPPPATQAPRTLHYYRNWLGQIAAFDQDQWASGRITHSYRNGSEDCALAYKIL	824
FT	DOMAIN	1805	1825	Extracellular (Potential).		Db	828	NVYVWLEENKQLPKWMLHYPRDMLQGLQDAFSDWETGKIMNNYKNGSDGVLAYKLL	887
FT	TRANSMEM	1826	1846	Potential.		QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMVSSDPLGLAASQANFPPTT	884
FT	DOMAIN	1847	1867	Cytoplasmic (Potential).		Db	888	VOTGRDXPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947
FT	TRANSMEM	1868	1888	Potential.		QY	885	WLHDKVDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943
FT	DOMAIN	1889	1909	Extracellular (Potential).		Db	948	WVHDKADWPETRLRIPAAEPIEYAFPYLNGLRDTSDFVEAIEKVRTICSNYSLSLGS	1007
FT	TRANSMEM	1910	1930	Potential.		QY	944	AYPSGSPFLFWQYLGRLRRCFLLAVCIILVCTFLVCAILLNLPWTAGLIVLVLMVTEL	1003
FT	DOMAIN	1931	1951	Cytoplasmic (Potential).		Db	1008	SYPNGYPLFWQYIGRLHLLFIISVVLACTFLVCAVFLNPNWTAGIIVVLMVTEL	1067
FT	TRANSMEM	1952	1972	Gly-rich.		QY	1004	FGIMFGLIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1063
FT	DOMAIN	1973	1993	N-linked (GlcNAc. . .) (Potential).		Db	1068	FGMGLIGIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1127
FT	TRANSMEM	1994	2014	N-linked (GlcNAc. . .) (Potential).		QY	1064	DCAISTLLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121
FT	DOMAIN	2015	2035	N-linked (GlcNAc. . .) (Potential).		Db	1128	DCAVSTLLGLMLAGSEDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1187
FT	TRANSMEM	2036	2056	N-linked (GlcNAc. . .) (Potential).		QY	1122	---QMYKESP---ILSP---APQG	1139
FT	DOMAIN	2057	2077	N-linked (GlcNAc. . .) (Potential).		Db	1188	NGLNLPSPRPVPPVVRFPFPGHSGSDSSDYSSQTTVSGLSSELRHYEAQQA	1247
FT	TRANSMEM	2078	2098	N-linked (GlcNAc. . .) (Potential).		QY	1140	G---G---	1140
FT	DOMAIN	2099	2119	N-linked (GlcNAc. . .) (Potential).		Db	1248	GGPAHQVIVATEPVFAHSTVHPHPSNRQOPHLDGSLPFGRCQQRRDPP	1307
FT	TRANSMEM	2120	2140	N-linked (GlcNAc. . .) (Potential).		QY	1141	---LRWG---	1155
FT	DOMAIN	2141	2161	N-linked (GlcNAc. . .) (Potential).		Db	1308	REGLMPLVPRPRDAFEISTEGHSGPSNRMPGRGKSHNPNPASTAMGSSVPGYCP	1367
FT	TRANSMEM	2162	2182	N-linked (GlcNAc. . .) (Potential).		QY	1156	VTT-----SMTVAIHPPPLPGYIHP	1176
FT	DOMAIN	2183	2203	N-linked (GlcNAc. . .) (Potential).		Db	1368	ITVTASASVTVAVHPPPVPGGRNP	1393
FT	TRANSMEM	2204	2224	N-linked (GlcNAc. . .) (Potential).		QY	645	LLGQEEETROKAAKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLFGLLGLSLYGA	704
FT	DOMAIN	2225	2245	Extracellular (Potential).		Db	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768
FT	TRANSMEM	2246	2266	Potential.		QY	705	TLVQDGLATDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764
FT	DOMAIN	2267	2287	Cytoplasmic (Potential).		Db	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNIIVTQKA-DYPNIQHLIYDLHRSFS	827
FT	TRANSMEM	2288	2308	Potential.		QY	765	SLKAVLPPPATQAPRTLHYYRNWLGQIAAFDQDQWASGRITHSYRNGSEDCALAYKIL	824
FT	DOMAIN	2309	2329	Extracellular (Potential).		Db	828	NVYVWLEENKQLPKWMLHYPRDMLQGLQDAFSDWETGKIMNNYKNGSDGVLAYKLL	887
FT	TRANSMEM	2330	2350	Potential.		QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMVSSDPLGLAASQANFPPTT	884
FT	DOMAIN	2351	2371	Cytoplasmic (Potential).		Db	888	VOTGRDXPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947
FT	TRANSMEM	2372	2392	Potential.		QY	885	WLHDKVDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943
FT	DOMAIN	2393	2413	Extracellular (Potential).		Db	948	WVHDKADWPETRLRIPAAEPIEYAFPYLNGLRDTSDFVEAIEKVRTICSNYSLSLGS	1007
FT	TRANSMEM	2414	2434	Potential.		QY	944	AYPSGSPFLFWQYLGRLRRCFLLAVCIILVCTFLVCAILLNLPWTAGLIVLVLMVTEL	1003
FT	DOMAIN	2435	2455	Cytoplasmic (Potential).		Db	1008	SYPNGYPLFWQYIGRLHLLFIISVVLACTFLVCAVFLNPNWTAGIIVVLMVTEL	1067
FT	TRANSMEM	2456	2476	Gly-rich.		QY	1004	FGIMFGLIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1063
FT	DOMAIN	2477	2497	N-linked (GlcNAc. . .) (Potential).		Db	1068	FGMGLIGIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1127
FT	TRANSMEM	2498	2518	N-linked (GlcNAc. . .) (Potential).		QY	1064	DCAISTLLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121
FT	DOMAIN	2519	2539	N-linked (GlcNAc. . .) (Potential).		Db	1128	DCAVSTLLGLMLAGSEDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1187
FT	TRANSMEM	2540	2560	N-linked (GlcNAc. . .) (Potential).		QY	1122	---QMYKESP---ILSP---APQG	1139
FT	DOMAIN	2561	2581	N-linked (GlcNAc. . .) (Potential).		Db	1188	NGLNLPSPRPVPPVVRFPFPGHSGSDSSDYSSQTTVSGLSSELRHYEAQQA	1247
FT	TRANSMEM	2582	2602	N-linked (GlcNAc. . .) (Potential).		QY	1140	G---G---	1140
FT	DOMAIN	2603	2623	N-linked (GlcNAc. . .) (Potential).		Db	1248	GGPAHQVIVATEPVFAHSTVHPHPSNRQOPHLDGSLPFGRCQQRRDPP	1307
FT	TRANSMEM	2624	2644	N-linked (GlcNAc. . .) (Potential).		QY	1141	---LRWG---	1155
FT	DOMAIN	2645	2665	N-linked (GlcNAc. . .) (Potential).		Db	1308	REGLMPLVPRPRDAFEISTEGHSGPSNRMPGRGKSHNPNPASTAMGSSVPGYCP	1367
FT	TRANSMEM	2666	2686	N-linked (GlcNAc. . .) (Potential).		QY	1156	VTT-----SMTVAIHPPPLPGYIHP	1176
FT	DOMAIN	2687	2707	N-linked (GlcNAc. . .) (Potential).		Db	1368	ITVTASASVTVAVHPPPVPGGRNP	1393
FT	TRANSMEM	2708	2728	N-linked (GlcNAc. . .) (Potential).		QY	645	LLGQEEETROKAAKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLFGLLGLSLYGA	704
FT	DOMAIN	2729	2749	Extracellular (Potential).		Db	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768
FT	TRANSMEM	2750	2770	Potential.		QY	705	TLVQDGLATDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764
FT	DOMAIN	2771	2791	Cytoplasmic (Potential).		Db	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNIIVTQKA-DYPNIQHLIYDLHRSFS	827
FT	TRANSMEM	2792	2812	Potential.		QY	765	SLKAVLPPPATQAPRTLHYYRNWLGQIAAFDQDQWASGRITHSYRNGSEDCALAYKIL	824
FT	DOMAIN	2813	2833	Extracellular (Potential).		Db	828	NVYVWLEENKQLPKWMLHYPRDMLQGLQDAFSDWETGKIMNNYKNGSDGVLAYKLL	887
FT	TRANSMEM	2834	2854	Potential.		QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMVSSDPLGLAASQANFPPTT	884
FT	DOMAIN	2855	2875	Cytoplasmic (Potential).		Db	888	VOTGRDXPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947
FT	TRANSMEM	2876	2896	Potential.		QY	885	WLHDKVDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943
FT	DOMAIN	2897	2917	Extracellular (Potential).		Db	948	WVHDKADWPETRLRIPAAEPIEYAFPYLNGLRDTSDFVEAIEKVRTICSNYSLSLGS	1007
FT	TRANSMEM	2918	2938	Potential.		QY	944	AYPSGSPFLFWQYLGRLRRCFLLAVCIILVCTFLVCAILLNLPWTAGLIVLVLMVTEL	1003
FT	DOMAIN	2939	2959	Cytoplasmic (Potential).		Db	1008	SYPNGYPLFWQYIGRLHLLFIISVVLACTFLVCAVFLNPNWTAGIIVVLMVTEL	1067
FT	TRANSMEM	2960	2980	Gly-rich.		QY	1004	FGIMFGLIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1063
FT	DOMAIN	2981	3001	N-linked (GlcNAc. . .) (Potential).		Db	1068	FGMGLIGIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1127
FT	TRANSMEM	3002	3022	N-linked (GlcNAc. . .) (Potential).		QY	1064	DCAISTLLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121
FT	DOMAIN	3023	3043	N-linked (GlcNAc. . .) (Potential).		Db	1128	DCAVSTLLGLMLAGSEDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1187
FT	TRANSMEM	3044	3064	N-linked (GlcNAc. . .) (Potential).		QY	1122	---QMYKESP---ILSP---APQG	1139
FT	DOMAIN	3065	3085	N-linked (GlcNAc. . .) (Potential).		Db	1188	NGLNLPSPRPVPPVVRFPFPGHSGSDSSDYSSQTTVSGLSSELRHYEAQQA	1247
FT	TRANSMEM	3086	3106	N-linked (GlcNAc. . .) (Potential).		QY	1140	G---G---	1140
FT	DOMAIN	3107	3127	N-linked (GlcNAc. . .) (Potential).		Db	1248	GGPAHQVIVATEPVFAHSTVHPHPSNRQOPHLDGSLPFGRCQQRRDPP	1307
FT	TRANSMEM	3128	3148	N-linked (GlcNAc. . .) (Potential).		QY	1141	---LRWG---	1155
FT	DOMAIN	3149	3169	N-linked (GlcNAc. . .) (Potential).		Db	1308	REGLMPLVPRPRDAFEISTEGHSGPSNRMPGRGKSHNPNPASTAMGSSVPGYCP	1367
FT	TRANSMEM	3170	3190	N-linked (GlcNAc. . .) (Potential).		QY	1156	VTT-----SMTVAIHPPPLPGYIHP	1176
FT	DOMAIN	3191	3211	N-linked (GlcNAc. . .) (Potential).		Db	1368	ITVTASASVTVAVHPPPVPGGRNP	1393
FT	TRANSMEM	3212	3232	N-linked (GlcNAc. . .) (Potential).		QY	645	LLGQEEETROKAAKSLPCARWNLAHFARYQAPLILQSHAKAIVLVLFGLLGLSLYGA	704
FT	DOMAIN	3233	3253	Extracellular (Potential).		Db	711	LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVWVIFLFLGLGLVSLYGT	768
FT	TRANSMEM	3254	3274	Potential.		QY	705	TLVQDGLATDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHOREFS	764
FT	DOMAIN	3275	3295	Cytoplasmic (Potential).		Db	769	TRVRDGLDLDIVPRETREYDFIAAQFKYFSYNNIIVTQKA-DYPNIQHLIYDLHRSFS	827
FT	TRANSMEM	3296	3316	Potential.		QY	765	SLKAVLPPPATQAPRTLHYYRNWLGQIAAFDQDQWASGRITHSYRNGSEDCALAYKIL	824
FT	DOMAIN	3317	3337	Extracellular (Potential).		Db	828	NVYVWLEENKQLPKWMLHYPRDMLQGLQDAFSDWETGKIMNNYKNGSDGVLAYKLL	887
FT	TRANSMEM	3338	3358	Potential.		QY	825	IOTGAQAPLDPFSQLTTRKLVDRREGLIPPELPMGLTVMVSSDPLGLAASQANFPPTT	884
FT	DOMAIN	3359	3379	Cytoplasmic (Potential).		Db	888	VOTGRDXPIDISQLTQKRLVDADGIINPSAFYIYLTAWVSDPVAYASQANIRPHRE	947
FT	TRANSMEM	3380	3400	Potential.		QY	885	WLHDKVDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADEFVIAEGARAAEAGQAGVH	943
FT	DOMAIN	3401	3421	Extracellular (Potential).		Db	948	WVHDKADWPETRLRIPAAEPIEYAFPYLNGLRDTSDFVEAIEKVRTICSNYSLSLGS	1007
FT	TRANSMEM	3422	3442	Potential.		QY	944	AYPSGSPFLFWQYLGRLRRCFLLAVCIILVCTFLVCAILLNLPWTAGLIVLVLMVTEL	1003
FT	DOMAIN	3443	3463	Cytoplasmic (Potential).		Db	1008	SYPNGYPLFWQYIGRLHLLFIISVVLACTFLVCAVFLNPNWTAGIIVVLMVTEL	1067
FT	TRANSMEM	3464	3484	Gly-rich.		QY	1004	FGIMFGLIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1063
FT	DOMAIN	3485	3505	N-linked (GlcNAc. . .) (Potential).		Db	1068	FGMGLIGIKLSAIPWVILVASVGVERTVVALGFLTQGSRLRAAHAEHTFAPVT	1127
FT	TRANSMEM	3506	3526	N-linked (GlcNAc. . .) (Potential).		QY	1064	DCAISTLLGLMLAGSHDFIVRYFFAALTUTLTLGLLHGLVLLPVLISILGPPPEVI--	1121

DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS0156; SSD; 1.
FT NON TER 913 913
SQ SEQUENCE 913 AA; 101047 MW; DBD8117E5D842F33 CRC64;

Query Match 53.3%; Score 3344; DB 2; Length 913;
Best Local Similarity 69.5%; Pred. No. 7.5e-216;
Matches 631; Conservative 112; Mismatches 139; Indels 26; Gaps 4;
QY 17 PARTAPQILLAGSLK-----APLWRAVFGGLFSLGCGIQRHCGKVLFLGLLARGA 68
Db 5 PRSAPPRAAAARALKALPEGRAPLWLRARFALLFALGCRIGRCHGKVLFGVLLLFGA 64
QY 69 LALGLRMAIETNLEQLVVEGSRVSGELHYTKELGEEAAAYTSQMLIQIOTARQEGENILT 128
Db 65 LAVGLRVASVETDIEHLWVEAGSRVSGELRYTKELGEEVYTSQMLIQIOTPREGENILT 124
QY 129 PEALGHILQALTASKVQVSLYKSWDLNKICVKSGVPLIENGMIEMIEKLPFPCVILTP 188
Db 125 QEALQHLHLEAALAASKVQVSLYKSWDLNKICVKSGVPIIENGMIEMIEKLPFPCVILTP 184
QY 189 LDCFWGAKLQGGSAVLPGRPDIDQNTNLDPEQLLELGPFALEGFRELLDKAQVQAYV 248
Db 185 LDCFWGAKLQGGSAVLPGRPDIDQNTNLDPEQLLELGPFALEGFRELLDKAQVQAYV 244
QY 249 GRPCLHPDDLHCPPSPAPNHHSQAPNVAHELSCGCHGFSGHKFMWQEEILLGGMARDPOG 308
Db 245 ERPCLDPRPHCPSPAPNKSQSQSPDIPAEILSCGCHGFSGHKFMWQEEILLGTTKDSQG 304
QY 309 ELLRAEALQSTFLMSPRQLYEHFRGDYQTHDIGNSEEQASTVLAQWRFRVQLAQEALP 368
Db 305 KLLSABALQTMFLMSPRQLYEHFRGDYQTHDIGNSEEQASTVLAQWRFRVQLAQEALP 364
QY 369 ENASQOIHAFSSFTLDDILHAPESVAARVGGYLLMLAYACVTMLRWDCASQSGVGLA 428
Db 365 PNATQNIHAFSTTLNDIMKSFSDVSAIRVAGYLLMLAYACVTMLRWDCASQSGVGLA 424
QY 429 GVLVLAVALASGLGLCALLGITFNAATQVLPALGIGVDVFLLAHAFTALPTPIQ 488
Db 425 GVLVLAVALASGLGLCALLGITFNAATQVLPALGIGVDVFLLAHAFTALPTPIQ 484
QY 489 ERMGECLORTGTSVLTSTNNMAFLMAALVPIPALRAFSLQAAIVVGCITFVAMLVFPA 548
Db 485 ERMGECLORTGTSVLTSTNNMAFLMAALVPIPALRAFSLQAAIVVGCITFVAMLVFPA 544
QY 549 ILSLDLRRRHCRDLVLCFSSPCSAQVIOILPOELGD-----GTVPVG-----IAHL 596
Db 545 ILSLDLYREKRLDILCCFYSPCSSRVIOIPOELADANDNHASTVPYGHGVATSTQI 604
QY 597 TATVQAFTHCEASSQHVITLPPQAH-----LVPPSPDLGSELSPGSGSTRDLGQBE 650
Db 605 TTTVQAFTHCEASSQHVITLPPQAH-----LVPPSPDLGSELSPGSGSTRDLGQBE 644
QY 651 ETQRKAACKSLCARNLAAHAFYQFAPILLQSHAKAIYVNLFGALLGLSLYCATILVQDG 710
Db 665 EAKGREGCVPLPLCRWLSLDFAREKAPILLQSHAKAIYVNLFGALLGLSLYCATILVQDG 724
QY 711 LALTDVVPRTGKEHAFSLAQRLYFSLYVALVTQGGFDVAHSQALFDLHQRFSSLKAYL 770
Db 725 LYLTDVVPRTGKEHAFSLAQRLYFSLYVALVTQGGFDVAHSQALFDLHQRFSSLKAYL 784
QY 771 PPATQAPRTWLYHYRNWVQGAQADQWASGRITRHSYRNGSEDEGALAYKLLIQTGDA 830
Db 785 REGNHDLPKWLHYFQDWLRGLQATDRDQWAGRIITRHSYRNGSEDEGALAYKLLIQTGDA 844
QY 831 QEPDPSQLTTRKLVDRGLIPPELFYMGTLVWVSSDPLGLAASQANFYPPPEMHLHXY 890
Db 845 KPEFFNQLTTRLVDENGIIPDPTIYICLTWASNDPLGFAASQANFYPPPEMHLHXY 904

QY 891 DTTGENLR 898
Db 905 DTTGENLR 912
RESULT 13
PTCI_CHICK
ID_PTCI_CHICK STANDARD; PRT; 1442 AA.
AC Q90693;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 1 (PTC1) (PTC).
GN Name=PTCH; Synonyms=PTC;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC TISSUE=Limb bud;
RX MEDLINE=96205046; PubMed=8620849;
RA Marigo V., Scott M.P., Johnson R.L., Goodrich L.V., Tabin C.J.;
RT "Conservation in hedgehog signaling: induction of a chicken patched homolog by Sonic hedgehog in the developing limb.";
RT Development 122:1225-1233 (1996).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97064175; PubMed=8906794;
RA Marigo V., Davey R.A., Zuo Y., Cunningham J.M., Tabin C.J.;
RT "Biochemical evidence that patched is the Hedgehog receptor.";
RL Nature 384:176-179 (1996).
CC -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian hedgehog (IHH) and desert hedgehog (DHH). Associates with the smoothened protein (SMO) to transduce the hedgehog's proteins signal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expression is seen in the embryonic neural tube, sclerotome, visceral mesoderm, and limb bud.
CC -!- DEVELOPMENTAL STAGE: In stage 10 embryo, expression is seen in neural tube, and at lower levels in the notochord, epithelial somites, endoderm and splanchnic mesoderm. At stage 18, PTC is broadly expressed in the neural tube but excluded from the cells of the floor plate. At stage 32, expression occurs in the mesodermal cells of the gastrointestinal tract.
CC -!- INDUCTION: Activated by hedgehog; repressed by itself (Probable).
CC -!- PTM: Glycosylation is necessary for SHH binding.
CC -!- SIMILARITY: Belongs to the patched family.
CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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CC -----
CC EMBL; U40074; AAC59898.1; -.
CC PIR; T18538; T18538.
CC InterPro; IPR003392; Patched.
CC InterPro; IPR004766; Patchedtm_recept.
CC InterPro; IPR000731; SSD_5TM.
CC Pfam; PF02460; Patched; 1.
CC TIGRFAMs; TIGR00918; 2A060602; 1.
CC PROSITE; PS0156; SSD; 1.
CC Glycoprotein; Receptor; Transmembrane.
CC DOMAIN 1 101 Cytoplasmic (Potential).
FT TRANSMEM 102 122 Potential.
FT DOMAIN 123 436 Extracellular (Potential).
FT TRANSMEM 437 457 Potential.
FT DOMAIN 458 472 Cytoplasmic (Potential).

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FT TRANSMEM 473 493 Potential.
FT DOMAIN 494 501 Extracellular (Potential).
FT TRANSMEM 502 522 Potential.
FT DOMAIN 523 547 Cytoplasmic (Potential).
FT TRANSMEM 548 568 Potential.
FT DOMAIN 569 577 Extracellular (Potential).
FT TRANSMEM 578 598 Potential.
FT DOMAIN 599 747 Cytoplasmic (Potential).
FT TRANSMEM 748 768 Potential.
FT DOMAIN 769 1026 Extracellular (Potential).
FT TRANSMEM 1027 1047 Potential.
FT DOMAIN 1048 1053 Cytoplasmic (Potential).
FT TRANSMEM 1054 1074 Potential.
FT DOMAIN 1075 1082 Extracellular (Potential).
FT TRANSMEM 1083 1101 Potential.
FT DOMAIN 1102 1120 Cytoplasmic (Potential).
FT TRANSMEM 1121 1141 Potential.
FT DOMAIN 1142 1153 Extracellular (Potential).
FT TRANSMEM 1154 1174 Potential.
FT DOMAIN 1175 1442 Cytoplasmic (Potential).
FT TRANSMEM 1443 160577 MW; 973E5F17FB8B6E43 CRC64;
FT CARBOHYD 141 141 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 312 312 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 349 349 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 414 414 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 827 827 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 874 874 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 999 999 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1442 AA; 160577 MW; 973E5F17FB8B6E43 CRC64;

Query Match 53.3%; Score 3340; DB 1; Length 1442;
Best Local Similarity 54.3%; Pred. No. 2,6e-215; Indels 50; Gaps 17;
Matches 663; Conservative 204; Mismatches 304;

QY 12 PSYTPARTAAQILAG---SLKAPLWLRAYFQGLLFLSLGCGIQRHCGKVLFLGLAFA 68
DB 54 PSYC-DAAPALQIAKGRATGRAPLWLRKQRULLFNLGCIYQKNCGRFLVUGLL-YSA 111
QY 69 LALGURMAIENLEOLWVEGSRVSGELHYKEKLGEEAAYTSQMLIOTARQEGNILT 128
DB 112 FAVGLRAANLETNVEELWVEGSRVRELNYTRQKIGEEAMFNQPMIQTPOEDGTNVL 171
QY 129 PEALGHLOAALTASKVOVSLYKCKWDANKIYKSGVPLIENGMIEMMLEKFLPCVILTP 188
DB 172 TEALQKQLDSALQAKGRVHYMYNRQMKLEHLCYKSGELITEAGYMDPILEYLPCLIITP 231
QY 189 LDCFWEGAKLQGSAYLPGRDPIQWNLDPQLLELPGF-ASLEGFRELLEKAAQVGQAY 247
DB 232 LDCFWEGAKLQGSTAYLLGKPPQLQWLNFDPLFLFLEELKKINYQVESWEMLNKAEGVGY 291
QY 248 VGRPCLPDLDLHCPSPAPNHSRQAPNVAHELSCGCHGSHKFMKMQBELLLGGWARDPQ 307
DB 292 MDPRCLNFPADPCPTAPNKNSTKPLDVALVLSGGCYGLSRKYMHWQEBLLIIGGTVKNS 351
QY 308 GELLRAEALQSTFLMSRQLYEHFRG-DYQTHDIGWSEEQASTVLQAWQRFRVQLAQRA 366
DB 352 GKLVSAQALQWFLMTPKQMEHFYGVSH-INWNEKKAAILLEAWQRYVEVHOS 410
QY 367 LPENASQIHAFSSTTLDILHAFSVSAARVVGGYLLMLAYACVTMLRWDCAQSGSVG 426
DB 411 VAQNSTQKVLSTFTTTLDLILKSPFSDSVIRVASGYLLMLAYACVTMLRWDCAKSQGAVG 470
QY 427 LAGVLLVALAVASGLGCLALLGITFNAAITQVLPFLALGIGVDDVFLLAHATEALPG-- 484
DB 471 LAGVLLVALSVAAGLCLSLIGTSENAATTQVLPFLALGVGDVDDVFLLAHAFSETQNKR 530
QY 485 TPLQERMGCLORTGTSVSVLTNNMAAFMLAALVPIPALRAFSLQAAIVGCTFVAVML 544
DB 531 IPEFQRTGCLKRTGASVALTSLSNVTAFPMALIPALRAFSLQAAVVVFNFAVML 590
QY 545 VFPAILSLDLRRRHCRQLDVLCCFSFSCSAQVITQILPQELGD-----GTVPVGLAH--- 595
DB 591 IFPAILSMDLXRRDRRLDIFCCFTSPCVTRVIQIEPQAYAENDNICYSSPPYSSHPA 650

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QY 596 -----LTATVQAFTHCEASSQHVVITLPPQAHLYVPPP-----SDPLGSELFPGGGSTRDL 645
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QY 646 LGOEBETRQKAACKSLPCARWNLAHFARYQFAPLLOSHAKAIVLVLFQALLGLSLYGAT 705
DB 711 LSQFSDS--SVHCLEPPCTKWTLSFAEKHYAPFLKPKRAKVUVIFLGLGLSLYGT 768
QY 706 LVQDGLALTDVVPRGTKEHAFSLAQRLYFSLYEVALVTQGGFDYAHQSRALEFDLHORFSS 765
DB 769 RVRDGLDLTDIVPRTREYDFIAAQFKYFSEYNNMIVTQKA-DYENVOQLLXELHRSFSN 827
QY 766 LKAVLPPPATQAPRTLHYRNWLOGIAAFQDQNASGRITHSRHSYRNGSEDEGALAYKLILI 825
DB 828 VTYVILLEGDRQLPKMWLHYFRDLWLOGLQDAFDWETGKITYSNYKNGSDDAVLAYKLIV 887
QY 826 QTGDAQEPLDFESOLTRKLVDRGLIPPELFYMGVLTVMVSSDPLGLAASQANFYPPPEW 885
DB 888 QTGNRAKPIDISQLTQRKQRLVDADGIINPNAFYIYLTAWVNSDPVAYASQANIRPHRPEW 947
QY 886 LHDKYDTTGE-NLRIPPAQPLEFAQFPFLRLGLQKTADFVEAIEGARAAACABAGQAGVHA 944
DB 948 VHDKADYMPETRLRIPAAEPIEYAOFPFYNGLRSETDFEAELEKVRACNNVYSLGIAS 1007
QY 945 YPSGSPFFLFWBOYLGLRRCFLLAVALCILLVCTFLVCAALLLNPTWAGLIVLVAMTVLELF 1004
DB 1008 YPNGYPFLFWBOYIGLRHMLLSISVLACTFLVCAFLLNPTWAGIIVVVALAMTVLELF 1067
QY 1005 GIMGFLGIKLSAIPVVLIVASVIGVEFTVHVVALGFLTTQGSRNLRRAHALHETAPVTD 1064
DB 1068 GMMGLIGIKLSAVPVVILLASVIGVEFTVHVVALGFLTTQGSRNLRRAHALHETAPVTD 1127
QY 1065 GAISTLLGLMLAGSHDFIVRYFFAALTVLTLLGLLHGLVLLPVLLSLILGPPPEVI--- 1121
DB 1128 GAVSTLLGLVLAGSEDFIVRYFFAVLAILITLGLVNGLVLLPVLLSPFFGYPPEVSPAC 1187
QY 1122 ---QMKYSPELLSPPA-----POGGGLRWGASSLSPOSFARVTTSMVAIH---PPPL 1169
DB 1188 GRNRLFTPSPE--PPSIVRFALPFGHTNNGSDSDSEYSSQTTVSGISELHHEATOS 1245
QY 1170 PGAYTHPAPDEPPMSPAATSS 1190
DB 1246 PGIPVHVQVVVEATENPVFARS 1266

RESULT 14
Q6UY90 PRELIMINARY; PRT; 1434 AA.
AC Q6UY90;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Patched.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=P344;
RX MEDLINE=22381811; PubMed=12469128;
RA Lai K., Kaspar B.K., Gage F.H., Schaffer D.V.;
RT "Sonic hedgehog regulates adult neural progenitor proliferation in
RT vitro and in vivo.";
RL Nat. Neurosci. 6:21-27(2003).
DR BMBL; AY357891; BAA067738.1;
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patched.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; I.
DR TIGRFam; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.

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416	QY	WDCAQSGSVGLAGVLLVALAVASGLGECALLGIFTNAAATQVLPFLALGIGVDDVPFLA	475
446	Db	WDCSKSGAVGLAGVLLVALSVAAAGLGLSIGISFNAAATQVLPFLALGIGVDDVPFLA	505
476	QY	HAFTEALPG--TPOERMGECLORTGTSVVLTSINMAAFALFMAALVPIPALRAFSLOAAI	533
506	Db	HAFSETGQNKRIFFEDRTGKCLKRTGASVALTSISNVTAFFMAALVPIPALRAFSLOAAV	565
534	QY	VWGCTFVAVMLVFPAILSLDRRRHRCQLDVLCCFSSPCSAQVITQILPQBLGDGTVP---	590
566	Db	VVVFNFAWVLLIPPAILSMDLYRREDRLDOI FCCFTSPCVSRVIOVEPQAV---TEPHSN	622
591	QY	-----VGIAHUT-----ATVOAQFTHCEASSOHVVTILPQAHLVPPP-----SDP	630
623	Db	TRYSPPPYPSSHFAHEHTHIMOSTVOLRTEYDPHTHYVYTTPRSEISVQPVVTITQDT	682
631	QY	LGSELPFGSGSTRDLLGOEBETRKAACKSLPCARWNLAHFARYQFAPAPLILQSHAKAIVL	690
683	Db	LSCQSPBSTSTRDLLSQFSDS--SLHCLPEPCTKWTLSFEAKHYAPFLRPKAKVVVI	740
691	QY	VLFGALLGLSLYGATLVQDGLAITDVVPRGTKEHAFLSAQLRVPSLYEVALVTQGGDYA	750
741	Db	LLFLGLLGLSVLYGTVTRVDCGLDLTDIVPERETREYDFIAAQFKYFSPFNMVITQKA-DYP	799
751	QY	HSQRAFLDLHORSSILKAVLPPATQAPRTHLYRNNWLOGIOAAQPDQWASGRITHSY	810
800	Db	NIQHLLYDLHKSPSSVKYVMLEENKQUPQMWLHYFRDWLQGLQDAFDSDETGRIMPNNY	859
811	QY	RNGSEDCALAYKLIIOTGDAQEPDLDFSQLTRKLIVDREGILPELFGMLTVMVSSDPLG	870
860	Db	KNGSDDGVLAYKLIVQTRGSRDKPIDISQTKQRLVDADGIINPSAFYIYLTAWVSNDPVA	919
871	QY	LAASQANFYPPPEWLHKDYDTTGE-NLRTPPQPLEFAQFPFLRLGLQKTAQDFVEAIEG	929
920	Db	YAAASQANIRHPREWHDKADYMPETRLRIPAAEPIEYQAFPEFYNLGRUOTSDFVEAIEK	979
930	QY	ARAAACAEGAQGVHAYPSGSPFLFWEQYGLRRCFLIACVILVCTELVCALLLNPWTA	989
980	Db	VRVICNNYTSGLSHSSYPNGVPFFWEQYISLRHWLLLAISVULACTELVCAPFLNPWTA	1039
990	QY	GLIVLVAMMTVELFGIMFGLIGIKLSAIPVVILVASVIGIVEFTHVALGFLTQGSRNIL	1049
1040	Db	GIIVMVLLAMTVELFGMWGLIGIKLSAVPVVILLIASVIGIVEFTHVALAFLTAIGDKNH	1099
1050	QY	RAAHALEHTPAPYTDGAI STLGLLMLAGSHFPFIVRYFFAALTVLTLGLLGLVLPLPV	1109
1100	Db	RAMLALEHMFAPVLDGAVSTLLGVMLAGSEFPFIVRYFFFAVLAILTVLGVMLGLVLLPV	1159
1110	QY	LLSILGPPPPVEVIQWYKESPEILSPAPQGGGLRWGASSSLPQSFARVTTSMTVAIHPPL	1169
1160	Db	LLSFFGCEPVE-----SPANG-----INRLP-----TSPPEPPS	1189
1170	QY	PGAYIHPADPPWSPAASTSGNLSL	1195
1190	Db	VWRFAYVE-----PGHTNNGSDSS	1207

Search completed: November 22, 2004, 07:57:32
Job time : 99 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 05:38:23 ; Search time 78 Seconds

(without alignments)
5532.710 Million cell updates/sec

Title: US-09-990-046-2

Perfect score: 6272

Sequence: 1 MTRSPPLRELPSYTPPART.....SPAATSSGNLSRGPGPATG 1203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6272	100.0	1203	2	AAY43261 Human pat
2	6272	100.0	1203	5	AAE19829 Human pat
3	6272	100.0	1203	6	ABG74104 Human pat
4	6248	99.6	1203	2	AAW28444 Human pat
5	6238	99.5	1203	3	AAW28444 Human pat
6	5911	94.2	1146	3	AAW28444 Human pat
7	5599	89.3	1182	5	AAE19831 Human pat
8	3348	53.4	1447	2	AAW75375 Human pat
9	3348	53.4	1447	2	AAW52200 Human pat
10	3348	53.4	1447	2	AAW72969 Human pat
11	3348	53.4	1447	4	AAW72969 Human pat
12	3348	53.4	1447	5	AAE19830 Human pat
13	3348	53.4	1447	5	ABJ10931 Human pat
14	3348	53.4	1447	5	ABG79571 Human pat
15	3348	53.4	1447	7	ABU62275 Human pat
16	3348	53.4	1447	7	ADD46678 Human pat
17	3348	53.4	1447	7	ADH62731 Human pat
18	3348	53.4	1447	8	ADH62731 Human pat
19	3348	53.4	1447	8	ADH62731 Human pat
20	3337	53.2	1434	2	AAW52199 Human pat
21	3337	53.2	1434	2	AAW72968 Human pat
22	3337	53.2	1434	4	AAW72968 Human pat
23	3337	53.2	1434	5	AAW72968 Human pat
24	3337	53.2	1434	7	ABU62271 Human pat
25	3337	53.2	1434	7	ADH62731 Human pat

ALIGNMENTS

RESULT 1

AA43261
ID AAY43261 standard; protein; 1203 AA.

XX AC AAY43261;

DT 19-JAN-2000 (first entry)

XX XX Human patched-2 protein sequence.

XX Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
XX cell proliferation; cell differentiation; testicular cancer; gut disease;
XX degenerative disorder; nervous system disorder; Parkinson's disease;
XX memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
XX Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
XX infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
XX therapy.

XX OS Homo sapiens.

XX WO9953058-A1.

XX 21-OCT-1999.

XX 02-APR-1999; 99WO-US007417.

XX 15-APR-1998; 98US-00060939.

XX (GETH) GENENTECH INC.

XX De Sauvage FJ, Carpenter DA;

XX WPI; 1999-620428/53.

XX N-PSDB; AAZ31717.

XX New isolated human patched-2 gene, used to develop products for treating,
XX e.g. cancer and Alzheimer's disease.

XX Claim 14; Fig 1; 124pp; English.

XX This sequence represents the human patched-2 (ptch-2) protein of the
XX invention. The patched-2 polypeptides are signalling molecules,
XX specifically for signalling and mediator molecules in the hedgehog (hh)
XX cascade which are involved in cell proliferation and differentiation.
XX They can be used for the treatment of disorders which are mediated at
XX least in part by Hh, especially Dhh, e.g. testicular cancer. They can
XX also be used for treating degenerative disorders of the nervous system,
XX e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou

Adh62722 Mouse pat
Ade48980 Mouse pat
Aar94380 Mouse pat
Aaw47157 Nevoid ba
Aaw82586 Human pat
Aaw52197 Precis co
Aaw72971 Precis co
Aab67156 Butterfly
Aag79573 Butterfly
Abu62149 Buckeye p
Ade94209 Peacock b
Adh62716 Butterfly
Ade48974 Butterfly
Abj10929 TRC8 rela
Aar86304 Drosophil
Aae05389 Human pat
Aab85751 Hedgehog
Aab31232 A consens
Abb79150 Patched p

26 3337 53.2 1434 7 ADH62722
27 3337 53.2 1434 8 ADE48980
28 3335 53.2 1434 2 AAR94380
29 3048 48.6 1296 2 AAW47157
30 2627 41.9 529 2 AAW82586
31 2236 35.7 1311 2 AAW52197
32 2235 35.6 1311 2 AAW72971
33 2235 35.6 1311 4 AAB67156
34 2235 35.6 1311 5 AAG79573
35 2235 35.6 1311 7 ABU62149
36 2235 35.6 1311 7 ADE94209
37 2235 35.6 1311 7 ADH62716
38 2235 35.6 1311 8 ADE48974
39 1992 31.8 1286 4 ABB59092
40 1992 31.8 1286 5 ABJ10929
41 1961.5 31.3 1299 2 AAR86304
42 1961.5 31.3 1299 4 AAE05389
43 1961.5 31.3 1299 4 AAB85751
44 1961.5 31.3 1299 4 AAB31232
45 1961.5 31.3 1299 5 ABB79150

CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
CC addiction. Patched-2 agonists can be used to treat gut diseases, bone
CC addition. Patched-2 agonists can be used to treat gut diseases, bone
CC diseases, skin diseases, diseases of the testis (including infertility),
CC ulcers, lung diseases, diseases of the pancreas, diabetes, and
CC osteoporosis. Antagonists or agonists of patched-2 may be used for
CC treating disorders or creating a desirable physiological condition
CC effected by blocking Hh signalling, especially Dhh signalling, e.g.
CC contraception or infertility treatment. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic animals
XX

SQ Sequence 1203 AA;

Query Match 100.0%; Score 6272; DB 2; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LGLAFGALALGLRMAIIEETNEQLWVEGSRVSQELHYTKELGEEAAYTSQMLIOTAR 120
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DB 121 QGENILTPALGLHLQAALTASKQVSLYKSWDLNKKICYKSGVPLIENGMIENWIEKL 180
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DB 181 FFCVILTPDLDFWEGAKLGGSAAYLFGRPDIQWTLNLDPEQLLELGGFASLEGFRELDDK 240
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QY 841 TRKLVDREGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDITGTENLRIP 900

841 TRKLVDREGLIPPELFYMGTLVWVSDPLGLAASQANFYPPPEWLHDKYDITGTENLRIP 900
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DB 1141 LRWGASSLSLPOSFAVTTSMTVAIHPPLPGAYIHPADEPPWSPAATSSGNLSRGP 1200
QY 1201 ATG 1203
DB 1201 ATG 1203

RESULT 2
AAE19829
ID AAE19829 standard; protein; 1203 AA.
XX AAE19829;
XX 18-JUN-2002 (first entry)
XX Human patched-2 (Ptc-2) protein.
XX Human; patched-2; Ptc-2; cell proliferation; differentiation; therapy;
XX cytosolic; testicular cancer; hedgehog protein signalling.
XX Homo sapiens.
XX Key
XX Location/Qualifiers
XX 57..76
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XX /note= "Transmembrane domain"
XX 394..414
XX /label= TM2
XX /note= "Transmembrane domain"
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XX 502..524
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XX 1014..1033
XX /label= TM10

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FT      /note= "Transmembrane domain"
FT      1058..1077
FT      /label= TM11
FT      /note= "Transmembrane domain"
FT      1091..1114
FT      /label= TM12
FT      /note= "Transmembrane domain"
XX      US6348575-B1.
PN      19-FEB-2002.
PD      15-APR-1999; 99US-00293505.
XX      15-APR-1998; 98US-0081884P.
XX      (GETH ) GENENTECH INC.
XX      De Sauvage F, Carpenter DA;
XX      WPI: 2002-215260/27.
XX      N-PSDB; AAD31576.
XX      Native human patched-2 polypeptide for treating disorders caused by
XX      Hedgehog protein signaling such as testicular cancer, and for screening
XX      cDNA libraries.
XX      Example 1; Fig 1; 82pp; English.
XX      The invention relates to an isolated sequence comprising a native human
XX      patched-2 (Ptc-2) polypeptide. The invention also relates to signalling
XX      and mediator molecules in the hedgehog (Hh) cascade which are involved in
XX      cell proliferation and differentiation. The isolated sequence is useful
XX      for the treatment of disorders which are linked to Hedgehog, especially
XX      desert hedgehog expression, such as testicular cancer. It may also be
XX      used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its
XX      homologues, and to diagnose whether a disorder is driven by Ptc-2 or
XX      Hedgehog protein signalling. The present sequence is human patched-2
XX      (Ptc-2) protein
XX      SQ      Sequence 1203 AA;

Query Match      100.0%; Score 6272; DB 5; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLCGIGRHCGRVLF 60
DB      1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLCGIGRHCGRVLF 60
QY      61 LGLLAFGALGLRMAIITETNLEQLWVEVGRSVQELHYTKELGEEAAYSQMLIQIAR 120
DB      61 LGLLAFGALGLRMAIITETNLEQLWVEVGRSVQELHYTKELGEEAAYSQMLIQIAR 120
QY      121 QEGENILTPREALGLHQAALTASKVQVSLYKGSMDLNKI CYKSGVPLIENGMIEMIEKL 180
DB      121 QEGENILTPREALGLHQAALTASKVQVSLYKGSMDLNKI CYKSGVPLIENGMIEMIEKL 180
QY      181 FPCVILTPDQCFWEGAKLQGSAYLPGRPDIQWNTNLDPELLELGPFAISLEGPRELLDK 240
DB      181 FPCVILTPDQCFWEGAKLQGSAYLPGRPDIQWNTNLDPELLELGPFAISLEGPRELLDK 240
QY      241 AQVGAYVGRPCLPDHLHCPSPAPNHHSRQAPNVAAHLSGCGCHGFSKFMHWQBELLLG 300
DB      241 AQVGAYVGRPCLPDHLHCPSPAPNHHSRQAPNVAAHLSGCGCHGFSKFMHWQBELLLG 300
QY      301 GMARDPQCELLRAEALQSTFLLMSRQLYEPRGDIQTHDVGWSEQAQSTVLQAWQREFV 360
DB      301 GMARDPQCELLRAEALQSTFLLMSRQLYEPRGDIQTHDVGWSEQAQSTVLQAWQREFV 360
QY      361 QLAQEALPENASQIHFASSTTLDLHAFSEVSAARVVGGLMLAYACVTMLRWDCQAQ 420
DB      361 QLAQEALPENASQIHFASSTTLDLHAFSEVSAARVVGGLMLAYACVTMLRWDCQAQ 420

QY      421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
DB      421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
QY      481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSQAAIIVGCTFV 540
DB      481 ALPGTPLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSQAAIIVGCTFV 540
QY      541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIOILPOELGDTGTVPGVIAHLTATV 600
DB      541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIOILPOELGDTGTVPGVIAHLTATV 600
QY      601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFSPGSGTRDLGQEEETRQKAACKS 660
DB      601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFSPGSGTRDLGQEEETRQKAACKS 660
QY      661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFQALLGLSLYGATLVQDGLALTQVVRG 720
DB      661 LPCARWNLAHFARYQFAPILLQSHAKAIVLVLFQALLGLSLYGATLVQDGLALTQVVRG 720
QY      721 TKEHAFSLAQRYFSLYEVALVTQGFQDYAHQSQRALFDLHQRFSSIKAVLPPPAQAPRT 780
DB      721 TKEHAFSLAQRYFSLYEVALVTQGFQDYAHQSQRALFDLHQRFSSIKAVLPPPAQAPRT 780
QY      781 WLHYRNWLQGIQAAFDQDQWASGRITRHSYRNGSEDEGALAYKLLIQTQDAQBPLOFSQLT 840
DB      781 WLHYRNWLQGIQAAFDQDQWASGRITRHSYRNGSEDEGALAYKLLIQTQDAQBPLOFSQLT 840
QY      841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
DB      841 TRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY      901 PAQPLEFAQFPFLRLGLOKTADFVEAIEGARACAAEQAGVHAYPSGSPFLFWQYLG 960
DB      901 PAQPLEFAQFPFLRLGLOKTADFVEAIEGARACAAEQAGVHAYPSGSPFLFWQYLG 960
QY      961 RRCFLAVCIILVCTFLVCALLLNPWTAGLIVLVAMTVLVELFGIMFGIKLSAIPV 1020
DB      961 RRCFLAVCIILVCTFLVCALLLNPWTAGLIVLVAMTVLVELFGIMFGIKLSAIPV 1020
QY      1021 ILVASVGIGVSTVHVHVALGELTQGSRLRAHALEHTFAPVTDCAISTLGLMLAGSH 1080
DB      1021 ILVASVGIGVSTVHVHVALGELTQGSRLRAHALEHTFAPVTDCAISTLGLMLAGSH 1080
QY      1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVIQMYKESPEILSPAPQGG 1140
DB      1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVIQMYKESPEILSPAPQGG 1140
QY      1141 LRWGASSSLPOSFARVTTMTVAIHPPPLPGAYIHPADPEPPWSPAATSSGNLSRGPGP 1200
DB      1141 LRWGASSSLPOSFARVTTMTVAIHPPPLPGAYIHPADPEPPWSPAATSSGNLSRGPGP 1200
QY      1201 ATG 1203
DB      1201 ATG 1203

RESULT 3
ABG74104
ID ABG74104 standard; protein; 1203 AA.
XX ABG74104;
AC ABG74104;
XX 02-APR-2003 (first entry)
XX Human patched-2 protein.
XX Human; patched-2; Dhh signalling; proliferation; differentiation;
XX chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;
XX basal cell carcinoma; neurodegenerative disorder; memory deficit;
XX Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease;
XX Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;

```

KW bone disease; skin disease; testicular disease; ulcer; lung disease;
KW pancreatic disease; diabetes; osteoporosis; desert hedgehog.
XX Homo sapiens.
XX US2002156245-A1.
XX 24-OCT-2002.
XX 20-NOV-2001; 2001US-009900045.
XX 15-APR-1998; 98US-0081884P.
XX 15-APR-1999; 99US-00293505.
XX (GETH) GENENTECH INC.
XX De Sauvage FJ, Carpenter DA;
XX WPI: 2003-182650/18.
XX N-PSDB; ABX15919.
XX New nucleic acid, useful for manufacturing a medicament for diagnosing or
XX treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
XX e.g., testicular cancer.
XX Claim 14; Fig 1; 85pp; English.
XX The invention relates to a new isolated nucleic acid encoding a
XX polypeptide having patched-2 biological activity, comprises DNA having at
XX least 95% sequence identity with a DNA molecule or its complement
XX encoding: (a) a human patched-2 polypeptide comprising the sequence
XX ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
XX Deposit No. 299778 designation). Also included are a vector comprising
XX the nucleic acid, a host cell transformed with the vector, a process for
XX producing patched-2 polypeptides, an isolated native sequence of human
XX patched-2 polypeptide, a chimeraic molecule comprising the vertebrate
XX patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
XX patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
XX hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
XX patched-2 that stimulates or enhances the normal functioning of patched-2
XX in the Dhh signalling pathway, screening for ant/agonists of patched-2
XX and diagnosing to determine whether a particular disorder is modulated
XX The nucleic acid is useful for manufacturing a medicament for diagnosing
XX or treating a disorder that is modulated by Dhh signalling e.g. tumour,
XX basal cell carcinoma, neurodegenerative disorders, memory deficit,
XX Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
XX Huntington's disease, schizophrenia, stroke, drug addiction, gut
XX diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
XX diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
XX Patched-2 may also be used to develop male contraceptives. The gene for
XX Patched-2 is located on human chromosome 1p33-34. The present sequence
XX represents human patched-2 protein
XX Sequence 1203 AA;
Query Match 100.0%; Score 6272; DB 6; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRSPPLRLPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLGCGIORHCKVLF 60
DB 1 MTRSPPLRLPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLGCGIORHCKVLF 60
QY 61 LGLAFGALALGRMAIETNLEQLMVVEGSRVSRVQELHYTKELKGBEAAVTSOMLIQTAR 120
DB 61 LGLAFGALALGRMAIETNLEQLMVVEGSRVSRVQELHYTKELKGBEAAVTSOMLIQTAR 120
QY 121 QGENTLTPEALGLHQAALTASKVOVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
DB 121 QGENTLTPEALGLHQAALTASKVOVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLCFWEKAKLQGSAYLPGRPDIQWTNLDPEQLLEELGFASLEGFRELLDK 240

DB 181 FPCVILTPDLCFWEKAKLQGSAYLPGRPDIQWTNLDPEQLLEELGFASLEGFRELLDK 240
QY 241 AQVQAYVGRPCCLHPDDDLHCPSPAPNHHSRQAPNVVAHELSCGCHGFSKFKMHWQBELLLG 300
DB 241 AQVQAYVGRPCCLHPDDDLHCPSPAPNHHSRQAPNVVAHELSCGCHGFSKFKMHWQBELLLG 300
QY 301 GWARDPQGBELLRAEALQSTFELLMSPROLYEHFRGRDYQTHDIGWSEQASTVLQAWORREV 360
DB 301 GWARDPQGBELLRAEALQSTFELLMSPROLYEHFRGRDYQTHDIGWSEQASTVLQAWORREV 360
QY 361 QLAQEALPENASQOIHFASSTTDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
DB 361 QLAQEALPENASQOIHFASSTTDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
DB 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAITQVLPFLALGIGVDDVFLAHAFTE 480
QY 481 ALPGTPLQERMGECLORTGTSVWLTSINMAAFMAALVPIPALRAFSLQAAIVVGCTEV 540
DB 481 ALPGTPLQERMGECLORTGTSVWLTSINMAAFMAALVPIPALRAFSLQAAIVVGCTEV 540
QY 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPOELGDTVPVGIHLTATV 600
DB 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPOELGDTVPVGIHLTATV 600
QY 601 QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFSFGGSTRDILGQEEETROKAAKS 660
DB 601 QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFSFGGSTRDILGQEEETROKAAKS 660
QY 661 LPCARWNLHAHFARYOFAPLLQSHAKATVLPFGALLGLSLYGATLVQDGLALTVDVVRG 720
DB 661 LPCARWNLHAHFARYOFAPLLQSHAKATVLPFGALLGLSLYGATLVQDGLALTVDVVRG 720
QY 721 TKHEAFLSAQLRFLSYEVALVTQGGFDYAHSQORALFDLHQRFSSLKAVLPPTAQAPT 780
DB 721 TKHEAFLSAQLRFLSYEVALVTQGGFDYAHSQORALFDLHQRFSSLKAVLPPTAQAPT 780
QY 781 WLHYRNWMLQTOAADFQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQPLDFSQLT 840
DB 781 WLHYRNWMLQTOAADFQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQPLDFSQLT 840
QY 841 TKRLVDREGLIPELFPYMGITVWVSDPLGLAASQANFYPPPEWHLHDKYDTTGENLRIP 900
DB 841 TKRLVDREGLIPELFPYMGITVWVSDPLGLAASQANFYPPPEWHLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQFPPELLRGLQKTADFVEAIEGARAACAAGQAGVHAYPSGSPFLFWEOYLGL 960
DB 901 PAQPLEFAQFPPELLRGLQKTADFVEAIEGARAACAAGQAGVHAYPSGSPFLFWEOYLGL 960
QY 961 RRCFLAVCILLVCTFLVCALLLNPWTAGLVVLAMMTVELFGIMGLGKLSAIPV 1020
DB 961 RRCFLAVCILLVCTFLVCALLLNPWTAGLVVLAMMTVELFGIMGLGKLSAIPV 1020
QY 1021 ILVAVSGIGVEFTVHVALGFLTTCGRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
DB 1021 ILVAVSGIGVEFTVHVALGFLTTCGRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
QY 1081 FDFIVRYFFAALTTLTLLGLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
DB 1081 FDFIVRYFFAALTTLTLLGLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
QY 1141 LWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPADDEPKWSPAATSSGNLSRGPGP 1200
DB 1141 LWGASSSLPQSFARVTTSMTVAIHPPPLPGAYIHPADDEPKWSPAATSSGNLSRGPGP 1200
QY 1201 ATG 1203
DB 1201 ATG 1203

ID AAY28444 standard; protein; 1203 AA.
 AC AAY28444;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE Human ptc-2 protein.
 XX
 KW Patched-2; ptc-2; human; hedgehog receptor; nontropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW basal injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
 KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 KW lesion-induced death; neuron regeneration; damage repair; skeletal;
 KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
 XX
 OS Homo sapiens.
 XX
 PN WO929854-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 08-DEC-1998; 98WO-US026009.
 XX
 PR 08-DEC-1997; 97US-0067940P.
 XX
 PA (ONTO-) ONTOGENY INC.
 XX
 PI Bumcrot DA;
 XX
 XX WPI; 1999-561298/47.
 DR N-PSDB; MAX89478.
 DR
 XX
 PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 PT prevention and/or reduction of the severity of neurological conditions.
 PS
 PS Claim 3; Page 73-77; 80pp; English.
 XX
 CC This invention describes a novel recombinantly produced human patched-2
 CC (ptc-2) polypeptide which has nontropic, neuroprotective, cardiant,
 CC antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
 CC protein is a hedgehog receptor and is therefore capable of modulating
 CC hedgehog signalling, and so affect a number of hedgehog-mediated
 CC biological activities. The human patched-2 (ptc-2) protein can be used to
 CC screen for modulators, antagonists and agonists, which are likely to play
 CC an important role in the modulation of cellular proliferation and
 CC maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
 CC tissues during disease states. Modulators of ptc-2 protein can be used
 CC for in vivo reformation of tissue, to improve grafting and morphology of
 CC transplanted tissue; for the treatment, prevention and/or reduction of
 CC the severity of neurological conditions deriving from: injury to the
 CC nervous system including traumatic injury, chemical injury, vascular injury
 CC and deficits (such as ischemia resulting from stroke), together with
 CC infectious/inflammatory and tumor-induced injury; ageing of the nervous
 CC system including Alzheimer's disease; chronic neurodegenerative diseases
 CC of the nervous system including Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis, as well as spinocerebellar degeneration;
 CC and chronic immunological diseases of the nervous system including
 CC multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
 CC of autonomic disorders of the peripheral nervous system, including
 CC disorders affecting the innervation of smooth muscle and endocrine
 CC tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
 CC Antagonists of ptc-2 protein can be used to prevent differentiation of
 CC cells in culture, as well as for treatment of chronic pain syndromes.
 CC Agonists may be used to rescue neurons from lesion-induced death as well
 CC as neuron regeneration, in diseases such CNS trauma infarction, (viral)

CC infection, metabolic disease, nutritional deficiency, toxic agents, and
 CC so on. ptc-2 therapeutics may also be used for the repair of central and
 CC peripheral nerve damage, for repair and regeneration of non-neuronal
 CC tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
 CC osteogenesis, arthritis, bone fractures, hereditary disease, as well as
 CC for generation of prosthetic cartilage devices, and to induce
 CC spermatogenesis and as fertility enhancers. This sequence represents the
 CC human ptc-2 protein described in the invention
 XX
 SQ Sequence 1203 AA;

Query Match 99.6%; Score 6248; DB 2; Length 1203;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPRLPSPYTPPARTAAPQIILAGSLKAPLMRLRAYFQGLLPSGLGGIQRHCKGVLF 60
 DB 1 MTRSPRLPSPYTPPARTAAPQIILAGSLKAPLMRLRAYFQGLLPSGLGGIQRHCKGVLF 60
 QY 61 LGLLAFGALALGLRMAIETNLEQLWVEVSGRSVQELHYTKELGEEAAYTSQMLIOTAR 120
 DB 61 LGLLAFGALALGLRMAIETNLEQLWVEVSGRSVQELHYTKELGEEAAYTSQMLIOTAR 120
 QY 121 QSGENILTPALGLHLQAALTASKVQVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
 DB 121 QSGENILTPALGLHLQAALTASKVQVSLYKSWDLNKICYKSGVPLIENGMIEMIEKL 180
 QY 181 FFCVILTPDLCFWEKALQGGSAIYLPGRPDIOIWTNLDPEQLLEELGPPASLGGFRELDDK 240
 DB 181 FFCVILTPDLCFWEKALQGGSAIYLPGRPDIOIWTNLDPEQLLEELGPPASLGGFRELDDK 240
 QY 241 AQVGQAYVGRPCILHPDDLHCPPSAPNHHSRQAPNVAHELGGCHGFSGHFKFMHQEELLG 300
 DB 241 AQVGQAYVGRPCILHPDDLHCPPSAPNHHSRQAPNVAHELGGCHGFSGHFKFMHQEELLG 300
 QY 301 GWARDPQCELLRAEALQSTFELLMSPROLYEYHPRGDYOTHDICWSEQASTVLQAWQRRFV 360
 DB 301 GWARDPQCELLRAEALQSTFELLMSPROLYEYHPRGDYOTHDICWSEQASTVLQAWQRRFV 360
 QY 361 QLAQALPENASQIIFAFSSITLDDIILHAFSEVSARVVGYYLLMALVACVTMLRWDCAQ 420
 DB 361 QLAQALPENASQIIFAFSSITLDDIILHAFSEVSARVVGYYLLMALVACVTMLRWDCAQ 420
 QY 421 SQGSVGLAGVILVALAVASGLGCLCALLGITFNAATTQVLPFLALGIGVDDVELLAHAFTE 480
 DB 421 SQGSVGLAGVILVALAVASGLGCLCALLGITFNAATTQVLPFLALGIGVDDVELLAHAFTE 480
 QY 481 ALPGTFLQRMGECLOQTGTSVLTSSINMAAFMAALVPPALRAFSLQAAIVVGCTFV 540
 DB 481 ALPGTFLQRMGECLOQTGTSVLTSSINMAAFMAALVPPALRAFSLQAAIVVGCTFV 540
 QY 541 AVMLVFPAILSLDRLRRHRCORLDVLCFSSPCSAQVIOILPQELGDDGTVPVGGIAHLTATV 600
 DB 541 AVMLVFPAILSLDRLRRHRCORLDVLCFSSPCSAQVIOILPQELGDDGTVPVGGIAHLTATV 600
 QY 601 QAFTHCEASSOHVVTILPPQAHVLPVPPSDPLGSELSFSGSTRDLGQEEETROKAAKCS 660
 DB 601 QAFTHCEASSOHVVTILPPQAHVLPVPPSDPLGSELSFSGSTRDLGQEEETROKAAKCS 660
 QY 661 LPCARWNLAHFARYOFAPLLQSHAKAIVLFGALLGLSLYGATLVQDGLALTDVVRG 720
 DB 661 LPCARWNLAHFARYOFAPLLQSHAKAIVLFGALLGLSLYGATLVQDGLALTDVVRG 720
 QY 721 TKEHAFSAQRYSLSLVEVALVTGGFDYAHSQBALFDLHORFSSSLKAVLPPPTQAPRT 780
 DB 721 TKEHAFSAQRYSLSLVEVALVTGGFDYAHSQBALFDLHORFSSSLKAVLPPPTQAPRT 780
 QY 781 WLHYRNWLOGIOAFAFDQDWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSQLT 840
 DB 781 WLHYRNWLOGIOAFAFDQDWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSQLT 840
 QY 841 TRKLVDREGILPPELFYMGLTVMVSSDPLGLAASQAFYPPPPWHLHDKYDTTGENLRIP 900

Db 841 TRKLVDRGLTPELFFYMCLTVWVSSDPLGLAASQANFYPPPEMLHDKYDTTGENLRIP 900
 QY 901 PAQPLEFAQFPFLRLGLQKTADFVAIEGARAACACAGQVHAYPSGPFLEWQYLG 960
 Db 901 PAQPLEFAQFPFLRLGLQKTADFVAIEGARAACACAGQVHAYPSGPFLEWQYLG 960
 QY 961 RECFLLAVCILVAVCTFLVCAALLNPWTAGLIVLVLMMTVLFGIMGFLGKLSAIPV 1020
 Db 961 RECFLLAVCILVAVCTFLVCAALLNPWTAGLIVLVLMMTVLFGIMGFLGKLSAIPV 1020
 QY 1021 ILVASGVIGVETVHVAGFLTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
 Db 1021 ILVASGVIGVETVHVAGFLTTQGSRLNRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
 QY 1081 FDFIVRYFPAALTUTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG 1140
 Db 1081 FDFIVRYFPAALTUTLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPIILSPAPQGG 1140
 QY 1141 LRWASSSLPQSFARVTTGTMVAIHPPPLPGAYIHPADPPWSPATSSGNLSRGPGP 1200
 Db 1141 LRWASSSLPQSFARVTTGTMVAIHPPPLPGAYIHPADPPWSPATSSGNLSRGPGP 1200
 QY 1201 ATG 1203
 Db 1201 ATG 1203
 RESULT 5
 ID AAY92703 standard; protein; 1203 AA.
 XX AAY92703;
 AC
 AC
 DT 10-AUG-2000 (first entry)
 XX
 DE Human patched 2 (PTCH2) protein splice variant.
 DE
 KW Patched 2; PTCH2; 1p32-35; tumour suppressor; familial melanoma CMML;
 KW familial adenomatous polyposis; hMOM1; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; gene therapy; chromosome 1p32-35; splice variant.
 XX
 OS Homo sapiens.
 XX
 PN WO200020037-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-SE001784.
 XX
 PR 06-OCT-1998; 98SE-00003393.
 XX
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
 PI Hollingsworth RE;
 PI
 XX WPI; 2000-303645/26.
 DR N-PSDB; AAA09084.
 DR
 XX Isolated human protein capable of participating in human patched
 PT gene/sonic hedgehog pathway during embryonic development is used in
 PT medicament for treatment of condition involving tumors such as basal cell
 PT carcinoma.
 XX
 PS Disclosure; Page; 55pp; English.
 XX
 CC This protein is a splice variant encoded by the novel human patched 2
 CC gene (PTCH2), which has been localised by radiation hybrid mapping to
 CC chromosome 1p32-35 with D1S211 and W1404 as closest flanking markers and
 CC with an estimated localisation 5.5 cR from D1S443. This region is often
 CC lost by LOH in various different tumour types, such as neuroblastoma,

CC melanoma and breast and colon cancer. PTCH2 is a candidate for a tumour
 CC suppressor gene in this region. It is also a candidate gene for
 CC involvement in familial melanoma CMML, modifier locus for familial
 CC adenomatous polyposis hMOM1 and Michelin Tire Baby Syndrome. PTCH2 is
 CC capable of participating in the human patched gene/sonic hedgehog
 CC (PTCH/SHH) pathway during embryonic development and/or carcinogenesis.
 CC The isolated human protein is useful as a medicament for the treatment of
 CC a condition involving tumours such as BCC (basal cell carcinoma). The
 CC nucleic acid is useful in gene therapy, and for use as a probe, primer or
 CC a diagnostic agent. Note: this sequence was constructed using information
 CC from Figure 2B and the protein sequence given on pages 41-44 of the
 CC specification
 XX
 SQ Sequence 1203 AA;
 Query Match 99.5%; Score 6238; DB 3; Length 1203;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1199; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFSLGCGIQRHCKVLF 60
 Db 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFSLGCGIQRHCKVLF 60
 QY 61 LGLAFGALALGLRMAIITETNLEQLWVEVGSRSVSELHYTKELGEEAAYTSQMLTQTAR 120
 Db 61 LGLAFGALALGLRMAIITETNLEQLWVEVGSRSVSELHYTKELGEEAAYTSQMLTQTAR 120
 QY 121 QEGENILTPREALGLHQAALTASKQVSLYSGSWDLNKICYKSGVPLIENGMIEMIEKL 180
 Db 121 QEGENILTPREALGLHQAALTASKQVSLYSGSWDLNKICYKSGVPLIENGMIEMIEKL 180
 QY 181 FFCVILTPLDCFEWAKLQGGSSAYLPGRPDIQWTLNLDPEQLLEELGFFASLEGFRELDDK 240
 Db 181 FFCVILTPLDCFEWAKLQGGSSAYLPGRPDIQWTLNLDPEQLLEELGFFASLEGFRELDDK 240
 QY 241 AQVQAYVGRPCILHPDDLHCPPSAPNHHRSQAPNVAHELSCGGCHGSHKFMHQBELLG 300
 Db 241 AQVQAYVGRPCILHPDDLHCPPSAPNHHRSQAPNVAHELSCGGCHGSHKFMHQBELLG 300
 QY 301 GMDPQGBLLRAEALQSTFLLMSRQLYHEHGRDYQTHDIGMSEQAQSTVLQAWORRFV 360
 Db 301 GMDPQGBLLRAEALQSTFLLMSRQLYHEHGRDYQTHDIGMSEQAQSTVLQAWORRFV 360
 QY 361 QLAQREALPENASQOIHAFSSTLDDILHAFSEVSARVVGYYLLMAYACVIMLRWDCAQ 420
 Db 361 QLAQREALPENASQOIHAFSSTLDDILHAFSEVSARVVGYYLLMAYACVIMLRWDCAQ 420
 QY 421 SQGSVGLAGVLLVALAVASGLGALLGITFNAATTQVLFFALGIGVDVDFLLAHAFTE 480
 Db 421 SQGSVGLAGVLLVALAVASGLGALLGITFNAATTQVLFFALGIGVDVDFLLAHAFTE 480
 QY 481 ALPGTQLQRMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAATVVGCTFV 540
 Db 481 ALPGTQLQRMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAATVVGCTFV 540
 QY 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGDTGVPGVIAHLTATV 600
 Db 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGDTGVPGVIAHLTATV 600
 QY 601 QAPTHCEASSQHVVTITLPPQAHVLPVPPSPGLSELSPSGSSTRDLLGQBEETRQKAACKS 660
 Db 601 QAPTHCEASSQHVVTITLPPQAHVLPVPPSPGLSELSPSGSSTRDLLGQBEETRQKAACKS 660
 QY 661 LPCARNWLAHFARYQAPLLOSHAKAIIVLFGALLGLSLYGATLVQDGLATDVVVRG 720
 Db 661 LPCARNWLAHFARYQAPLLOSHAKAIIVLFGALLGLSLYGATLVQDGLATDVVVRG 720
 QY 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
 Db 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFFSSLKAVLPPPATQAPRT 780
 QY 781 WLHYRNWLGIOQAADFQDQWASGRITRHSYRNSGEGALAYKLLIQTGDAQEPLDPSQLT 840

Db 781 WLHYRNWLQGIQAAPDQDQWASGRITRHSYRNGSEGDALAYKLLIQTDQAQLLDFSQLT 840
 Qy 841 TRKLVREGLIPPELFYMGLTWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
 Db 841 TRKLVREGLIPPELFYMGLTWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENFRIP 900
 Qy 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYGLG 960
 Db 901 PAQPLEFAQFPFLRLGLQKTADFVEAIEGARAAACAEAGQAGVHAYPSGSPFLFWEQYGLG 960
 Qy 961 RCFLLAVCILLVCTFLVCAALLLNPWTAGLIVLVMAMTVLFGIMGFLGKLSAIPVY 1020
 Db 961 RCFLLAVCILLVCTFLVCAALLLNPWTAGLIVLVMAMTVLFGIMGFLGKLSAIPVY 1020
 Qy 1021 ILVASGVIGVEFTVHALGFLTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
 Db 1021 ILVASGVIGVEFTVHALGFLTTQGSRLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
 Qy 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPPAQGGG 1140
 Db 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPPAQGGG 1140
 Qy 1141 LRWGASSSLPQSFAVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSRGPGP 1200
 Db 1141 LRWGASSSLPQSFAVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSRGPGP 1200
 Qy 1201 ATG 1203
 Db 1201 ATG 1203

RESULT 6

AA92225
 ID AA92225 standard; protein; 1146 AA.
 AC AA92225;
 XX
 DT 10-AUG-2000 (first entry)
 DE Human patched 2 (PTCH2) protein.
 XX
 KW Patched 2; PTCH2; tumour suppressor; familial melanoma CMM1;
 KW familial adenomatous polyposis; hMomi; Michelin Tire Baby Syndrome;
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;
 KW basal cell carcinoma; chromosome 1p32-35; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO200020037-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-SE001784.
 XX
 PR 06-OCT-1998; 98SE-00003393.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
 PI Hollingsworth RE;
 XX
 DR WPI; 2000-303645/26.
 DR N-FSDB; AAA09081, AAA09084.
 XX
 PT Isolated human protein capable of participating in human patched
 PT gene/sonic hedgehog pathway during embryonic development is used in
 PT medicament for treatment of condition involving tumors such as basal cell
 PT carcinoma.
 XX
 PS Claim 2; Page 41-44; 55pp; English.
 XX
 CC This protein is encoded by the novel human patched 2 gene (PTCH2), which

CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
 CC DIS11 and W1404 as closest flanking markers and with an estimated
 CC localisation 5.5 cR from DIS443. This region is often lost by LOH in
 CC various different tumour types, such as neuroblastoma, melanoma and
 CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
 CC gene in this region. It is also a candidate gene for involvement in
 CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis
 CC hMomi and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
 CC exist (see AAA09082-84). PTCH2 is capable of participating in the human
 CC patched gene/sonic hedgehog (PTCH/SHH) pathway during embryonic
 CC development and/or carcinogenesis. The isolated human protein is useful
 CC as a medicament for the treatment of a condition involving tumours such
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
 CC therapy, and for use as a probe, primer or a diagnostic agent

XX Sequence 1146 AA;

Query Match 94.2%; Score 5911; DB 3; Length 1146;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1139; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFSGLCGIORHCGKVL 60
 Db 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLMRAYFQGLLFSGLCGIORHCGKVL 60
 Qy 61 LGLAFGALALGLRMAIETNLEQWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAT 120
 Db 61 LGLAFGALALGLRMAIETNLEQWVEVGSVSOELHYTKEKLGEEAAYTSQMLIQAT 120
 Qy 121 QEGENILTPREALGLHQAALTASKVOVSLYKGSWDLNKICYKSGVPLTENGMIEMIEKL 180
 Db 121 QEGENILTPREALGLHQAALTASKVOVSLYKGSWDLNKICYKSGVPLTENGMIEMIEKL 180
 Qy 181 PFCVILTPDCFWEGAKLQGSAYLPGRPDIQWNLDPQELLEELGPFASLEGFRELDDK 240
 Db 181 PFCVILTPDCFWEGAKLQGSAYLPGRPDIQWNLDPQELLEELGPFASLEGFRELDDK 240
 Qy 241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSCGCHGFSHKFWHQBELLG 300
 Db 241 AQVGQAYVGRPCLHPDDLHCPPSAPNHHSRQAPNVAHELSCGCHGFSHKFWHQBELLG 300
 Qy 301 GWARDPOGELARAFALOSTFLLMSPROLYEYFRGDYQTHDIGNSEBOASTVLOAWQRFV 360
 Db 301 GWARDPOGELARAFALOSTFLLMSPROLYEYFRGDYQTHDIGNSEBOASTVLOAWQRFV 360
 Qy 361 QLAQEALPENASQOIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
 Db 361 QLAQEALPENASQOIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
 Qy 421 SQGSVGLAGVLLVALAVASGLGALLGITNAATTQVLPFLALIGIVDDVFLLAHAFTE 480
 Db 421 SQGSVGLAGVLLVALAVASGLGALLGITNAATTQVLPFLALIGIVDDVFLLAHAFTE 480
 Qy 481 ALPGTPIQERMGECLQRTGTSVLTSTNNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
 Db 481 ALPGTPIQERMGECLQRTGTSVLTSTNNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
 Qy 541 AVMLVFPAILSLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGVVPGVIAHLTATV 600
 Db 541 AVMLVFPAILSLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGVVPGVIAHLTATV 600
 Qy 601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFPGGSTRDLLGQEEETROKAAACKS 660
 Db 601 QAFTHCEASSQHVVTILPPQAHLVPPSPDPLGSELSFPGGSTRDLLGQEEETROKAAACKS 660
 Qy 661 LPCARNWLAHFARYQFAPLILQSHAKAIVLVFQALLGLSLYATLVQDGLALTDVVPGR 720
 Db 661 LPCARNWLAHFARYQFAPLILQSHAKAIVLVFQALLGLSLYATLVQDGLALTDVVPGR 720
 Qy 721 TKEHAFLSAQLRVFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTATQAPT 780
 Db 721 TKEHAFLSAQLRVFSLYEVALVTQGGFDYAHQSORALFDLHQRFSLSKAVLPPPTATQAPT 780

QY 1140 G----- 1140
 Db 1248 GGAHQVIVEATENVFAHSTVVVHPESHHPSPNPRQPHLDGSLPGRGQQQRPRDP 1307
 QY 1141 -----LRWG-----ASSLPQSFAR 1155
 Db 1308 REGLPPLPRDFAFETEGHSGPSNRAWGPGRGARNPRNPASTAMGSSVFGYQCP 1367
 QY 1156 VTT-----SMTVAIHPPLPGAYIHP 1176
 Db 1368 ITTVTASAVTVAVHPPVPVPGGRNP 1393

RESULT 9

AAW52200
 ID AAW52200 standard; protein; 1447 AA.

XX AC AAW52200;
 XX DT 25-JUN-1998 (first entry)
 XX DE Human patched (ptc) protein.
 XX KW Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
 XX KW wound healing; ageing; human.
 XX OS Homo sapiens.
 XX PN WO9745541-A2.
 XX PD 04-DEC-1997.
 XX PF 02-JUN-1997; 97WO-US009553.
 XX PR 31-MAY-1996; 96US-00656055.
 XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Scott MP, Goodrich LV, Johnson RL, Epstein E, Oro A;
 XX WPI; 1998-032648/03.
 XX DR N-PSDB; AAW21590.
 XX PT patched protein other than Drosophila melanogaster patched protein - used
 XX PS for characterising the phenotype of a tumour.
 XX PS Claim 4; Page 76-80; 86pp; English.

CC This is a human patched (ptc) protein. The encoding DNA can be used to
 CC construct an expression cassette comprising an altered patch or hedgehog
 CC gene. The expression cassette comprises a nucleic acid encoding a patched
 CC protein other than a Drosophila melanogaster patched protein, or fragment
 CC of at least 12 nucleotides in length, as other than an intact chromosome
 CC under transcriptional control of a transcriptional initiation region, and
 CC a transcriptional termination region, both functional in an expression
 CC host. A genetically engineered mammalian cell comprising this expression
 CC cassette as an extrachromosomal element or integrated into the genome of
 CC the cell can be predisposed to develop basal cell carcinoma as a result
 CC of the transfection. By analysing DNA, functional analysis of patched
 CC protein function, or by detecting antibody binding to abnormal patched
 CC protein, a genetic predisposition to developmental abnormalities and
 CC cancer can be diagnosed. This analysis can also be used for
 CC characterising the phenotype of a tumour, particularly a carcinoma,
 CC especially a basal cell carcinoma. The methods can also be used for
 CC characterising transitional cell carcinoma of the bladder, meningiomas
 CC medulloblastomas, etc. The modified cells comprising the expression
 CC cassette can be used to determine the role of different exons of the
 CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal
 CC models created from these cells can be used as animal models for
 CC carcinomas of the skin. The patched protein of mosquito, butterfly or
 CC beetle or alternatively, a mammalian patched protein of human or mouse

CC can be used to identify ligands or substrates that bind to, modulate, or
 CC mimic the action of patched gene. These agents could be used as tumour
 CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing)
 XX SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 2; Length 1447;
 Best Local Similarity 49.9%; Pred No. 1.5e-291;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
 QY 12 PSYTPPAPTAAPQILAGSL---KAPLWLRAYFQGLLSGLGCIQRHCKGVFLGLLAFGA 68
 Db 53 PSYC-DAAFALAEQISKGKATCGKAPLWLRKFORLLFKLGCYIQKNCCKFLVGLLIFGA 111
 QY 69 LALGLRMAIETNLEOLWVEYGRSVSOELHYTKELGHEAAYTSQMLTQTARQEGENILIT 128
 Db 112 FAVGLKAANDTNVEELWVEYGRSVRELNTYRQKIGBEAMFNPOIMTQTPKEGANVLT 171
 QY 129 PEALGLHLQAALTASKVQVSLYKGSWDLNKKI CYKSGVPLIENGMIEMIEKLFPCVILTP 188
 Db 172 TEALLQHLDSALQASRVHVMYKWKLEHLICYKSGELITETGYMDQIIEVLYPCLITP 231
 QY 189 LDCFWEKAKOGGSAYLPREDIOWNLDPQLLEELGPF-ASLEGFRELILDKAQQVQAY 247
 Db 232 LDCFWEKAKLQSGTAYLLGKPLRWTFNDFLEELKKINQVDSWEMLNKAEGVGHY 291
 QY 248 VGRPCLHPDDLHCPPSAPNHHSRQAPVAHELSCGCHGFSHKFMHWOBELLGCVARDPQ 307
 Db 292 MDRPCLNPADPCFATAPFNKNSTKPLDMALVINGCHGLSRKYMHWQBELIVGGTVKNS 351
 QY 308 GELLRAEALQSTFLLMSPRQLYEHPRG-DYOTHDIGWSEEOASTVLQAWQRFFVLOA 366
 Db 352 GKLSVAHALQTMFQLMTPKQYEHFKGYEYVSH-INWNEDKRAALILEAWQTYVEVHQ 410
 QY 367 LPENASQIQIHAFSSTLDDIILHAFSEVSAARVGVGYLLMLAYACVTMLRWCAQSGSVG 426
 Db 411 VAQNSTQKVLSTFTTTTDDILKSFSDSVIRVASGYLLMLAYACVTMLRWDCSKQGA 470
 QY 427 LAGVLLVALAVASGLGICALLGITFNAATTQVLPALGIGVDDVFLAHAFTEALPG-- 484
 Db 471 LAGVLLVALVAAGLGLCSLIGISFNAATTQVLPALGIGVDDVFLAHAFSETPGQNK 530
 QY 485 TPLQERMGECLORTGTSVLTISINMAAFMAALVPIPALRAFSLQAAIVVVGCTFVAVML 544
 Db 531 IFFEDRTGECLEKRGASVALTISINVTAFMAALVPIPALRAFSLQAAIVVVFNFAMVL 590
 QY 545 VFPAILSDLRHRCQRLDVLCCFSSPCSAQVQLPQELGD-----GTVPVGIH-- 595
 Db 591 IFFAILSDLYRRDRDLDFCCFTSPCVSRVQVEPOAYTDTHDNTYSPPPYSSHSF 650
 QY 596 -----LTATVQAFTHCEASSQHVVTILPQAHLVPPP-----SDPLGSELSFGSGSTD 644
 Db 651 AHETQITWQSTVQLRTDYDPHTHYVYTTAEPRSEISVQFVTVTQTLSCQSESTSTRD 710
 QY 645 ILGQEEETRQKAAKSLPCARWLAHFARYQFAPLLQSHAKAIVLVLFGLALLGLSLYGA 704
 Db 711 LLSQFSDS-SLHCLPEPCTKWTLSFAEKHYAPLLKPAKVVIFFLGLGLVSLYGT 768
 QY 705 TLVDQGLALTVDVPRGTKEHAFPLSAQLRYFSLYEVALVTQGGFDYAHASORALFDLHQ 764
 Db 769 TRVRDGLDLTIVPRETREYDFIAAQFKYFSGFYNNYIVTQKA-DYPNIQHLLYDLHRS 827
 QY 765 SLKAVLPPATCAPRTWLAHYVYNNWLOQIQAAPDQDWSAGRITRYSYRNGSDGALAYKL 824
 Db 828 NVKYVMLEENKQLPKMWLHYFRDMLQGLQDAPDSWETGKIMPNNNKNGSDGVLAYKLL 887
 QY 825 IQTDAQEPDLFSQLTTRKLVDRGLIPPELFYMGTLVWSSDPLGLAASQANFYPPPPPE 884
 Db 888 VQTGSRDKPIDISQLTQRLVDADGIINPSAFYIVLTAVVSNDPVAYAAQANIRHPRE 947
 QY 895 WLHKYDVTGE-NLRIPPAQPLEFAQPFLLRGLQKTADFVEAIEGARAACAEAGQGVH 943
 Db 948 WHDKADYWPETRLRIPAAEPIEVAQFPFYLNGLRDTSDFEAIEKVRTICSNYTSGLS 1007


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QY 765 SLKAVLPPPPATQRTWLHYRNWLOGIOAAPDQDNASGRITRHSYRNGSEDCALAYKLL 824
Db 828 NVKYVWLEENKQPKRWLHYFRDMLQGLQAFQSDWETGKIMPNYKNGSDGVLAYKLL 887
QY 825 IQTDAQEPLDFSQLTRKLVREGILIPPELFYMGTLVWSSDPLGLAASQANFYPPPPPE 884
Db 888 VQTGRDKPIDISQLTKQRLVDADGIINPSAFIYILTAWVSDPDVAYAAQANIRPHRPE 947
QY 885 WLHDKYDTTGE-NLRTPPAQPIEFQFPFLRLGLOKQADTQFVEAIEGARAAACABAGAGYH 943
Db 948 WWHDKADYMPETRLRIPAAEPIEYQFPFLYNGLRDTSDFVEAIEKVRTICSNYTSLGLS 1007
QY 944 AYESGSPFLFWEGYGLRRCFLAVCILAVCTFLVCALLILNPWTAGLVLVLAAMTVEL 1003
Db 1008 SYPNGYPLFWEGYIGIRHLLFISVLVACTFLVCALLILNPWTAGIIVMLALMTVEL 1067
QY 1004 FGIMFGIKLSAIPVILVASVIGIVETVHVVALGFLTTQGSRLNRAAAHALEHTFAPVT 1063
Db 1068 FGMWGLIGIKLSAIPVILVASVIGIVETVHVVALAFLTAIGDKNRAVLALEHMEFAPVL 1127
QY 1064 DGAISTLLGLLMLAGSHDFIVRYFFPAALTVLTLGLLHGLVLLPVLLSLTGLPPPEVI-- 1121
Db 1128 DGAISTLLGLVLMAGSEDFIVRYFFFAVLAAILTLGLVNLGLVLLPVLLSFFGFPYPSVPA 1187
QY 1122 ----QMYKESPE-----ILSPP-----APQGG 1139
Db 1188 NGNLRLPTSPSPPPSVVRFPMPGGTHSGSDSDSEYSSQTTVSGLSBELRHYEAQQA 1247
QY 1140 G-----LRWG-----ASSLPOSFAR 1155
Db 1248 GGPAAQVIVEATENPVFAHSTVVHPESRHHPPSPNPQQPHLDGSLPPGRCQQQPRDRPP 1307
QY 1141 -----LRWG-----ASSLPOSFAR 1155
Db 1308 REGLMPLPYRRDFAFEISTEGHSGFSNRARWGPRGARSHNPNRNPASTAMGSSVPGYCQP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAVIHP 1176
Db 1368 ITVTASASVTVAVHPPPVPGFGRNP 1393

RESULT 12
AAEI9830
ID AAEI9830 standard; protein; 1447 AA.
AC AAEI9830;
DE 18-JUN-2002 (first entry)
DT Human patched (Ptch) protein.
DE Human; patched; Ptch; cell proliferation; differentiation; therapy;
KW cytosstatic; testicular cancer; hedgehog protein signalling.
XX Homo sapiens.
FH Key Location/Qualifiers
FT 100..119
FT /label= TM1
FT /note= "Transmembrane domain"
FT 438..458
FT /label= TM2
FT /note= "Transmembrane domain"
FT 471..493
FT /label= TM3
FT /note= "Transmembrane domain"
FT 502..521
FT /label= TM4
FT /note= "Transmembrane domain"
FT 548..570
FT /label= TM5
FT /note= "Transmembrane domain"

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FT Domain 578..599
FT /label= TM6
FT /note= "Transmembrane domain"
FT 751..769
FT /label= TM7
FT /note= "Transmembrane domain"
FT 1028..1048
FT /label= TM8
FT /note= "Transmembrane domain"
FT 1052..1074
FT /label= TM9
FT /note= "Transmembrane domain"
FT 1078..1097
FT /label= TM10
FT /note= "Transmembrane domain"
FT 1122..1141
FT /label= TM11
FT /note= "Transmembrane domain"
FT 1155..1178
FT /label= TM12
FT /note= "Transmembrane domain"
FT XX
US6348575-B1.
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081884P.
XX
PA (GETH ) GENENTECH INC.
XX
PI De Sauvage F, Carpenter DA;
XX
DR WPI; 2002-215260/27.
XX
PT Native human patched-2 polypeptide for treating disorders caused by
PT Hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 3; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to Hedgehog, especially
CC Desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC Hedgehog protein signalling. The present sequence is human patched (Ptch)
CC protein. Note: The sequence shown as SEQ ID NO: 4 in sequence listing of
CC the specification is a fragment of the sequence shown as SEQ ID NO: 4 in
CC fig 3 of the specification
XX
SQ Sequence 1447 AA;
Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPPARTAAPQILAGSL---KAPLMIRAYFQGLLPSLGGCIQRHCKVFLGLLAFGA 68
Db 53 PSYC-DAFALEQISKGATGRKAPLWLRKAFQRLLPKLGCVIQKCGKFLVWGLLIFGA 111
QY 69 LALGLRMAIETNLEQLWVEGSRVSOELHYTEKEKLEEAAYTSOMLIQTARQEGENTLT 128
Db 112 FAVGLKAANLETNVEELWVEGSRVSRLENTYTRQKIGEEAMFNQPMIQTPKEGANVLT 171
QY 129 PEALGLHLQAALTASKVQVSLYKGSWDLNKLTCYKSGVPLIENGMEIEMWIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYNNRWQKLEHLCYKSGELITETGYMDQIIEYLYPCLLIPT 231

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QY 189 LDCWEGAKLOGSAYLPGRPDIOWNTLNDPEOLLEELGPF-ASLEGFRLLDKAQQGAY 247
Db 232 LDCWEGAKLOGSAYLPGRPDIOWNTLNDPEOLLEELGPF-ASLEGFRLLDKAQQGAY 291
QY 248 VGRPCILHPDDLCPSPAPNHHQAPNVAHELSGGCHGFSHKFMHQEBELLGGMARDPQ 307
Db 292 MDRPCINPADPCAPATAPNKNSTKPLDMALVNLGGCHGLSKYMKHMQEBELIVGGTVKNST 351
QY 308 GELLRAEALQSTFLMSPOLYHEHFG-DYQTHDIGNWSEEQASTVLQAWQRFFVOLAQPA 366
Db 352 GKLVSAAHALQTMFQMTKPMQYHEFKGYEVSH-INWNEDEKAAALILAEWQRTYEVVHQS 410
QY 367 LPENASQOIHAFSSITLDDILHAFSEVSAAVVGGVLLMLAVACVTMLRMDCAQSGSVG 426
Db 411 VAQNSTQKVLSTTTTLLDILKSFSDSVIRVASGYLLMLAYACLMLRWDCKSGGAVG 470
QY 427 LAGVLLVALAVASGLGCLALLGITFNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGLGLCLSLIGISFNAATQVLPFLALGIGVDDVFLLAHAFSETQONKR 530
QY 485 TPLQRMGECLQRTGTSVLTINNNWAAFLMAALVPIPALRAFSLQAAIVVGCFTFVAVML 544
Db 531 IFFEDRTGECLEKRTGASVALTSISNVTAFMAALIPIPALRAFSLQAAVVVNFAMVLL 590
QY 545 VFPAILSLDRRHQRDLVLCFSPSCSAQVITQILPQELGP-----GTPVVGIAH-- 595
Db 591 IFFAILSDMLYRREBRDLDFCFTSPCVSRVIOVEPOAYTTHDNTRYSPPPSSHFSF 650
QY 596 -----LTAATVQAFTHCASSQHVVTIIPQAHVPPP-----SDPLGSELFSPGSTRD 644
Db 651 AHETQITWQSTVOLRTYEPHTHYVYTTAEPRSEISVQPVTVQDTLSQSPSESTSTRD 710
QY 645 ILGQBEETQKACKSLPCARNLAHAFARYQAPLILLOSHAKAIVLVFGALIGLSLYCA 704
Db 711 LLSQFSDS--SUHCLPEPPCKTSLSFABEKHYAPFLPKPKAVWVIFLGLGLVSLYKT 768
QY 705 TLVQDGLALTDVVRGTEKHAFLSAQLRYFSIYEVALVTQGGFDVAHSQALFDLHQRES 764
Db 769 TVRUGLDLTDIVPRETRYDIFIAQFKYFSFNMYIVTQKA-DYDNIQHLLYDLHRSFS 827
QY 765 SLKAVLPPPATQPTWLYHYRNWLOGIAAFDQDQWASGRITRHSYRNGSEGALAYKLL 824
Db 828 NVKYVMLEENKQLPKMWHYFRDMLQGLQDAFSDWETGKIMPNYKNGSDGCVLAYKLL 887
QY 825 IGTGDAQEPLDPSOLTRKLVDBEGLIIPPELFWGLTWVWSSDPLGLAASQANFYPPPE 884
Db 888 VQTGRDKPDIDISQTKQRLVDADGILNPSAFYIYLTAWVSNPDVAYAAASQANIRPHRE 947
QY 885 WLHDKYDTTGE-NLRITPPAQPLEFAQFPFLRLGLQKTADFVEAIEGARACAEAGQGVH 943
Db 948 WHDXADYMPETELRIPAREPIEYAQFPFLNGLRDTSDFVEAIEKVRITCSNYTSLGLS 1007
QY 944 AYPGSPFLFWQYGLRCFLAVCILVCTFLVCAILLNPNWTAAGLVVLVMMTVEL 1003
Db 1008 SYPNGYFPLFWQYGLRHLWLLFISVWLACTPLVCVAFLLNPNWTAAGLVVLVMMTVEL 1067
QY 1004 FGIMFLGKLGAIPVWILVASGIGVEFTVHVALGFLTQGSNLRRAHLEHTFAPYT 1063
Db 1068 FGMGLGILKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRAVLALEHMFAPVL 1127
QY 1064 DGAISTLLGLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLSTLGLPPEPVI-- 1121
Db 1128 DGAISTLLGLMLAGSEDFIVRYFFAVLAILTLGLVGLVLLPVLSTLGLPPEVSPA 1187
QY 1122 ----QMYKSPE-----ILGPP-----APQGG 1139
Db 1188 NGNLRLFTSPSPPPSVFVAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHYEAQQA 1247
QY 1140 G----- 1140
Db 1248 GGAHQVIVEATENPVFAHSTVVHPSRHPPSNPQQPHLDGSLPPGQCGQPPRDP 1307
QY 1141 -----LRWG-----ASSLSQSFAR 1155
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Db 1308 REGLMWPLVPRDPAFEISTEGHSPSNRARGPRGARSHNPRNPASTAMGSSVPGYQCP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTVTASASVTVAHVPPFPVPGGRNP 1393

RESULT 13
ABU10931
ID ABJ10931 standard; protein; 1447 AA.
XX
AC ABJ10931;
XX
DT 12-DEC-2002 (first entry)
XX
DE TRC8 related human patched protein SEQ ID No 5.
XX
KW TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3,2;
KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
KW human chromosomal translocation.
XX
OS Homo sapiens.
XX
US 2002106656-A1.
XX
PD 08-AUG-2002.
XX
PF 02-JUL-2001; 2001US-00898533.
XX
PR 12-MAR-1998; 98US-0077723P.
PR 12-MAR-1999; 99US-00268140.
XX
PA (GEMM/) GENMILL R M.
PA (DRAB/) DRABKIN H A.
XX
PI Gemmill RM, Drabkin HA;
XX
WPI; 2002-712395/77.
XX
PT Novel Translocation in Renal cancer from Chromosome 8 genes, useful for
PT detection of tumors, comprises rearrangements in the t(3;8)(p14.2;q24.1)
PT chromosomal translocation which occurs in renal and thyroid carcinomas.
XX
PS Disclosure; Fig 2D; 49pp; English.
XX
CC The invention relates to an isolated TRC8 (Translocation in Renal cancer
CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
CC comprising a sequence of 664 amino acids fully defined in the
CC specification and comprising a sequence located in the 5' flanking region
CC to the coding region of TRC8 and a sequence which occurs in certain
CC sporadic renal cell carcinomas. The methods are useful for detecting the
CC presence of the TRC8 gene in a biological sample, detecting alterations
CC to the gene, such as a 3;2 human chromosomal translocation, and fused DNA
CC containing the fused site of TRC8/FHIT. A nucleic acid probe is useful
CC for detecting the 3;8 human chromosomal translocation, by contacting the
CC nucleic acid probe with a biological sample to be tested, and determining
CC whether the nucleic acid probe specifically hybridizes to the TRC8/FHIT or
CC FHIT/TRC8 fusion DNA. This sequence represents a TRC8 related protein of
CC the invention
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYTQGLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAPALQISGKATGRKAPLWLRARFQRLFLKGCYIQKCGKFLVVGLLIFGA 111
QY 69 LALGLEMALEIENLEQLWVEVSGSELHYKEKLEGEAAAYTSOMLIQTARQEGENILT 128
Db 128 LALGLEMALEIENLEQLWVEVSGSELHYKEKLEGEAAAYTSOMLIQTARQEGENILT 128
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Db 112 FAVGLKAANLETNVEELWVEGVRVSRELNYTRQKIGEEAMFNPQLMIQTPKXEGANVLT 171
Qy 129 PEALGHLHQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMTEKULFPVCVILTP 188
Db 172 TEALQHLDSALQAQSRVHYMYNRQWKLHLCYKSGELITETGYMDQIIYEIYLPCLIIPT 231
Qy 189 LDCFWEGAKLQGSAYLPGRPDIQWNLDPQLLELPGF-ASLEGFRELLDKAOGVQAY 247
Db 232 LDCFWEGAKLQGSAYLPGRPDIQWNLDPQLLELPGF-ASLEGFRELLDKAOGVQAY 291
Qy 248 VGRPCILHDDHCPSPAPNHHSRQAPNAHVELSGGCHGFSKFMHWEQELLGGMARDPQ 307
Db 292 MDRPCINPADPCPATAPNKNSTKPLDMALVNGGCHGLSRKYMHWQEBELIVGVTVKST 351
Qy 308 GELLPAEALQSTFLMLSPQLYEHFRG-DYQTHDTCWSEEQASTVLQAWQRFPVOLAQBA 366
Db 352 GKLVSALHQLTNFQMTPKQMYEHFKGYEVVSH-INWNEDKAAALEAWQRTYVEVHQS 410
Qy 367 LPENASQOIHAFSSTLDDILHAFSEVSAARVVGGVLLMLAYACVTLRWDCQAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTLLDILKFSFSDSVIRVASGYLLMLAYACVTLRWDCSKSQGAVG 470
Qy 427 LAGVLLAVASGLGLCALLGITTNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGIGVDDVFLLAHAFSETQNK 530
Qy 485 TPLQRMRECLORTGTSVVLTSINNMAFLMAALVPIPALRAFSLOAIVUGCTFVAVML 544
Db 531 IPFEDTGECLKRTGASVALTSISNVTAFPMALIPALRAFSLOAIVVVFNFAMVLL 590
Qy 545 VFPAILSLDLRRHRCORLDVLCFSPCSAOVIQILPOELGP-----GTVPVGIAH-- 595
Db 591 IFPAILSMDLRYRDERLDIFCCFSPCVSRVQVPEQAYDTHNTRYSPPPVSSHSF 650
Qy 596 -----LTATVQAFTHCEASSQHVVTILPPOAHLVPPP-----SDPLGSELSFGGSTRD 644
Db 651 AHETQITWQSTVQLRTEYDPHTVHYTTAEPRSEISVQPVTVTQDTLSCQSPESSTRD 710
Qy 645 LLQBEETROKAAKSLCARWNLHAFARYQAPLILLOSHAKAIVLILFGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPECTKWTLSFAEKHYAPFLPKAKRVVIFLFLGLVLSYGT 768
Qy 705 TLVODGLALTDPVPRGTKEHAFSLAQRLVSELYVALVTOGGFDYAHQSORALFDLHOREFS 764
Db 769 TRVRDGLDLDIVPRETREYDFIAAQKFPSYNNIYVTKA-DYPNIQHLIDYDHRFS 827
Qy 765 SLKAVLPPATQAPRTWLHYRNWILQGIQAAPDQDMSGRITRHSYRNGSDGALAYKLL 824
Db 828 NVKYVMLEENKQPKWMLHYFRDMLQGLQDAPFSDMETGKIMPNYKNGSDDGVLAYKLL 887
Qy 825 IOTGDAQEPDLSQLTTRKLVDRGLIPPELFYMGILTVMVSSDPLGLAASQANFYPPPPPE 884
Db 888 VOTGSRDKPIDISQTKQRLVDADGIINPESAFYIYLTAWNSNDPVAYASQANIRPHRPE 947
Qy 885 WLHDKYDTTGE-NLRIPPAQPLEPAQFPFLRLGLOKTADEVEAIEGARAACAQAQGVH 943
Db 948 WHDXADYMPETRLRIPAEIEYVQAFPPYLNGLRDTSDFVEAIEKVITICSNYTSLGUS 1007
Qy 944 AYPGSPFLFWEQYGLRRCFLAVCILLVCTFLVCALLNLPWTAGIIVLVLAMMTVEL 1003
Db 1008 SYPNGYPFLFWEQYGLRHLLLFISVVLACTFLVCVFLNPNWTAGIIVVVLAMMTVEL 1067
Qy 1004 FGIMGFLGKLSAIPVWILVASGVIGVEFTTHVALGFLTTQGSRLRAHALEHTFAPVT 1063
Db 1068 FGIMGFLGKLSAIPVWILVASGVIGVEFTTHVALGFLTTQGSRLRAHALEHTFAPVT 1127
Qy 1064 DGAITLLGLMLAGSHDFIVRYEFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSEDFIVRYEFAALTVLTLGLLHGLVLLPVLVLSILGPPPEVI-- 1187
Qy 1122 ---QMYKESPE-----ILSP-----APOGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRPAMPPTHGSDSDSEYSSQTTVTSGLSEELRHYEAQQA 1247
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Qy 1140 G----- 1140
Db 1248 GGPAHQVIVEATENVEFAHSTVVPESRRHPPSPRQOPHLDSGSLPPGRQCGQRRDPP 1307
Qy 1141 -----LRWG-----ASSLPOSFAR 1155
Db 1308 REGMLPPLYRPRDADFELISTEGHSPSRARWPRGARSHNPRNPASTAMGSSVPGYQCP 1367
Qy 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTWTASAVTVAVHPVPVPGFGRNP 1393

RESULT 24
AAG79571
ID AAG79571 standard; protein; 1447 AA.
XX AC AAG79571;
XX DT 23-DEC-2002 (first entry)
XX DE Human patched protein.
XX KW Patched; ptc; basal cell nevus syndrome; BCNS; wound healing;
KW developmental disorder; spina bifida; craniofacial abnormality;
KW basal cell carcinoma; skin; brain tumour; transgenic; mouse;
KW proliferation; oncogenesis; signal transduction; cancer; aging.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 113 /note= "Encoded by CCG"
FT Misc-difference 413 /note= "Encoded by GAG"
FT Misc-difference 864 /note= "Encoded by GAA"
XX US6429354-B1.
XX PD 06-AUG-2002.
XX PF 22-AUG-1997; 97US-00918658.
XX PR 07-OCT-1994; 94US-00319745.
XX PR 06-OCT-1995; 95US-00540406.
XX PR 31-MAY-1996; 96US-00656055.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Scott MP, Goodrich LV, Johnson RL, Epstein B;
XX DR WPI; 2002-722086/78.
XX DR N-FSDB; ABA00374.
XX PT Transgenic mouse, useful for cancer drug screening, comprises disruption
XX PT of allele of patched locus which predisposes the mouse to develop a
XX PT proliferative disorder.
XX PS Disclosure; Col 85-92; 58pp; English.
XX This sequence shows human patched (ptc) protein. Human patched gene has
XX been mapped to human chromosome band 9q22.3 and lies between two
XX polymorphic markers D9S196 and D9S287. Mutations in the patched gene are
XX characteristic in basal cell nevus syndrome (BCNS), an inherited disorder
XX with an increased risk of developmental disorders such as spina bifida
XX and craniofacial abnormalities, basal cell carcinoma of the skin and
XX brain tumours. The human and mouse ptc sequences show 86% homology. The
XX transgenic mouse of the invention has a genome comprising a disruption of
XX at least one allele of a patched locus, where the disruption predisposes
XX the mouse to develop a proliferative disorder. The transgenic mouse is
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CC useful for studying patched function and regulation, for e.g. a series of
CC small deletions and/or substitutions made in the patched gene, to
CC determine the role of different exons in oncogenesis, signal
CC transduction, etc; and for drug screening which is useful for treating
CC cancer or developmental abnormalities attributed to a defect in patched
CC function such as wound healing and aging
XX
SQ Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.5e-291;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
QY 12 PSYTPARTAAQILAGSL--KAPLWRAVYQGLLFSLGCGIORHCGVLFGLLAFGA 68
DB 53 PSYC-DAPALQISKGKATGRKAPLWRAKQRLFLKGLGCIQKNCGLFVVGILLIGA 111
QY 69 LALGLRMALITNLEQLVEVSRYSQELHYTKELIGEBAAYTSQWLIQTARQEGENIIT 128
DB 112 FAVGLKAANLETNVELWVEVGRVSRRELNYTRQKIGEBAEFPQLMIQTPKEEGANVLT 171
QY 129 PFALGLHQAALITASKVQVSLYKGSWDLNKKIYKSGVPLIENGMIEMIEKLFPCVILTP 188
DB 172 TEALLQLHLSALQASRVHYMYNRQWKLHLCYKSELITETCYMDQIIEYLYPCLIITP 231
QY 189 LDCFEWAGLQGSAYLPCRPDIQWNTLDPLOELLELPF-ASLGEFRELLDKAQQVQAY 247
DB 232 LDCFEWAGLQGSAYLPCRPDIQWNTLDPLOELLELPF-ASLGEFRELLDKAQQVQAY 291
QY 248 VGRPCLLHPDDLCPSPAPNHHRSQAPNVAHELSGGCHGFHMFHWEQELLGGMARDPQ 307
DB 292 MDRPCINPADPCPATAPKNSTKPLDMALVNGGCHGLSKRYMHWQEELIVGGIVKST 351
QY 308 GELLRAEALQSTFLMSPQLYEHFRG-DYQTHDTCWSEEQASTVLQAWRRFVLAQBA 366
DB 352 GLKVSAAHALQTMFQMTKPMQYEHFKGYEVSH-INWNEDKAAALAEAWQRTYVEVHOS 410
QY 367 LPENASQOIHAFSTTLLDILHAFSEVSAARVGVGVLMLAYACVTMLRWDCAQSGSVG 426
DB 411 VAQNSTQKVLSTTTTLLDILKSFSDSVIRVASGYLLMLAYACVTMLRWDCSKQAGV 470
QY 427 LAGVLLVALAVASGLCALGCLGITRNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
DB 471 LAGVLLVALSVAAGLGLCSLIGISFNAATQVLPFLALGVGDDVFLLAHAFSETQONKR 530
QY 485 TPLQRMGHCICLORTGTSVVLTSINWMAAPLMAALPIPALRAFSLQAAIVVCTFVAVML 544
DB 531 IPEDRTGECIKRTGASVALTSISNVTAFMAALPIPALRAFSLQAAIVVVFNFAMVLL 590
QY 545 VFPAILSLDLRRRHCRDLVLCFCSPSCSAQVITQILPQELGD-----GTPVGVIAH-- 595
DB 591 IFPAILSMDLRYREDRLDIFCCTSPCVSRVIOVEQAYTTHDNTRYSPPPYSSHSF 650
QY 596 -----ITATVQAFTHCBASSQHVVTILPQAHLVPPP-----SDPLGSELSPGSGSTRD 644
DB 651 AHETQITWQSTVQLRTEYDPHTHYVYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710
QY 645 LLGQEEETQKACAKSLPCARNWLAHAFYQAPLQLQSHAKAIVLVLPFALLGLSLYGA 704
DB 711 LLSQFSDS--SLHCLPEPPCTKWLTSFAEKHYAPFLPKKRVVIFLGLGLVSLYGT 768
QY 705 TLVQDGLALTDVVPRTGKHAFLSAQLRYFSLYEVALVTQGGFDVAHSORALFDLHORFS 764
DB 769 FTVRUGLDLTDIVPRETRYEDRIAQPKYFSFYNMVIYTKA-DYPNIOHLLYDLHRSFS 827
QY 765 SLKAVLPPPPATQAPRWLHYRNWLGIOAAFDQDQWASGRITRHAYRNGSEGCALAYKLL 824
DB 828 NVKYVMLENKQLPKMWLHYFRDLQGLQDAFSDWQTKIMPNYKNGSDDDGLVAYKLL 887
QY 825 IOTGDAQEPLDPSQLTRKLVDBEGLIPPELFVWGLTVMVSSDPLGLAASQANFYPPPE 884
DB 888 VQTGSRDKPIDISQLTKQRLVADAGIINPSAFYIYLTAWVSNPDVAYAAASQANIRPHREE 947

QY 885 WLHDKYDVTGGE-NLRIPPAQPLEFAQFPFLLRGLQKTDFAVEAIEGARACAEAGQGVH 943
DB 948 WYHDKADYWPETRLRIPRAEPYEQAFPFYLNGLRDTSDFAIEKVRITCSNYISLGLS 1007
QY 944 AYPGSPFLFWBQYIQLRRRCFLAYCILLVCTFLVCALLLMPWTAGLIVLVAMMTVEL 1003
DB 1008 SYPNGYPFLFWBQYIQLRRHLLIFISVVLACTFLVCAVFLNPWTAGIIVVVLMTVEL 1067
QY 1004 FGIMFLGILKLSAIPVILVASVGVGVFVHVALGELTTCQSRNLRRAHALEHTFAPVT 1063
DB 1068 FGMWGLIGLKSAPVWILIASVGVGVFVHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127
QY 1064 DGAISTLLGLMLAGSHFDFIVRYEFAALTIVTLGLLHGLVLLPVLISILGPPPEVI-- 1121
DB 1128 DGAISTLLGLMLAGSEDFIVRYEFAVLAITILGLVNLGLVLLPVLISFFGYPPEVSA 1187
QY 1122 ----QMYKESP-----IISPP-----APQG 1139
DB 1188 NGLNRLPTSPPPPPSVVRFAFMPGHTHSGSDSDSEYSSQTTVSGLSSELRYEAAQGA 1247
QY 1140 G-----LRWG-----ASSSLPQSFA 1155
DB 1248 GGAHQVIVEATENPVFAHSTVVVHPSRHHPPSNPQQPHLDGSLPPGRCQQRRDDPP 1307
QY 1141 -----LRWG-----ASSSLPQSFA 1155
DB 1308 REGLMPLLYRPRDAFEISTEGHSGPSNRWGPGRASHNFRNPASTAMGSSVPGYCOP 1367
QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
DB 1368 ITTWTASASVTVAVHPPPVPGSGRNP 1393
RESULT 15
ABU62275
ID ABU62275 standard; protein; 1447 AA.
XX
AC ABU62275;
XX
DT 25-AUG-2003 (first entry)
XX
DE Human patched gene PTC product.
XX
KW Human; patched gene; PTC; hedgehog protein; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003032085-A1.
XX
PD 13-FEB-2003.
XX
PF 20-OCT-1997; 97US-00954701.
XX
PR 07-OCT-1994; 94US-00319745.
XX
PR 06-OCT-1995; 95US-00540406.
XX
PA (SCOT/) SCOTT M P.
PA (GOOD/) GOODRICH L V.
PA (JOHN/) JOHNSON R L.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
WPI; 2003-492065/46.
XX
PT New DNA sequence other than present in a chromosome encoding patched gene
PT other than Drosophila patched gene, useful for preparing transgenic
PT laboratory animals and to knock out patched protein in embryonic stem
PT cells.
XX
PS Disclosure; Page 8-10; 40pp; English.
XX
XX The invention relates to a DNA sequence other than present in chromosome
CC encoding a patched (ptc) gene other than Drosophila patched gene. A cell

expressing the DNA sequence is useful for producing patched protein, by growing the cell expressing the DNA sequence, where the patched protein is expressed and isolating the patched protein free of other proteins. The cell expressing the DNA sequence is also useful for screening candidate compounds for binding affinity to the patched protein, by combining the candidate protein with the cell expressing the DNA sequence where the DNA sequence comprises the entire coding sequence under the transcriptional regulation of the transcriptional initiation region and a transcriptional termination region functional in the cell, expressing the patched protein in the cell and assaying for the binding of the candidate compound to the patched protein. The above cell is useful for screening candidate compounds for agonist activity with the patched protein. The DNA sequence is useful for producing all or portions of the patched protein, as probes for research, diagnosis, binding of hedgehog protein for its isolation and purification and in gene therapy. The DNA sequence is also useful as primers for investigating other species and for isolating genes from various mammalian sources of interest, particularly from humans or from domestic animals. The DNA sequence is further useful for preparing transgenic laboratory animals and to knock out the PTC protein in the embryonic stem cells, so as to produce hosts with single functional patched gene. The present sequence represents the amino acid sequence of the human patched gene PTC product

Sequence 1447 AA;

Query Match 53.4%; Score 3348; DB 7; Length 1447;

Best Local Similarity 49.9%; Pred. No. 1.5e-291;

Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

12 PSYTPARTAPQIILAGSL---KAPLWLRAYFQGLLFLSLGCGIQRHCGKVLFLGLLAFGA 68
 53 PSYC-DAAPALEQISKGATGRKAPLWLRKAFQRLFLKGLCVIQKCGKFLVVGILLIGA 111
 69 LALGLRMAIETNLBQLWVEGSRVSOELHYTKELGSEAAVTSQMLIQTARQEGENILT 128
 112 FAVGLKAANLETNBELWVEGSRVSRLENYTRQKIGSEAMENPQLMIQTKEGANVLT 171
 129 PEALGLHQAALTASKVQVSLYKSKNDLKNICKYKSGVPLIENGMEIWEKLEKLPFCVILT 188
 172 TEALQHLDSALQASRHHVYMYNRMQWKEHLCKYSGELITETGYMDQIIIEYDPLCLITP 231
 189 LDCFWEGAKLOGGSAYLPCRPDIOWTNLDPEQLLELGPFF-ASLRGFRLELDKAQVQAY 247
 232 LDCFWEGAKLOGGTAYLLGKPLRWNTNFDPLFLELKKINYQVDSWEMLNKAEGVGHY 291
 248 VGRPLCHPDDLHCPSPANHHSRQAPNVAAHLSGCGHFSKFMHWQBELLGGMWARDPQ 307
 292 MDRPCLNADPDCEPATENKNSKTPDLMAVLINGGCHGLSRKRYMEHWQBELIVGGTVKNST 351
 308 GELLRAEALQSTFLMSPROLYEHPRG-DYQTHDIGMSEEQASTVLOAWORRFVQLAQEA 366
 352 GKLVSNAHALQTNFQMTPKQMEHPKGYEYVSH-INWNEDKAAALILEAWQRTYVEVHQ 410
 367 LPENASQOIHAFSFTLDDILHAFSEVSAARVVGGLYMLLAYACVTMLRWDCASQSGSVG 426
 411 VAQNSTQKVLSPFTTTLLDDILKSFSDSVIRVASCYLLMLAYACLTMLRWDCSKSQGAVG 470
 427 LAGVLLVALAVASGLGALLGITTNAAATTVQLPFLAIGIVDDVFLLAHAFTALPG-- 484
 471 LAGVLLVALVSAAGLGLGIGISFNAAATTVQLPFLAIGVDDVFLLAHAFTSETGQNK 530
 485 TPLQRMGECLORTGTSVVLTSINNMAAFMLAALVPIPALRAFSLOAAIVVGCITVAVML 544
 531 IFFDRTGECUKRTGASVALTISINVTAFMAALIPIPALRAFSLOAAIVVVFNFAMVLL 590
 545 VFPAILSLDLRRRHRCORLDVLCFSSPCSAOVIQILPOELGD-----GTVPVGIAH-- 595
 591 IFFAILSMDLVREDRRLDIFCCFTSPCVSRVQVQEPQAYTDTHTNTRYSPPPPYSSHSF 650
 596 -----LTATVQAATHCEASSQHVVVTLPPQAHLVPPP-----SDPLGSELFSPGGSTRD 644
 651 AHETQITMQSTVQLRTEYDPHTVHYVYTTAEPRSEISVQPVTVTQDTLSCQSPESSTSTRD 710

QY 645 ILGQEEETQKAAKSLPCARNLHAHARYQAPILLOSHAKAIYVLVFLGALLGLSLYGA 704
 DB 711 LLSQSDS--SLHCLPEPCTKTWLSFAEKHVPFLPKAKVWVIFLFLGLGLVSLYGT 768
 QY 705 TLVQDGLALTVDVVRGTTEHAFSLAQRLVFSLYEVALVTQGGFDYAHQSORALFDLHOREFS 764
 DB 769 FVRUGLDLTDIVPRETREYDFIAAQFKYFSFYNNYVITOKA-DPNTIOHLYDLSHRSF 827
 QY 765 SUKAVLPPPTAQPRTWLHYRNWLGQIQAAFDQDQWASGRITRHSYRNSESGALAYKLL 824
 DB 828 NVKYVMLEENKQLPKWMLHYFRDWLQGLQDAFDSWETGKIMPNYKNGSDDGVLAYKLL 887
 QY 825 IOTGDAQEPDLSQLTTRKLVDRGLIIPPELFYMGILTVMWSSDPGLAASQANFPFPPPE 884
 DB 888 VQTGRDPEIDISQTLKORLVADAGIINPSAFYIYLTAWVSNDFVAYASQANIRHPRE 947
 QY 885 WLHDKYDTTGE-NLRIIPPAQPLEFAQFPFLRLGLQKTADEFVAIEGARAACAEGAGVH 943
 DB 948 WYHDKADYMPETRLIPAAEPLEYAQFFYLNGLDRTSDTFVEAIEKVRTICSNYTSLSLS 1007
 QY 944 AYPGSGPFLFWQYXGLRRCFLAVCIILVCTFLVCALLLLNPTAGLIVLVLAMTVEL 1003
 DB 1008 SYNGYPFLFWQYIGLRHLLIFTSVVLACTFLVCAVFLNPTAGIIVMLALMTVEL 1067
 QY 1004 PCIMGFLGKLSAIPWILVASVGIGVEFTHVALGFLTTQGSRLNRAHALEHTFAPVT 1063
 DB 1068 FMMGLIGKLSAVPWWILIASVGIGVEFTHVALAFLTAIGDKRRRAVLAEHMFAPVL 1127
 QY 1064 DCAISTLLGLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVI-- 1121
 DB 1128 DGAVSTLLGLVMLAGSEEDFIVRYFFAVLAILITLGLVNLGLVLLPVLLSFFGYPPEVSPA 1187
 QY 1122 ---QMYKESPE-----ILSP-----APQGG 1139
 DB 1188 NGLNELPTSPPEPPSVVRFAMP PGHTHSGSDSDSEYSSOTTVSGLSEELRHVEAQGA 1247
 QY 1140 G-----LRWG-----ASSLPPQSFAR 1155
 DB 1248 GGAHQVIVEATENPVFAHSTVWHPSRHHPPSNRQOPHLDGSLPPGROQQQRRDPP 1307
 QY 1141 -----LRWG-----ASSLPPQSFAR 1155
 DB 1308 REGLWPPLYRRDRDAFEISTEHSCHSPSNRARGPGRGASHNRPNPASTAMGSSVPGYCP 1367
 QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
 DB 1368 ITTVTASAVTVAVHPPVPVPGGRNP 1393

Search completed: November 22, 2004, 07:55:54
 Job time : 89 secs

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